



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 94941

TO: Phillip Gambel
Location: 8b03 / 9e12
Saturday, May 24, 2003
Au: 1644
Serial Number: 919408

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

NOTE :

Nucleic acid search results will be forwarded to you when they are available.

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

94941
Delaval, Jan

From: Gambel, Phillip
Sent: Saturday, May 24, 2003 8:34 AM
To: Delaval, Jan
Subject: 09/919,408 lemischka amd

jan

please perform a sequence and a sequence interference search for

ussn 09/919,408 (lemischka amd)

SEQ ID NO: 1

SEQ ID NO: 2

SEQ ID NO: 3

SEQ ID NO: 4

thanx

phillip gambel
art unit 1644
308--3997

if there is going to be a delay with the nucleic acid sequences,
then searching the amino acid sequences would be sufficient
thanx

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

Set Name Query

side by side

Hit Count Set Name

result set

*DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ*L4 L3 same (antibod\$ or immunoglobulin\$ or hybridoma\$)36 L4L3 'flk-2'86 L3*DB=USPT,PGPB; PLUR=YES; OP=ADJ*L2 L1 and 'flk-2'10 L2L1 lemischka-ihor\$11 L1

END OF SEARCH HISTORY

WEST[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)[Cases](#)**Search Results -**

Term	Documents
ANTIBOD\$	0
ANTIBOD.DWPI,EPAB,JPAB,USPT,PGPB.	731
ANTIBODANTIBODA.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODAY.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODEES.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODEIES.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODEIS.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODES.DWPI,EPAB,JPAB,USPT,PGPB.	213
ANTIBODEY.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODFIES.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODHYBRIDOMAS.DWPI,EPAB,JPAB,USPT,PGPB.	1
(L3 SAME (ANTIBOD\$ OR IMMUNOGLOBULIN\$ OR HYBRIDOMAS\$)).USPT,PGPB,JPAB,EPAB,DWPI.	36

[There are more results than shown above. Click here to view the entire set.](#)

Database:

US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search:

L4

[Refine Search](#)[Recall Text](#)[Clear](#)**Search History**

DATE: Saturday, May 24, 2003 [Printable Copy](#) [Create Case](#)

Set Name Query
side by side**Hit Count Set Name**
result set*DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ*L4 L3 same (antibod\$ or immunoglobulin\$ or hybridoma\$)36 L4L3 'flk-2'86 L3*DB=USPT,PGPB; PLUR=YES; OP=ADJ*L2 L1 and 'flk-2'10 L2L1 lemischka-ihor\$11 L1

END OF SEARCH HISTORY

U.S. DEPARTMENT OF COMMERCE
PATENT AND TRADEMARK OFFICE

EXAMINER'S CASE ACTION WORKSHEET

Application No. <div style="text-align: center;">09/919,408</div>		Legal Instrument Examiner
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CHECK TYPE OF ACTION		DATE OF COUNT _____
<input checked="" type="checkbox"/> Non-Final Rejection	<input type="checkbox"/> Restriction/Election Only	<input type="checkbox"/> Final Rejection
<input type="checkbox"/> Ex Parte Quayle	<input type="checkbox"/> Allowance	<input type="checkbox"/> Advisory Action
<input type="checkbox"/> Examiner's Answer	<input type="checkbox"/> Reply Brief Noted	<input type="checkbox"/> Non-Entry of Late Paper
<input type="checkbox"/> Defective Notice of Appeal or Defective Appeal Brief	<input type="checkbox"/> Interference SPE <small>(Approval for Disposal)</small>	<input type="checkbox"/> Suspension SPE <small>(Initial)</small>
<input type="checkbox"/> Allowance After Examiner's Answer	<input type="checkbox"/> SIR Disposal <small>(use only after FAOM)</small>	<input type="checkbox"/> Post-Allowance Communication
<input type="checkbox"/> Miscellaneous Office Letter <small>(With Shortened Statutory Period Set)</small>	<input type="checkbox"/> Notice of Non-Responsive Amendment <small>(With One Month Time Period Set)</small>	<input type="checkbox"/> Miscellaneous Office Letter <small>(No Response Period Set)</small>
<input type="checkbox"/> Letter Requiring Formal Drawings	<input type="checkbox"/> Supplemental Action <small>(Excluding Examiner's Answer)</small>	<input type="checkbox"/> Response to a Rule 312 Amendment
<input type="checkbox"/> Restart Time Period <small>(e.g., Missing References)</small>	<input type="checkbox"/> Interview Summary	<input type="checkbox"/> Authorization to Change Previous Office Action SPE: <small>(Initial)</small>
<input type="checkbox"/> Abandonment	<input type="checkbox"/> Express Abandonment <small>Date: _____</small>	<input type="checkbox"/> Abandonment After Examiner's Answer

Examiner's Name : _____ First Last AU: _____ 1234

[Generate Collection](#)[Print](#)**Search Results - Record(s) 21 through 30 of 36 returned.**

-
- ☐ 21. 5747651. 15 Feb 96; 05 May 98. Antibodies against tyrosine kinase receptor flk-1. Lemischka; Ihor R.. 530/387.9; 530/388.22 530/388.7 530/389.1 530/389.6. C07K016/28 C12P021/08.
-
- ☐ 22. 5710134. 19 May 95; 20 Jan 98. Combination of necrosis-inducing substances with substances which are activated by necroses for the selective therapy of tumors and inflammatory disorders. Bosslet; Klaus, et al. 514/34; 536/6.4. A61K031/70.
-
- ☐ 23. 5635388. 04 Apr 94; 03 Jun 97. Agonist antibodies against the flk2/flt3 receptor and uses thereof. Bennett; Brian D., et al. 435/334; 424/85.1 424/85.2 424/85.5 435/320.1 435/328 435/70.21 530/351 530/387.3 530/388.22 530/389.1 536/23.53. C12N005/20 C07K016/28 C07H015/12.
-
- ☐ 24. 5621090. 26 Jun 92; 15 Apr 97. Nucleic acids encoding soluble human FLK-2 extracellular domain. Lemischka; Ihor R.. 536/23.5; 435/69.1. C07H021/00.
-
- ☐ 25. 5548065. 31 Oct 94; 20 Aug 96. Tyrosine kinase receptor human flk-2-specific antibodies. Lemischka; Ihor R.. 530/388.22; 530/387.9 530/388.23 530/388.7 530/389.2 530/389.6. C07K016/18 C07K016/28.
-
- ☐ 26. 5367057. 30 Apr 93; 22 Nov 94. Tyrosine kinase receptor flk-2 and fragments thereof. Lemischka; Ihor R.. 530/350; 530/403. C07K013/00.
-
- ☐ 27. 5283354. 17 Sep 92; 01 Feb 94. Nucleic acids encoding hematopoietic stem cells receptors flk-1. Lemischka; Ihor R.. 536/23.5; 435/69.1 530/350 530/403. C07H021/00.
-
- ☐ 28. 5270458. 19 Nov 92; 14 Dec 93. Nucleic acids encoding fragments of hematopoietic stem cell receptor flk-2. Lemischka; Ihor R.. 536/23.5; 435/320.1 435/69.1 530/350 530/403. C07H021/00.
-
- ☐ 29. 5185438. 24 Dec 91; 09 Feb 93. Nucleic acids encoding hencatoporetic stem cell receptor flk-2. Lemischka; Ihor R.. 536/23.2; 435/320.1 435/69.1 530/350 530/403. C07H021/00.
-
- ☒ 30. EP 1186301 A2. 07 Sep 94. 13 Mar 02. Monoclonal antibodies that recognize flk-2 receptors and the isolation of primitive hematopoietic stem cell populations. GOLDSTEIN, NEIL I, et al. A61K039/395; A61P035/02.
-

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Term	Documents
ANTIBOD\$	0
ANTIBOD.DWPI,EPAB,JPAB,USPT,PGPB.	731
ANTIBODANTIBODA.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODAY.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODEES.DWPI,EPAB,JPAB,USPT,PGPB.	.2
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(L3 SAME (ANTIBOD\$ OR IMMUNOGLOBULIN\$ OR HYBRIDOMAS)).USPT,PGPB,JPAB,EPAB,DWPI.	36

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Term	Documents
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ANTIBOD.DWPI,EPAB,JPAB,USPT,PGPB.	731
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ANTIBODEIS.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODES.DWPI,EPAB,JPAB,USPT,PGPB.	213
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ANTIBODFIES.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODHYBRIDOMAS.DWPI,EPAB,JPAB,USPT,PGPB.	1
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Database: US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
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Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search:

L4

[Refine Search](#)[Recall Text](#)[Clear](#)**Search History**

DATE: Saturday, May 24, 2003 [Printable Copy](#) [Create Case](#)

WEST[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 10 of 10 returned.**☐ 1. Document ID: US 20020119545 A1

L2: Entry 1 of 10

File: PGPB

Aug 29, 2002

PGPUB-DOCUMENT-NUMBER: 20020119545

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020119545 A1

TITLE: Soluble human flk-2 protein

PUBLICATION-DATE: August 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
<u>Lemischka, Ihor R.</u>	Princeton	NJ	US	

US-CL-CURRENT: 435/194; 435/320.1, 435/325, 435/69.1, 536/23.2

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	RWC	Draw Desc	Image
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☐ 2. Document ID: US 20020072077 A1

L2: Entry 2 of 10

File: PGPB

Jun 13, 2002

PGPUB-DOCUMENT-NUMBER: 20020072077

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020072077 A1

TITLE: Method for isolating cells expressing FLk-2 receptors and isolated populations of cells that express FLk-2 receptors

PUBLICATION-DATE: June 13, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
<u>Lemischka, Ihor R.</u>	Princeton	NJ	US	

US-CL-CURRENT: 435/7.21; 435/320.1, 435/325, 435/69.1, 536/23.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	RWC	Draw Desc	Image
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☐ 3. Document ID: US 5912133 A

L2: Entry 3 of 10

File: USPT

Jun 15, 1999

US-PAT-NO: 5912133

DOCUMENT-IDENTIFIER: US 5912133 A

**** See image for Certificate of Correction ****

TITLE: Method for isolating stem cells expressing flk-1 receptors

DATE-ISSUED: June 15, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 435/7.21; 435/971, 530/388.7, 530/389.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 4. Document ID: US 5747651 A

L2: Entry 4 of 10

File: USPT

May 5, 1998

US-PAT-NO: 5747651

DOCUMENT-IDENTIFIER: US 5747651 A

TITLE: Antibodies against tyrosine kinase receptor flk-1

DATE-ISSUED: May 5, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 530/387.9; 530/388.22, 530/388.7, 530/389.1, 530/389.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 5. Document ID: US 5621090 A

L2: Entry 5 of 10

File: USPT

Apr 15, 1997

US-PAT-NO: 5621090

DOCUMENT-IDENTIFIER: US 5621090 A

TITLE: Nucleic acids encoding soluble human FLK-2 extracellular domain

DATE-ISSUED: April 15, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.5; 435/69.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 6. Document ID: US 5548065 A

L2: Entry 6 of 10

File: USPT

Aug 20, 1996

US-PAT-NO: 5548065

DOCUMENT-IDENTIFIER: US 5548065 A

TITLE: Tyrosine kinase receptor human flk-2-specific antibodies

DATE-ISSUED: August 20, 1996

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 530/388.22; 530/387.9, 530/388.23, 530/388.7, 530/389.2, 530/389.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 7. Document ID: US 5367057 A

L2: Entry 7 of 10

File: USPT

Nov 22, 1994

US-PAT-NO: 5367057

DOCUMENT-IDENTIFIER: US 5367057 A

TITLE: Tyrosine kinase receptor flk-2 and fragments thereof

DATE-ISSUED: November 22, 1994

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 530/350; 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 8. Document ID: US 5283354 A

L2: Entry 8 of 10

File: USPT

Feb 1, 1994

US-PAT-NO: 5283354

DOCUMENT-IDENTIFIER: US 5283354 A

TITLE: Nucleic acids encoding hematopoietic stem cells receptors flk-1

DATE-ISSUED: February 1, 1994

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.5; 435/69.1, 530/350, 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 9. Document ID: US 5270458 A

L2: Entry 9 of 10

File: USPT

Dec 14, 1993

US-PAT-NO: 5270458

DOCUMENT-IDENTIFIER: US 5270458 A

TITLE: Nucleic acids encoding fragments of hematopoietic stem cell receptor flk-2

DATE-ISSUED: December 14, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.5; 435/320.1, 435/69.1, 530/350, 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 10. Document ID: US 5185438 A

L2: Entry 10 of 10

File: USPT

Feb 9, 1993

US-PAT-NO: 5185438

DOCUMENT-IDENTIFIER: US 5185438 A

**** See image for Certificate of Correction ****TITLE: Nucleic acids encoding hencatoporetic stem cell receptor flk-2

DATE-ISSUED: February 9, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.2; 435/320.1, 435/69.1, 530/350, 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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Term	Documents
FLK-2.USPT,PGPB.	70
FLK-2S	0
(1 AND FLK-2).USPT,PGPB.	10
(L1 AND 'FLK-2').USPT,PGPB.	10

Display Format:

-

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identifying ligands which stimulate stem cell hematopoiesis
? s flk(w)2

2948 FLK
8736730 2

S4 279 FLK(W)2

? s s4 and py<1993

Processing

Processing

279 S4
32335638 PY<1993

S5 4 S4 AND PY<1993

? rd s5

...completed examining records

S6 1 RD S5 (unique items)

? t s6/3/all

6/3/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All.rts. reserv.

07768231 BIOSIS NO.: 000092071602

A RECEPTOR TYROSINE KINASE SPECIFIC TO HEMATOPOIETIC STEM AND PROGENITOR
CELL-ENRICHED POPULATIONS

AUTHOR: MATTHEWS W; JORDAN C T; WIEGAND G W; PARDOLL D; LEMISCHKA I R

AUTHOR ADDRESS: DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, N.J.
08540.

JOURNAL: CELL 65 (7). 1991. 1143-1152. 1991

FULL JOURNAL NAME: Cell

CODEN: CELLB

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

?

TEM:OS - DIALOG OneSearch

File 5: Biosis Previews(R) 1969-2003/May W3
(c) 2003 BIOSIS

*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 73: EMBASE 1974-2003/May W3
(c) 2003 Elsevier Science B.V.

*File 73: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 155: MEDLINE(R) 1966-2003/May W3
(c) format only 2003 The Dialog Corp.

*File 155: Medline has been reloaded and accession numbers have changed. Please see HELP NEWS 155.

File 399: CA SEARCH(R) 1967-2003/UD=13821
(c) 2003 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement. Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

? e au=lemischka ihor ?

Ref	Items	Index-term
E1	40	AU=LEMISCHKA I.R.
E2	9	AU=LEMISCHKA IHOR
E3	0	*AU=LEMISCHKA IHOR ?
E4	36	AU=LEMISCHKA IHOR R
E5	1	AU=LEMISCHKA, I. R.
E6	6	AU=LEMISCHKA, IHOR
E7	25	AU=LEMISCHKA, IHOR R.
E8	1	AU=LEMISH D
E9	10	AU=LEMISH G T
E10	4	AU=LEMISH G.T.
E11	3	AU=LEMISH I
E12	1	AU=LEMISH I.

Enter P or PAGE for more

? s e1-e7

40	AU=LEMISCHKA I.R.
9	AU=LEMISCHKA IHOR
0	AU=LEMISCHKA IHOR ?
36	AU=LEMISCHKA IHOR R
1	AU=LEMISCHKA, I. R.
6	AU=LEMISCHKA, IHOR
25	AU=LEMISCHKA, IHOR R.

S1 117 E1-E7

? s s1 and (flk(W)2)

Processing

117	S1
2948	FLK
8736730	2
279	FLK(W)2
S2 3	S1 AND (FLK(W)2)

? rd s2

...completed examining records

S3 2 RD S2 (unique items)

? t s3/7/all

3/7/1 (Item 1 from file: 73)

DIALOG(R) File 73: EMBASE

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04722255 EMBASE No: 1991215609

A receptor tyrosine kinase specific to hematopoietic stem and progenitor

cell-enriched populations

Matthews W.; Jordan C.T.; Wiegand G.W.; Pardoll D.; Lemischka I.R.
Department of Molecular Biology, Princeton University, Princeton, NJ
08540 United States
Cell (CELL) (United States) 1991, 65/7 (1143-1152)
CODEN: CELLB ISSN: 0092-8674
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

To elucidate the molecular biology of the hematopoietic stem cell, we have begun to isolate genes from murine cell populations enriched in stem cell activity. One such cDNA encodes a novel receptor tyrosine kinase, designated fetal liver kinase-2 or *flk-2*, which is related to the W locus gene product c-kit. Expression analyses suggest an extremely restricted distribution of *flk-2*. It is expressed in populations enriched for stem cells and primitive uncommitted progenitors, and is absent in populations containing more mature cells. Therefore, this receptor may be a key signal transducing component in the totipotent hematopoietic stem cell and its immediate self-renewing progeny.

3/7/2 (Item 1 from file: 399)
DIALOG(R) File 399:CA SEARCH(R)
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126289031 CA: 126(22)289031p PATENT
Recombinant production of human gene *flk-2* protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
INVENTOR(AUTHOR): Lemischka, Ihor R.
LOCATION: USA
ASSIGNEE: Princeton University
PATENT: United States ; US 5621090 A DATE: 19970415
APPLICATION: US 906397 (19920626) *US 679666 (19910402) *US 728913 (19910628) *US 793065 (19911115) *US 813593 (19911224)
PAGES: 55 pp. Cont.-in-part of U.S. 5,185,438. CODEN: USXXAM LANGUAGE: English CLASS: 536023500; C07H-021/00A
SECTION:
CA203002 Biochemical Genetics
CA207XXX Enzymes
CA213XXX Mammalian Biochemistry
IDENTIFIERS: gene *flk2* protein kinase ligand screening, human gene *flk2* protein kinase sequence, cDNA sequence *flk2* protein kinase human, hematopoiesis stem cell stimulation *flk2* ligand
DESCRIPTORS:
Genes (animal)...
 flk-2; recombinant prodn. of human gene *flk-2* protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
cDNA sequences... Hematopoietic stem cell... Ligands... mRNA... Protein sequences...
 recombinant prodn. of human gene *flk-2* protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
Hematopoiesis...
 stem cell; recombinant prodn. of human gene *flk-2* protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
CAS REGISTRY NUMBERS:
139569-91-8 146215-22-7 162394-09-4 nucleotide sequence; recombinant prodn. of human gene *flk-2* protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
80449-02-1P 139569-26-9 146215-24-9 155077-32-0P recombinant prodn. of human gene *flk-2* protein kinase extracellular domain and use for

egin 5,73,155,399
24may03 08:13:40 User208760 Session D2312.2
\$0.00 0.071 DialUnits File410
\$0.00 Estimated cost File410
\$0.01 TELNET
\$0.01 Estimated cost this search
\$0.28 Estimated total session cost 0.149 DialUnits

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*File 73: Alert feature enhanced for multiple files, duplicates
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File 155:MEDLINE(R) 1966-2003/May W3
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*File 155: Medline has been reloaded and accession numbers have
changed. Please see HELP NEWS 155.
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(c) 2003 American Chemical Society
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Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set	Items	Description
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? s flk(w)2		
	2948	FLK
	8736730	2
S1	279	FLK(W)2
? s flk(w)2(10n)(human)		
Processing		
	2948	FLK
	8736730	2
	19097961	HUMAN
S2	43	FLK(W)2(10N)(HUMAN)
? rd s2		
...completed examining records		
S3	24	RD S2 (unique items)
? t s3/3/all		

3/3/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13435527 BIOSIS NO.: 200200064348
Nucleic acids encoding soluble **human flk-2** extracellular
domain
AUTHOR: Lemischka I R
AUTHOR ADDRESS: Princeton, N.J.**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1197 (3):p1935 April 15, 1997
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Citation
LANGUAGE: English

3/3/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13419152 BIOSIS NO.: 200200047973
Tyrosine kinase receptor **human flk-2**-specific antibodies
AUTHOR: Lemischka I R
AUTHOR ADDRESS: Princeton, N.J.**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1189 (3):p2100 Aug. 20, 1996
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Citation
LANGUAGE: English

3/3/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13275375 BIOSIS NO.: 200100482524
Soluble Flk-2 sequence.
AUTHOR: Yang Zhi(a)
AUTHOR ADDRESS: (a)Palo Alto, CA**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1246 (2):pNo Pagination May 8, 2001
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

3/3/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13110077 BIOSIS NO.: 200100317226
Storage of factor VIII (FVIII) in the alpha-granules of human platelets
following retroviral transduction and transplantation of human CD34+
cells into NOD-SCID mice.
AUTHOR: Wilcox David A(a); Rosenberg Jonathan B; Johnson Bryon D(a);
Montgomery Robert R(a)
AUTHOR ADDRESS: (a)Department of Pediatrics, Medical College of Wisconsin,
Milwaukee, WI**USA
JOURNAL: Blood 96 (11 Part 1):p803a November 16, 2000
MEDIUM: print
CONFERENCE/MEETING: 42nd Annual Meeting of the American Society of
Hematology San Francisco, California, USA December 01-05, 2000
SPONSOR: American Society of Hematology
ISSN: 0006-4971
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12412955 BIOSIS NO.: 200000166457
Identification of CD19-B220+c-Kit+Flt3/Flk-2+ cells as early B lymphoid
precursors before pre-B-I cells in juvenile mouse bone marrow.
AUTHOR: Ogawa Minetaro(a); ten Boekel Edwin; Melchers Fritz
AUTHOR ADDRESS: (a)Department of Molecular Genetics, Graduate School of
Medicine, Kyoto University, Shogoin-Kawaharacho 53, Sakyo-ku, Kyoto,
606-8507**Japan
JOURNAL: International Immunology. 12 (3):p313-324 March, 2000

ISSN: 0953-8178
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12301577 BIOSIS NO.: 200000059444
Ex vivo generation of CD34+ cells from CD34- hematopoietic cells.
AUTHOR: Nakamura Yoshihiko; Ando Kiyoshi(a); Chargui Jamel; Kawada Hiroshi;
Sato Tadayuki; Tsuji Takashi; Hotta Tomomitsu; Kato Shunichi
AUTHOR ADDRESS: (a)Department of Hematology, Tokai University School of
Medicine, Bohseidai, Isehara, Kanagawa**Japan
JOURNAL: Blood 94 (12):p4053-4059 Dec. 15, 1999
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12258591 BIOSIS NO.: 200000012093
SZF1: A novel KRAB-zinc finger gene expressed in CD34+ stem/progenitor
cells.
AUTHOR: Liu Cheng; Levenstein Mark; Chen Joseph; Tsifrina Elina; Yonescu
Raluc; Griffin Constance; Civin Curt I; Small Donald(a)
AUTHOR ADDRESS: (a)The Johns Hopkins Oncology Center, 600 North Wolfe
Street, Rm. 3-109, Baltimore, MD, 21287-5001**USA
JOURNAL: Experimental Hematology (Charlottesville) 27 (2):p313-325 Feb.,
1999
ISSN: 0301-472X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12161736 BIOSIS NO.: 199900456585
Modulation of haematopoietic progenitor development by FLT-3 ligand.
AUTHOR: Banu Naheed; Deng Bijia; Lyman Stewart D; Avraham Hava(a)
AUTHOR ADDRESS: (a)Division of Experimental Medicine, Beth Israel Deaconess
Medical Center, Harvard Institutes of Medicine, 4 Blackfan Circle, 3rd
Floor, Boston, MA, 02115**USA
JOURNAL: Cytokine 11 (9):p679-688 Sept., 1999
ISSN: 1043-4666
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/9 (Item 9 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

11622695 BIOSIS NO.: 199800404830

Isolation and characterization of a cDNA for human, mouse, and rat
full-length stem cell growth factor, a new member of C-type lectin
superfamily.

AUTHOR: Mio Hiroyuki(a); Kagami Naofumi; Yokokawa Sachiko; Kawai Hironori;
Nakagawa Satoshi; Takeuchi Kyoko; Sekine Susumu; Hiraoka Atsunobu

AUTHOR ADDRESS: (a)Pharm. Res. Inst., Kyowa Hakko Kogyo Co. Ltd., 1188
Shimotogari, Nagaizumi-cho, Sunto-gun, Shizu**Japan

JOURNAL: Biochemical and Biophysical Research Communications 249 (1):p
124-130 Aug. 10, 1998

ISSN: 0006-291X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

3/3/10 (Item 10 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10851909 BIOSIS NO.: 199799473054

Expression of multiple forms of fetal liver kinase-2 (flk-2
/flt-3) ligand in cultured human keratinocytes.

AUTHOR: Morita Eishin(a); Tanaka Toshihiko; Shinoda Sumumu; Kameyoshi
Yoshikazu; Yamamoto Shoso; Lee Dong-Geun; Sugiyama Masanori

AUTHOR ADDRESS: (a)Dep. Dermatol., Hiroshima Univ. Sch. Med., Kasumi 1-2-3,
Minami-ku, Hiroshima 734**Japan

JOURNAL: Archives of Dermatological Research 289 (3):p177-179 1997

ISSN: 0340-3696

RECORD TYPE: Citation

LANGUAGE: English

3/3/11 (Item 11 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10219695 BIOSIS NO.: 199698674613

FLT3/FLK-2 (STK-1) ligand does not stimulate human
megakaryopoiesis in vitro.

AUTHOR: Ratajczak Mariusz Z; Ratajczak Janina; Ford John; Kregnow Robert;
Marlicz Wojtek; Gewirtz Alan M(a)

AUTHOR ADDRESS: (a)513B-Stellar-Chance Lab., Univ. Penna. Sch. Med., 422
Curie Blvd., Philadelphia, PA 19104**USA

JOURNAL: Stem Cells (Dayton) 14 (1):p146-150 1996

ISSN: 1066-5099

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

3/3/12 (Item 12 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10110680 BIOSIS NO.: 199698565598

Isolation and characterization of a monoclonal antibody binding to the
extracellular domain of the flk-2 tyrosine kinase receptor.

AUTHOR: Rose Caroline; Rockwell Patricia; Yang Jian-Quing; Pytowski
Bronislaw; Goldstein Neil I(a)

AUTHOR ADDRESS: (a)Immunol./Monoclonal Antibodies Dep., ImClone Systems

Inc., 180 Varick St., New York, NY 10014**USA
JOURNAL: Hybridoma 14 (5):p453-459 1995
ISSN: 0272-457X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

3/3/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09713826 BIOSIS NO.: 199598168744
FLK-2/FLT-3 ligand regulates the growth of early myeloid progenitors
isolated from human fetal liver.
AUTHOR: Muench Marcus O; Roncarolo Maria Grazia; Menon Satish; Xu Yuming;
Kastelein Robert; Zurawski Sandra; Hannum Charles H; Culpepper Janice;
Lee Frank; Namikawa Reiko(a)
AUTHOR ADDRESS: (a)DNAX Res. Inst. Mol. Cellular Biol., 901 California
Ave., Palo Alto, CA 94304-1104**USA
JOURNAL: Blood 85 (4):p963-972 1995
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

3/3/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09126484 BIOSIS NO.: 199497134854
STK-1, the **human** homology of **Flk-2/Flt-3**, is selectively
expressed in CD34+ **human** bone marrow cells and is involved in the
proliferation of early progenitor/stem cells.
AUTHOR: Small Donald(a); Levenstein Mark; Kim Eunkyung; Carow Cathy; Amin
Shahina; Rockwell Patricia; Witte Larry; Burrow Christopher; Ratajczak
Mariusz Z; et al
AUTHOR ADDRESS: (a)Oncol. Cent., Dep. Pediatr., Johns Hopkins Univ. Sch.
Med., 600 North Wolfe Street, Baltimore, M**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United
States of America 91 (2):p459-463 1994
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

3/3/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09098771 BIOSIS NO.: 199497107141
STK-1, a **human** homolog of **FLK-2/FLT3**, is aberrantly
expressed in **human** leukemias and may be involved in the growth
and/or differentiation of hematopoietic stem/progenitor cells.
AUTHOR: Small D(a); Levenstein M; Kim E; Carow C E; Amin S; Ratajczak M;
Gewirtz A M; Civin C I
AUTHOR ADDRESS: (a)Dep. Oncol., Johns Hopkins Univ. Sch. Lab. Med.,
Baltimore, MD**USA
JOURNAL: Blood 82 (10 SUPPL. 1):p325A 1993
CONFERENCE/MEETING: Thirty-fifth Annual Meeting of the American Society of
Hematology St. Louis, Missouri, USA December 3-7, 1993
ISSN: 0006-4971

RECORD TYPE: Citation

LANGUAGE: English

3/3/16 (Item 1 from file: 73)

DIALOG(R)File 73:EMBASE

(c) 2003 Elsevier Science B.V. All rts. reserv.

10630874 EMBASE No: 2000096239

Identification of CD19sup -B220sup +c-Kitsup +Flt3/Flk-2sup + cells as early B lymphoid precursors before pre-B-I cells in juvenile mouse bone marrow

Ogawa M.; Ten Boekel E.; Melchers F.

M. Ogawa, Department of Molecular Genetics, Graduate School of Medicine, Kyoto University, Shogoin-Kawaharacho 53, Sakyo-ku, Kyoto 606-8507 Japan
International Immunology (INT. IMMUNOL.) (United Kingdom) 2000, 12/3 (313-324)

CODEN: INIME ISSN: 0953-8178

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 58

3/3/17 (Item 2 from file: 73)

DIALOG(R)File 73:EMBASE

(c) 2003 Elsevier Science B.V. All rts. reserv.

10520866 EMBASE No: 1999431983

Ex vivo generation of CD34sup + cells from CD34sup - hematopoietic cells

Nakamura Y.; Ando K.; Chargui J.; Kawada H.; Sato T.; Tsuji T.; Hotta T.; Kato S.

Dr. K. Ando, Department of Hematology, Tokai University School of Medicine, Isehara, Kanagawa 259-1183 Japan

Blood (BLOOD) (United States) 1999, 94/12 (4053-4059)

CODEN: BLOOA ISSN: 0006-4971

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 21

3/3/18 (Item 3 from file: 73)

DIALOG(R)File 73:EMBASE

(c) 2003 Elsevier Science B.V. All rts. reserv.

05636203 EMBASE No: 1994041406

STK-1, the **human** homolog of **Flk-2/Flt-3**, is selectively expressed in CD34sup + **human** bone marrow cells and is involved in the proliferation of early progenitor/stem cells

Small D.; Levenstein M.; Kim E.; Carow C.; Amin S.; Rockwell P.; Witte L.; Burrow C.; Ratajczak M.Z.; Gewirtz A.M.; Civin C.I.

Department of Pediatrics, Oncology Center, Johns Hopkins Univ. Sch. of Medicine, 600 North Wolfe Street, Baltimore, MD 21287 United States

Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1994, 91/2 (459-463)

CODEN: PNASA ISSN: 0027-8424

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

3/3/19 (Item 1 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

134085068 CA: 134(7)85068m JOURNAL

Murine stromal cell line HESS-5 maintains reconstituting ability of ex vivo-generated hematopoietic stem cells from human bone marrow and cytokine-mobilized peripheral blood

AUTHOR(S): Shimakura, Yasuhito; Kawada, Hiroshi; Ando, Kiyoshi; Sato, Tadayuki; Nakamura, Yoshihiko; Tsuji, Takashi; Kato, Shunichi; Hotta, Tomomitsu

LOCATION: Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193

JOURNAL: Stem Cells (Miamisburg, Ohio) DATE: 2000 VOLUME: 18 NUMBER: 3

PAGES: 183-189 CODEN: STCEJ ISSN: 1066-5099 LANGUAGE: English

PUBLISHER: AlphaMed Press

3/3/20 (Item 2 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

131196610 CA: 131(15)196610q JOURNAL

Rapid ex vivo expansion of human umbilical cord hematopoietic progenitors using a novel culture system

AUTHOR(S): Kawada, Hiroshi; Ando, Kiyoshi; Tsuji, Takashi; Shimakura, Yasuhito; Nakamura, Yoshihiko; Chargui, Jamel; Hagihara, Masao; Itagaki, Hiroyuki; Shimizu, Takashi; Inokuchi, Sadaki; Kato, Shunichi; Hotta, Tomomitsu

LOCATION: Research Center for Genetic Engineering and Cell Transplantation, JT Inc., Kanagawa, Japan, 259-1193

JOURNAL: Exp. Hematol. (N. Y.) DATE: 1999 VOLUME: 27 NUMBER: 5

PAGES: 904-915 CODEN: EXHMA6 ISSN: 0301-472X

PUBLISHER ITEM IDENTIFIER: 0301-472X(99)00012-0 LANGUAGE: English

PUBLISHER: Elsevier Science Inc.

3/3/21 (Item 3 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

131196608 CA: 131(15)196608v JOURNAL

Ex vivo expansion of human cord blood stem cells and its application to gene therapy

AUTHOR(S): Ando, Kiyoshi; Kawada, Hiroshi; Shimizu, Takashi; Tsuji, Takashi; Nakamura, Yoshihiko; Kimura, Minoru; Miyatake, Hiroko; Shimakura, Yasuhito; Inokuchi, Sadaki; Kato, Shunichi; Hotta, Tomomitsu

LOCATION: Research Center for Genetic Engineering and Cell Transplantation, Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193

JOURNAL: Int. Congr. Ser. DATE: 1999 VOLUME: 1175 NUMBER: Tissue Engineering for Therapeutic Use 3 PAGES: 1-14 CODEN: EXMDA4 ISSN:

0531-5131 LANGUAGE: English PUBLISHER: Elsevier Science B.V.

3/3/22 (Item 4 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

126289031 CA: 126(22)289031p PATENT

Recombinant production of human gene flk-2 protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis

INVENTOR(AUTHOR): Lemischka, Ihor R.

LOCATION: USA

ASSIGNEE: Princeton University

PATENT: United States ; US 5621090 A DATE: 19970415

APPLICATION: US 906397 (19920626) *US 679666 (19910402) *US 728913

(19910628) *US 793065 (19911115) *US 813593 (19911224)
PAGES: 55 pp. Cont.-in-part of U.S. 5,185,438. CODEN: USXXAM LANGUAGE:
English CLASS: 536023500; C07H-021/00A

3/3/23 (Item 5 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

120290838 CA: 120(23)290838q PATENT
Soluble analogs of the mouse fetal liver kinase FLK-2 hemopoietic factor
INVENTOR(AUTHOR): Yang, Zhi
LOCATION: USA
ASSIGNEE: Systemix, Inc.
PATENT: PCT International ; WO 9401576 A1 DATE: 940120
APPLICATION: WO 93US6404 (930707) *US 912122 (920709)
PAGES: 21 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12P-021/06A;
C12N-015/00B; A61K-037/00B; C07K-013/00B DESIGNATED COUNTRIES: AU; CA; JP;
KR; NO; PL; RU; UA DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR
; IE; IT; LU; MC; NL; PT; SE

3/3/24 (Item 6 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

120154711 CA: 120(13)154711r JOURNAL
Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
receptor: a proliferative factor for primitive hematopoietic cells
AUTHOR(S): Lyman, Stewart D.; James, Laura; Vanden Bos, Tim; de Vries,
Peter; Brasel, Ken; Gliniak, Brian; Hollingsworth, L. T.; Picha, Kathleen
S.; McKenna, Hilary J.; et al.
LOCATION: Immunex Res. and Dev. Corp., Seattle, WA, 98101, USA
JOURNAL: Cell (Cambridge, Mass.) DATE: 1993 VOLUME: 75 NUMBER: 6
PAGES: 1157-67 CODEN: CELLB5 ISSN: 0092-8674 LANGUAGE: English
? s flt3
S4 3794 FLT3
? s s4 and py<1993
Processing
Processing
3794 S4
32335638 PY<1993
S5 20 S4 AND PY<1993
? rd s5
...completed examining records
S6 7 RD S5 (unique items)
? t s6/7/all

6/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

08751260 BIOSIS NO.: 199395040611
Expression of the FMS/KIT-like gene **FLT3** in human acute leukemias of
the myeloid and lymphoid lineages.
AUTHOR: Birg Françoise(a); Courcoul Marianne; Rosnet Olivier; Bardin
Florence; Pebusque Marie-Joséphé; Marchetto Sylvie; Tabilio Antonio;
Mannoni Patrice; Birnbaum Daniel
AUTHOR ADDRESS: (a)Unite 119 de l'INSERM, 27, Boulevard Lei Roure, 13009
Marseille**France
JOURNAL: Blood 80 (10):p2584-2593 1992
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: **FLT3**, a receptor belonging to the FMS/KIT family and localized to 13q12, could play a role in the biology of early hematopoietic progenitor cells. Because FMS and KIT are expressed in both normal progenitors and myeloid leukemias, we looked for **FLT3** expression in fresh human leukemic cells using Northern blot analysis. High levels of **FLT3** expression were detected in 92% of the cases of acute myeloid leukemia (AML) tested, ranging from the M1 to the M5 stages of differentiation assessed in the French-American-British classification. Immature (M0) AML cells, biphenotypic leukemias, and AML with megakaryocytic differentiation (M7 subtype) also expressed the **FLT3** transcript. **FLT3** was also expressed at high levels in acute lymphoid leukemias of T and B origins. Finally, it was not expressed in chronic myeloid leukemias in chronic phase, whereas it was expressed in most blast crisis samples. This pattern of expression of **FLT3** contrasts with the expression of FMS and KIT restricted to myeloid leukemias, and suggests that the **FLT3** product could play a role in the expansion of the leukemic blasts of both the myeloid and lymphoid lineages.

6/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08227172 BIOSIS NO.: 000094028136
CHROMOSOMAL LOCALIZATION OF FLT4 A NOVEL RECEPTOR-TYPE TYROSINE KINASE GENE
AUTHOR: GALLAND F; KARAMYSHEVA A; MATTEI M-G; ROSNET O; MARCHETTO S;
BIRNBAUM D
AUTHOR ADDRESS: LAB. MOLECULAR ONCOLOGY, U.119 INSERM, 27 BLVD., LEI ROURE,
13009 MARSEILLE, FR.
JOURNAL: GENOMICS 13 (2). 1992. 475-478. 1992
FULL JOURNAL NAME: Genomics
CODEN: GNMCE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A new human gene encoding a putative receptor-type tyrosine kinase (RTK) was isolated by screening a placenta cDNA library with a mouse **Flt3** probe. The deduced amino acid sequence of the intracellular region of the molecule showed that it was strongly related to the **FLT1** and **KDR/FLK1** gene products and to a lesser degree to members of the class III RTKs: **FMS/CSF1R**, **PDGFRA/B**, **KIT**, and **FLT3**. The gene was named **FLT4**. Cosmid clones of the mouse **Flt4** gene were isolated. The human gene was localized to bands q34-q35 of chromosome 5, i.e., slightly telomeric to the **CSF1R/PDGFRB** tandem of genes, and the mouse homolog to chromosome 11, region A5-B1.

6/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08181055 BIOSIS NO.: 000094004828
GENOMIC ORGANIZATION OF THE HUMAN C-KIT GENE EVOLUTION OF THE RECEPTOR
TYROSINE KINASE SUBCLASS III
AUTHOR: ANDRE C; MARTIN E; CORNU F; HU W-X; WANG X-P; GALIBERT F
AUTHOR ADDRESS: LAB. HEMATOLOGIE EXPERIMENTALE, CENTRE HAYEM, HOPITAL
SAINT-LOUIS, 75475 PARIS CEDEX 10, FR.
JOURNAL: ONCOGENE 7 (4). 1992. 685-691. 1992
FULL JOURNAL NAME: Oncogene
CODEN: ONCNE
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The c-kit proto-oncogene encodes a transmembrane tyrosine kinase receptor. It belongs to receptor tyrosine kinase subclass III, which also includes the colony-stimulating factor I receptor (c-fms), platelet-derived growth factor receptors A and B (PDGFRA and PDGFRB), as well as FLT1 and FLT3/FLK2. cis-kit and PDGFRA, c-fms and PDGFRB, FLT1 and FLT3/FLK2 are grouped by pair in three clusters in man on chromosome 4 band q11-q13, chromosome 5 band q31-q33 and chromosome 13 band q12 respectively. Here, we report the genomic organization of the human c-kit gene, which is composed of 21 small coding exons, distributed over 80 kb. Comparison of the c-kit and c-fms oncogenes shows that they share identical exon/intron boundaries in their two kinetic domains, as well as a similar exon/intron organization in the extracytoplasmic domain. Comparison with the kinase domains of tyrosine kinase genes not belonging to subclass III suggests that the exon/intron organization of c-kit and c-fms is a characteristic feature of subclass III. The genomic similarities between c-kit and c-fms, in conjunction with the location in pairs on different chromosomes of the subclass III genes, has led us to hypothesize that cis and trans duplications gave rise to this group of genes.

6/7/4 (Item 4 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

07886735 BIOSIS NO.: 000092135727
MURINE FLT3 A GENE ENCODING A NOVEL TYROSINE KINASE RECEPTOR OF THE PDGFR-CSF1R FAMILY
AUTHOR: ROSNET O; MARCHETTO S; DELAPEYRIERE O; BIRNBAUM D
AUTHOR ADDRESS: U.119 INSERM, 27 BLD LEI ROURE, 13009 MARSEILLE, FR.
JOURNAL: ONCOGENE 6 (9). 1991. 1641-1650. 1991
FULL JOURNAL NAME: Oncogene
CODEN: ONCNE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Receptor-type tyrosine kinases presenting an extracellular region with five immunoglobulin-like domains, and strongly related by sequence similarities in the intracellular region, constitute a family of receptors involved in development and function of various cell lineages. We have isolated and characterized the mouse Flt3 gene, encoding the sixth member of this family. The Flt3 gene possesses an open reading frame of 3000 nucleotides, and therefore appears to code for a protein of 1000 amino acids. The deduced structure of the FLT3 protein presents all the characteristics of a receptor-type kinase of this family. The gene is expressed in placenta, in various adult tissues including gonads and brain, and in hematopoietic cells. The Flt3 transcript is 3.7 kb long, except in the testis, where two shorter post-meiotic transcripts are detected. These results suggest a role for this novel receptor and its yet unidentified ligand in placenta, gonads and hematopoietic and nervous systems.

6/7/5 (Item 5 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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04802506 BIOSIS NO.: 000080105634
IDENTIFICATION OF MULTIPLE VARIANTS OF FAST MUSCLE TROPONIN T IN THE CHICKEN USING MONOCLONAL ANTIBODIES
AUTHOR: BIRD I M; DHOOT G K; WILKINSON J M
AUTHOR ADDRESS: DEP. BIOCHEMISTRY, ROAYL COLLEGE SURGEONS OF ENGLAND,

LINCOLN'S INN FIELDS, LONDON, ENGLAND WC2A 3PN.
JOURNAL: EUR J BIOCHEM 150 (3). 1985. 517-526. 1985
FULL JOURNAL NAME: European Journal of Biochemistry
CODEN: EJBCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Two monoclonal antibodies, T1/7 and T1/61, were prepared which are specific for chicken fast muscle troponin T. Both are of the IgG.gamma.1 subclass. Both antibodies cross-react strongly with human fast and chicken cardiac troponin T, but while T1/7 reacts weakly with rabbit fast troponin T, T1/61 does not. The antibodies can be used for fiber typing of both chicken and human muscle. The antibodies were used to identify fast troponin T on 2-dimensional maps of proteins from a variety of chicken muscles by electrophoretic transfer to nitrocellulose followed by immunoperoxidase staining. Using this technique 5 variant forms of fast troponin T were identified. Two variants, fBT1 and fBT2, are expressed in breast muscle, while the other 3 fLT1, fLT2 and **fLT3** are expressed in leg muscle. Of the leg muscle variants, fLT1 and fLT2 correspond to the 2 forms described previously. The 3rd variant, **fLT3**, has not been described before and is expressed in muscles which have a high content of slow fibers. In addition to these clearly defined variant forms immunostaining reveals multiple minor variants of troponin T present in leg muscle which may reflect complex RNA processing of the troponin T gene transcript.

6/7/6 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

04577528 EMBASE No: 1991071571
Isolation and chromosomal localization of a novel FMS-like tyrosine kinase gene
Rosnet O.; Mattei M.-G.; Marchetto S.; Birnbaum D.
U.119 INSERM, 27 Bd. Lei Roure, 13009, Marseille France
Genomics (GENOMICS) (United States) 1991, 9/2 (380-385)
CODEN: GNMCE ISSN: 0888-7543
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

We have isolated and sequenced part of a new gene of the tyrosine kinase family. This gene, called **FLT3**, has strong sequence similarities with members of a group of genes encoding growth factor receptors: FMS, KIT, and PDGFR. We have localized the human **FLT3** gene to chromosome 13, band q12, and its mouse homolog to chromosome 5, region G.

6/7/7 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

07256996 92119639 PMID: 1310071
FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-qter.
Aprelikova O; Pajusola K; Partanen J; Armstrong E; Alitalo R; Bailey S K; McMahon J; Wasmuth J; Huebner K; Alitalo K
Department of Virology, University of Helsinki, Finland.
Cancer research (UNITED STATES) Feb 1 1992, 52 (3) p746-8,
ISSN 0008-5472 Journal Code: 2984705R
Contract/Grant No.: CA 21124; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The receptors for at least two hematopoietic growth factors, namely the stem cell factor and colony-stimulating factor 1, belong to class III receptor tyrosine kinases. Here we describe cloning of a partial complementary DNA for FLT4, an additional member of this gene family from human leukemia cells. The FLT4 tyrosine kinase domain is 79% homologous with the previously cloned FLT1 (M. Shibuya et al., Oncogene, 5: 519-524, 1990) tyrosine kinase and maps to the chromosomal region 5q33-qter. We have found FLT4 expression in human placenta, lung, heart, and kidney, whereas the pancreas and brain appeared to contain very little if any FLT4 RNA. The results suggest that FLT4 functions in multiple adult tissues.

Record Date Created: 19920225

Record Date Completed: 19920225

? s flk(W)2

2948 FLK

8736730 2

S7 279 FLK(W)2

? s s7 and py<1993

Processing

Processing

279 S7

32335638 PY<1993

S8 4 S7 AND PY<1993

? rd s8

...completed examining records

S9 1 RD S8 (unique items)

? t s9/7/all

9/7/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

07768231 BIOSIS NO.: 000092071602

A RECEPTOR TYROSINE KINASE SPECIFIC TO HEMATOPOIETIC STEM AND PROGENITOR
CELL-ENRICHED POPULATIONS

AUTHOR: MATTHEWS W; JORDAN C T; WIEGAND G W; PARDOLL D; LEMISCHKA I R

AUTHOR ADDRESS: DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, N.J.

08540.

JOURNAL: CELL 65 (7). 1991. 1143-1152. 1991

FULL JOURNAL NAME: Cell

CODEN: CELLB

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: To elucidate the molecular biology of the hematopoietic stem cell, we have begun to isolate genes from murine cell populations enriched in stem cell activity. One such cDNA encodes a novel receptor tryosine kinase, designated fetal liver kinase-2 or **flk-2**, which is related to the W locus gene product c-kit. Expression analyses suggest an extremely restricted distribution of **flk-2**. It is expressed in populations enriched for stem cells and primitive uncommitted progenitors, and is absent in populations containing more mature cells. Therefore, this receptor may be a key signal transduction component in the totipotent hematopoietic stem cell and its immediate self-renewing progeny.

? s s7 and review?

279 S7

3363995 REVIEW?

S10 9 S7 AND REVIEW?

? rd s10

...completed examining records

S11 9 RD S10 (unique items)

? t s11/7/all

11/7/1 (Item 1 from file: 5)

DIALOG(R) File 5: Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10420380 BIOSIS NO.: 199699041525

Expression of FLT3 receptor and response to FLT3 ligand by leukemia cells.

AUTHOR: Drexler H D

AUTHOR ADDRESS: DSMZ-German Collection Microorganisms Cell Cultures, Dep.

Human Animal Cell Cultures, Mascheroder Weg**Germany

JOURNAL: Leukemia (Basingstoke) 10 (4):p588-599 1996

ISSN: 0887-6924

DOCUMENT TYPE: Literature Review

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The novel hematopoietic growth factor FLT3 ligand (FL) is the cognate ligand for the FLT3 tyrosine kinase receptor (R), also referred to as **FLK-2** and **STK-1**. The FLT3R belongs to a family of receptor tyrosine kinases involved in hematopoiesis that also includes **KIT**, the receptor for **SCF** (stem cell factor), and **FMS**, the receptor for **M-CSF** (macrophage colony-stimulating factor). Restricted FLT3R expression was seen on human and murine hematopoietic progenitor cells. In functional assays recombinant FL stimulated the proliferation and colony formation of human hematopoietic progenitor cells, i.e. CD34+ cord and peripheral blood, bone marrow and fetal liver cells. Synergy was reported for co-stimulation with G-CSF (granulocyte-CSF), GM-CSF (granulocyte-macrophage CSF), M-CSF, interleukin-3 (IL-3), PIXY-321 (an IL-3/GM-CSF fusion protein) and SCF. In the mouse, FL potentially enhanced growth of various types of progenitor/precursor cells in synergy with G-CSF, GM-CSF, M-CSF, IL-3, IL-6, IL-7, IL-11, IL-12 and SCF. The well-documented involvement of this ligand-receptor pair in physiological hematopoiesis brought forth the question whether FLT3R and FL might also have a role in the pathobiology of leukemia. At the mRNA level FLT3R was expressed by most (80-100%) cases of AML (acute myeloid leukemia) throughout the different morphological subtypes (M0-M7), of ALL (acute lymphoblastic leukemia) of the immunological subtypes T-ALL and BCP-ALL (B cell precursor ALL including pre-pre B-ALL, cALL and pre B-ALL), of AMLL (acute mixed-lineage leukemia), and of CML (chronic myeloid leukemia) in lymphoid or mixed blast crisis. Analysis of cell surface expression of FLT3R by flow cytometry confirmed these observations for AML (66% positivity when the data from all studies are combined), BCP-ALL (64%) and CML lymphoid blast crisis (86%), whereas less than 30% of T-ALL were FLT3R+. The myeloid, monocytic and pre B cell type categories also contained the highest proportions of FLT3R+ leukemia cell lines. In contrast to the selective expression of the receptor, FL expression was detected in 90-100% of the various cell types of leukemia cell lines from all hematopoietic cell lineages. The potential of FL to induce proliferation of leukemia cells in vitro was also examined in primary and continuously cultured leukemia cells. The data on FL-stimulated leukemia cell growth underline the extensive heterogeneity of primary AML and ALL samples in terms of cytokine-inducible DNA synthesis that has been seen with other effective cytokines. While the majority of T-ALL (0-33% of the cases responded proliferatively; mean 11%) and BCP-ALL (0-30%; mean 20%) failed to proliferate in the presence of FL despite strong expression of surface FLT3R, FL caused a proliferative response in a significantly higher percentage of AML cases (22-90%; mean 53%). In the panel of leukemia cell lines examined only myeloid and monocytic growth factor-dependent cell lines increased their proliferation upon incubation with FL, whereas all growth factor-independent cell lines were refractory to stimulation. Combinations of FL with G-CSF, GM-CSF, M-CSF, IL-3, PIXY-321 or SCF and FL with IL-3 or IL-7 had synergistic or additive mitogenic effects on primary AML and ALL cells, respectively. The potent stimulation of the myelomonocytic cell lines was further augmented by addition of bFGF (basic fibroblast growth factor), GM-CSF, IL-3 or SCF. The inhibitory effects of TGF-beta-1 (transforming growth factor-beta-1)

on FL-supported proliferation were abrogated by bFGF. Taken together, these results demonstrate the expression of functional FLT3R capable of mediating FL-dependent mitogenic signaling in a subset of AML and ALL cases and further underline the heterogeneity of AML and ALL samples in their proliferative response to cytokines. The data reviewed here provided clear experimental evidence for the involvement of the FL-FLT3R ligand-receptor interaction in normal and possibly also in leukemic hematopoiesis.

11/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10243948 BIOSIS NO.: 199698698866
Role of protein tyrosine kinase receptors in cancer: Possibilities for therapeutic intervention.
AUTHOR: Rockwell Patricia(a); Goldstein Neil I
AUTHOR ADDRESS: (a)Immunol./Monoclonal Antibodies Dep., Imclone Systems Inc., 180 Varick St., New York, NY 10014**USA
JOURNAL: Molecular and Cellular Differentiation 3 (4):p315-335 1995
ISSN: 1065-3074
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: For many cancers, oncogenic activation by genetic alterations triggers a dysfunctional cell proliferation that may manifest itself as overexpression of growth factors and their cognate receptors on tumor cells. Secreted growth factors that promote cell proliferation are provided either by surrounding tumor-associated stroma (paracrine) or by the tumor cell itself (autocrine). In addition, receptors on quiescent endothelial cells are activated to stimulate new blood vessel formation (tumor angiogenesis). Therapeutic strategies for suppressing cancer growth and metastasis have focused on targeting the critical proteins that contribute to cancer progression. One approach is blocking the activation of receptors overexpressed in growth factor-dependent tumor cells. This review discusses the use of neutralizing monoclonal antibodies (Mab) to target three important protein tyrosine kinase receptors (PTK) that play a role in malignant transformation: the epidermal growth factor receptor (EGFR), fetal liver kinase-1 (flk-1), and fetal liver kinase-2 (flk-2). Experimental evidence is presented showing the use of neutralizing Mabs as efficacious immunotherapeutics in the treatment of solid tumors (EGFR), acute leukemias (flk-2), and in blocking tumor angiogenesis (flk-1). In addition, preclinical results from studies utilizing human carcinoma xenograft models have shown that a therapeutic approach of antireceptor monoclonal antibodies in combination with chemotherapy is synergistic. These data emphasize (1) the importance of targeting receptors that play a crucial role in tumor growth and progression, (2) the tumor vasculature as a major target for inhibiting tumor growth, and (3) the clinical relevance of these receptors for therapeutic intervention.

11/7/3 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
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10675228 EMBASE No: 2000159682
Ex vivo expansion of hematopoietic stem cells and their clinical application
Nakahata T.
Dr. T. Nakahata, Department of Pediatrics, Graduate School of Medicine,

Kyoto University, 54 Kawahara-cho, Shogoin, Sakyo-ku, Kyoto 606-8507
Japan
Biotherapy (BIOTHERAPY (JAPAN)) (Japan) 2000, 14/3 (270-275)
CODEN: BITPE ISSN: 0914-2223
DOCUMENT TYPE: Journal; Review
LANGUAGE: JAPANESE SUMMARY LANGUAGE: ENGLISH; JAPANESE
NUMBER OF REFERENCES: 16

We previously reported that most of immature progenitor cells such as CFU-Blast and LTCIC were included in CD34sup + gp130sup + IL-6Rsup - population, suggesting that sIL-6R/IL-6 but not IL-6 may be potent for the ex vivo expansion of immature progenitor cells. We also demonstrated that most immature progenitors in cord blood expressed c-Kit, Flk 2 /Flt 3 and mpl receptors. A significant ex vivo expansion of human hematopoietic stem cells capable of repopulating in NOD/SCID mice using a combination of stem cell factor (SCF), Flk 2/Flt 3 ligand (FL), thrombopoietin (TPO) and a complex of interleukin (IL)-6 and soluble IL-6 receptor (IL-6/sIL-6R). When fresh cord blood CD34sup + cells and their progenies cultured with SCF+FL+TPO+IL-6/sIL-6R for 7 days were transplanted into NOD/SCID mice, successful engraftment were highly observed in the mice who were transplanted with cultured cells, 10 to 12 weeks after the transplantation. The CD45sup + cells in the recipients engrafted with cultured cells consisted of various lineages and a large number of CD34sup + cells, which formed human hematopoietic colonies in in vitro clonal culture. The fold increase in the long-term repopulating hematopoietic stem cells was estimated at 4.0 by a limiting dilution method. The present study may provide a novel culture method for the expansion of human transplantable hematopoietic stem cells aimed for clinical application.

11/7/4 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE
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07513354 EMBASE No: 1998418902
Recent progress in identifying genes regulating hematopoietic stem cell function and fate
Jordan C.T.; Van Zant G.
C.T. Jordan, Blood Marrow Transplantation Program, Markey Cancer Center, University Kentucky Medical Center, 800 Rose Street, Lexington, KY 40536 United States
AUTHOR EMAIL: cjordan@pop.uky.edu
Current Opinion in Cell Biology (CURR. OPIN. CELL BIOL.) (United Kingdom) 1998, 10/6 (716-720)
CODEN: COCBE ISSN: 0955-0674
DOCUMENT TYPE: Journal; Review
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 46

Significant advances in the use of genetic and molecular biology strategies have recently begun to identify genes that have a major impact on the determination, commitment and developmental potential of hematopoietic stem cells. Using a variety of experimental strategies, genes such as SCL, GATA-2, HoxB4, Flk-2, c-mpl, dlk, and others have been implicated as important regulators of stem cell growth. In addition, genetic mapping has identified several loci that correlate strongly with stem cell numbers and proliferation.

11/7/5 (Item 3 from file: 73)
DIALOG(R)File 73:EMBASE
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07131889 EMBASE No: 1998019867

Regulation of hematopoiesis by microvascular endothelium

Rafii S.; Mohle R.; Shapiro F.; Frey B.M.; Moore M.A.S.

S. Rafii, Division of Hematology-Oncology, Cornell University Medical College, 1300 York Avenue, New York, NY 10021 United States

Leukemia and Lymphoma (LEUK. LYMPHOMA) (United Kingdom) 1997, 27/5-6 (375-386)

CODEN: LELYE ISSN: 1042-8194

DOCUMENT TYPE: Journal; Review

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 86

The bone marrow microenvironment is a complex three dimensional structure where hematopoietic stem cells proliferate, mature, migrate into the sinusoidal space, and enter the circulation in an exquisitely regulated fashion. Stromal cells within the BM microenvironment provide a suitable environment for self-renewal, proliferation and differentiation of hematopoietic stem cells. Within the hematopoietic microenvironment, whether it is embryonic yolk sac, fetal liver, or adult bone marrow, microvascular endothelium not only acts as a gatekeeper controlling the trafficking and homing of hematopoietic progenitors, but also provides cellular contact and secretes cytokines that allows for the preservation of the steady state hematopoiesis. Recently, homogenous monolayers of bone marrow endothelial cells (BMEC) have been isolated and cultivated in tissue culture. Long term coculture studies have shown that BMEC monolayers are unique type of endothelium and can support long-term proliferation of hematopoietic progenitor cells particularly megakaryocytic and myeloid progenitor cells by constitutive elaboration of lineage-specific cytokines such as G-CSF, GM-CSF, M-CSF, Kit-ligand, IL6, **FLK-2** ligand, and leukemia inhibitory factor. Direct cellular contact between hematopoietic progenitor cells and BMEC monolayers through specific adhesion molecules including beta1, beta2 integrins and selectins play a critical role in trafficking and possibly proliferation of hematopoietic stem cells. Dysfunction of microvascular endothelial cells within the hematopoietic microenvironment may result in stem cell disorders and progression to aplastic anemias, and contribute to graft failure during bone marrow transplantation. Further studies on the role of microvascular endothelium in the regulation of hematopoietic stem cell homing and proliferation may enhance our understanding of the pathophysiology of stem cell and leukemic disorders.

11/7/6 (Item 4 from file: 73)

DIALOG(R)File 73:EMBASE

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06382704 EMBASE No: 1996041629

FLT3/**FLK-2** (STK-1) ligand does not stimulate human megakaryopoiesis in vitro

Ratajczak M.Z.; Ratajczak J.; Ford J.; Kregenow R.; Marlicz W.; Gewirtz A.M.

513B-Stellar Chance Laboratories, University of Pennsylvania, School of Medicine, 422 Curie Blvd., Philadelphia, PA 19104 United States

Stem Cells (STEM CELLS) (United States) 1996, 14/1 (146-150)

CODEN: STCEE ISSN: 1066-5099

DOCUMENT TYPE: Journal; Review

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

It has not yet been determined if the FLT3/**FLK-2** or STK-1 Ligand (STK-1 L)FLT3/**FLK-2** or STK-1 receptor (STK-1R) axis has the ability to regulate human megakaryopoiesis in vitro. To address this question, we exposed normal human CD34sup + marrow mononuclear cells to recombinant human STK-11, alone, or in combination with other growth factors. Colony-forming unit- megakaryocytic/thrombocytes (CFU-Meg) and BEU-E-derived colonies were then enumerated, and effects on colony size and

maturation noted. As assessed by these parameters, STK-11, had no demonstrable effect on megakaryocyte colony formation. Similarly, suppressing STK-1R expression with oligodeoxynucleotides also had no influence on CFU-Meg-derived colony formation. To begin to derive a physiologic explanation for these findings, we examined freshly isolated normal human megakaryocytes for the presence of STK-11, and STK-1R mRNA. In contrast to a growing number of growth factors and growth factor receptors which appear to be expressed by megakaryocytes, normal mature human megakaryocytes express neither STK-1R or STK-1L, mRNA. Accordingly, our results led us to hypothesize that if STK-1/STK-1L, have any effects on megakaryocyte development in vitro, they are likely subtle and of uncertain physiologic significance.

11/7/7 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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137061596 CA: 137(5)61596t CONFERENCE PROCEEDING

Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells

AUTHOR(S): Nakahata, Tatsuhiko

LOCATION: School of Medicine, Kyoto University, Japan,

JOURNAL: Zoketsu Saitokain (Zoketsu Saitokain) EDITOR: Motoyoshi, Kazuo
(Ed), DATE: 2001 PAGES: 198-210 CODEN: 69CBMS LANGUAGE: Japanese

PUBLISHER: Medikaru Rebyusha, Tokyo, Japan

SECTION:

CA215000 Immunochemistry

IDENTIFIERS: review Flk2 Flt3 ligand hematopoietic stem cell

DESCRIPTORS:

Hematopoiesis...

Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells

Hematopoietins...

FLT3 ligand; Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells

Hematopoietin receptors...

FLT3 receptors; Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells

Hematopoietic precursor cell...

stem; Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells

11/7/8 (Item 2 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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131168819 CA: 131(13)168819w JOURNAL

B cell development in the mouse from early progenitors to mature B cells

AUTHOR(S): Rolink, Antonius G.; ten Boekel, Edwin; Yamagami, Tamotsu;

Ceredig, Rod; Andersson, Jan; Melchers, Fritz

LOCATION: Basel Institute for Immunology, CH-4005, Basel, Switz.

JOURNAL: Immunol. Lett. DATE: 1999 VOLUME: 68 NUMBER: 1 PAGES: 89-93

CODEN: IMLED6 ISSN: 0165-2478 PUBLISHER ITEM IDENTIFIER:

0165-2478(99)00035-8 LANGUAGE: English PUBLISHER: Elsevier Science
Ireland Ltd.

SECTION:

CA215000 Immunochemistry

IDENTIFIERS: review B cell development progenitor gene tyrosine kinase

DESCRIPTORS:

B cell(lymphocyte)... Cell differentiation...

B cell development in the mouse from early progenitors to mature B cells

Hematopoiesis...

B-cell lymphopoiesis; in B cell development in the mouse from early progenitors to mature B cells

Hematopoietic precursor cell...
 B-cell; B cell development in the mouse from early progenitors to
 mature B cells
 Hemopoietins...
 flk-2 ligand; in B cell development in the mouse from early progenitors
 to mature B cells
 Biomarkers(biological responses)... c-Kit(protein)... Gene,animal...
 Immunoglobulins...
 in B cell development in the mouse from early progenitors to mature B
 cells
 Recombination,genetic...
 rearrangement, Ig genes; in B cell development in the mouse from early
 progenitors to mature B cells
 CAS REGISTRY NUMBERS:
 138359-29-2 in B cell development in the mouse from early progenitors to
 mature B cells

11/7/9 (Item 3 from file: 399)
 DIALOG(R)File 399:CA SEARCH(R)
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123252066 CA: 123(19)252066r JOURNAL
 Flt 3/Flk 2 and its ligand
 AUTHOR(S): Komatsu, Norio
 LOCATION: Jichi Med. Coll., Tochigi, Japan, 329-04
 JOURNAL: Igaku no Ayumi DATE: 1995 VOLUME: 174 NUMBER: 2 PAGES: 131-4
 CODEN: IGAYAY ISSN: 0039-2359 LANGUAGE: Japanese
 SECTION:
 CA213000 Mammalian Biochemistry
 CA203XXX Biochemical Genetics
 IDENTIFIERS: review gene FLT3 receptor ligand hematopoiesis
 DESCRIPTORS:
 Hematopoiesis... Molecular cloning... Receptors, gene FLT3...
 FLT3/FLK2 receptor tyrosine kinase and its ligand in hematopoiesis
 ? ds

Set	Items	Description
S1	279	FLK(W)2
S2	43	FLK(W)2(10N)(HUMAN)
S3	24	RD S2 (unique items)
S4	3794	FLT3
S5	20	S4 AND PY<1993
S6	7	RD S5 (unique items)
S7	279	FLK(W)2
S8	4	S7 AND PY<1993
S9	1	RD S8 (unique items)
S10	9	S7 AND REVIEW?
S11	9	RD S10 (unique items)
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	279	S7
	19097961	HUMAN
	370744	MURINE
S12	37	S7 AND (HUMAN AND MURINE)
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S13	20	RD S12 (unique items)
? t s13/3/all		

13/3/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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13171516 BIOSIS NO.: 200100378665

Extensive and long-term ex vivo production of dendritic cells from CD34 positive umbilical cord blood or bone marrow cells by novel culture system using mouse stroma.

AUTHOR: Hagihara Masao(a); Li Changwen; Gansuud Balgansuren; Munkhbat Batmunkh; Inoue Hiroyasu; Shimakura Yasuhito; Tsuchiya Takahide; Ueda Yoko; Oki Masayuki; Ando Kiyoshi; Kato Shunichi; Hotta Tomomitsu

AUTHOR ADDRESS: (a)Department of Hematology and Rheumatology, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa, 259-1193: masao@is.icc.u-tokai.ac.jp**Japan

JOURNAL: Journal of Immunological Methods 253 (1-2):p45-55 1 July, 2001

MEDIUM: print

ISSN: 0022-1759

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/2 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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13110077 BIOSIS NO.: 200100317226

Storage of factor VIII (FVIII) in the alpha-granules of human platelets following retroviral transduction and transplantation of human CD34+ cells into NOD-SCID mice.

AUTHOR: Wilcox David A(a); Rosenberg Jonathan B; Johnson Bryon D(a); Montgomery Robert R(a)

AUTHOR ADDRESS: (a)Department of Pediatrics, Medical College of Wisconsin, Milwaukee, WI**USA

JOURNAL: Blood 96 (11 Part 1):p803a November 16, 2000

MEDIUM: print

CONFERENCE/MEETING: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000

SPONSOR: American Society of Hematology

ISSN: 0006-4971

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/3 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

12301577 BIOSIS NO.: 200000059444

Ex vivo generation of CD34+ cells from CD34- hematopoietic cells.

AUTHOR: Nakamura Yoshihiko; Ando Kiyoshi(a); Chargui Jamel; Kawada Hiroshi; Sato Tadayuki; Tsuji Takashi; Hotta Tomomitsu; Kato Shunichi

AUTHOR ADDRESS: (a)Department of Hematology, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa**Japan

JOURNAL: Blood 94 (12):p4053-4059 Dec. 15, 1999

ISSN: 0006-4971

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/4 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

12278689 BIOSIS NO.: 200000032191

Rapid ex vivo expansion of **human** umbilical cord hematopoietic progenitors using a novel culture system.

AUTHOR: Kawada Hiroshi; Ando Kiyoshi; Tsuji Takashi; Shimakura Yasuhito; Nakamura Yoshihiko; Chargui Jamel; Hagihara Masao; Itagaki Hiroyuki; Shimizu Takashi; Inokuchi Sadaki; Kato Shunichi; Hotta Tomomitsu(a)

AUTHOR ADDRESS: (a)Division of Hematology, Department of Internal Medicine, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa, 259-1193**Japan

JOURNAL: Experimental Hematology (Charlottesville) 27 (5):p904-915 May, 1999

ISSN: 0301-472X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/5 (Item 5 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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12161736 BIOSIS NO.: 199900456585

Modulation of haematopoietic progenitor development by FLT-3 ligand.

AUTHOR: Banu Naheed; Deng Bijia; Lyman Stewart D; Avraham Hava(a)

AUTHOR ADDRESS: (a)Division of Experimental Medicine, Beth Israel Deaconess Medical Center, Harvard Institutes of Medicine, 4 Blackfan Circle, 3rd Floor, Boston, MA, 02115**USA

JOURNAL: Cytokine 11 (9):p679-688 Sept., 1999

ISSN: 1043-4666

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/6 (Item 6 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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11661939 BIOSIS NO.: 199800443670

Leukemic predisposition of mice transplanted with gene-modified hematopoietic precursors expressing flt3 ligand.

AUTHOR: Hawley Teresa S; Fong Andrew Z C; Griesser Henrik; Lyman Stewart D; Hawley Robert G(a)

AUTHOR ADDRESS: (a)Toronto Hospital, CRCS-424, 67 College St., Toronto, Ontario M5G 2M1**Canada

JOURNAL: Blood 92 (6):p2003-2011 Sept. 15, 1998

ISSN: 0006-4971

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

13/3/7 (Item 7 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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11622695 BIOSIS NO.: 199800404830

Isolation and characterization of a cDNA for **human**, mouse, and rat full-length stem cell growth factor, a new member of C-type lectin superfamily.

AUTHOR: Mio Hiroyuki(a); Kagami Naofumi; Yokokawa Sachiko; Kawai Hironori;

Nakagawa Satoshi; Takeuchi Kyoko; Sekine Susumu; Hiraoka Atsunobu
AUTHOR ADDRESS: (a)Pharm. Res. Inst., Kyowa Hakko Kogyo Co. Ltd., 1188
Shimotogari, Nagaizumi-cho, Sunto-gun, Shizu**Japan
JOURNAL: Biochemical and Biophysical Research Communications 249 (1):p
124-130 Aug. 10, 1998
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

13/3/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10420380 BIOSIS NO.: 199699041525
Expression of FLT3 receptor and response to FLT3 ligand by leukemia cells.
AUTHOR: Drexler H D
AUTHOR ADDRESS: DSMZ-German Collection Microorganisms Cell Cultures, Dep.
Human Animal Cell Cultures, Mascheroder Weg**Germany
JOURNAL: Leukemia (Basingstoke) 10 (4):p588-599 1996
ISSN: 0887-6924
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

13/3/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10110680 BIOSIS NO.: 199698565598
Isolation and characterization of a monoclonal antibody binding to the
extracellular domain of the flk-2 tyrosine kinase receptor.
AUTHOR: Rose Caroline; Rockwell Patricia; Yang Jian-Quing; Pytowski
Bronislaw; Goldstein Neil I(a)
AUTHOR ADDRESS: (a)Immunol./Monoclonal Antibodies Dep., ImClone Systems
Inc., 180 Varick St., New York, NY 10014**USA
JOURNAL: Hybridoma 14 (5):p453-459 1995
ISSN: 0272-457X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

13/3/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09983617 BIOSIS NO.: 199598438535
Rationale for cytokine combinations for ex vivo expansion of hematopoietic
stem cells.
AUTHOR: Ogawa M(a); Johnson Ralph H
AUTHOR ADDRESS: (a)Dep. Veterans Affairs Med. Center, Charleston, SC**USA
JOURNAL: Experimental Hematology (Charlottesville) 23 (8):p839 1995
CONFERENCE/MEETING: 24th Annual Meeting of the International Society for
Experimental Hematology Duesseldorf, Germany August 27-31, 1995
ISSN: 0301-472X
RECORD TYPE: Citation
LANGUAGE: English

13/3/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

09546029 BIOSIS NO.: 199598000947

Cellular and molecular characterization of the role of the **FLK-2/FLT-3** receptor tyrosine kinase in hematopoietic stem cells.

AUTHOR: Zeigler Francis C; Bennett Brian D; Jordan Craig T; Spencer Susan D
; Baumhueter Susanne; Carroll Kathleen J; Hooley Jeffrey; Bauer Kenneth;
Matthews William(a)

AUTHOR ADDRESS: (a)Genentech, Inc., 460 Point San Bruno Blvd., South San
Francisco, CA 94080**USA

JOURNAL: Blood 84 (8):p2422-2430 1994

ISSN: 0006-4971

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

13/3/12 (Item 12 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

09154020 BIOSIS NO.: 199497162390

Molecular cloning of a ligand for the **FLT3/FLK-2** receptor: A
proliferative factor for early hematopoietic cells.

AUTHOR: Beckmann M Patricia; Vanden Bos Tim; James Laura; Brasel Ken; De
Vries Peter; Picha Kathleen S; Farrah Terry; Hollingsworth L T; Gliniak
Brian; et al

AUTHOR ADDRESS: Immunex Res. and Development Corp., Seattle, WA 98101**USA

JOURNAL: Journal of Cellular Biochemistry Supplement 0 (18B):p175 1994

CONFERENCE/MEETING: Keystone Symposium on Stem Cells Taos, New Mexico, USA
January 31-February 7, 1994

ISSN: 0733-1959

RECORD TYPE: Citation

LANGUAGE: English

13/3/13 (Item 13 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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09126484 BIOSIS NO.: 199497134854

STK-1, the **human** homology of **Flk-2/Flt-3**, is selectively
expressed in CD34+ **human** bone marrow cells and is involved in the
proliferation of early progenitor/stem cells.

AUTHOR: Small Donald(a); Levenstein Mark; Kim Eunkyung; Carow Cathy; Amin
Shahina; Rockwell Patricia; Witte Larry; Burrow Christopher; Ratajczak
Mariusz Z; et al

AUTHOR ADDRESS: (a)Oncol. Cent., Dep. Pediatr., Johns Hopkins Univ. Sch.
Med., 600 North Wolfe Street, Baltimore, M**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United
States of America 91 (2):p459-463 1994

ISSN: 0027-8424

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

13/3/14 (Item 14 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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09098771 BIOSIS NO.: 199497107141

STK-1, a **human** homolog of **FLK-2/FLT3**, is aberrantly
expressed in **human** leukemias and may be involved in the growth

and/or differentiation of hematopoietic stem/progenitor cells.
AUTHOR: Small D(a); Levenstein M; Kim E; Carow C E; Amin S; Ratajczak M;
Gewirtz A M; Civin C I
AUTHOR ADDRESS: (a)Dep. Oncol., Johns Hopkins Univ. Sch. Lab. Med.,
Baltimore, MD**USA
JOURNAL: Blood 82 (10 SUPPL. 1):p325A 1993
CONFERENCE/MEETING: Thirty-fifth Annual Meeting of the American Society of
Hematology St. Louis, Missouri, USA December 3-7, 1993
ISSN: 0006-4971
RECORD TYPE: Citation
LANGUAGE: English

13/3/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09076690 BIOSIS NO.: 199497085060
Molecular cloning of a ligand for the flt3/flk-2 tyrosine
kinase receptor: A proliferative factor for primitive hematopoietic
cells.
AUTHOR: Lyman Stewart D; James Laura; Vanden Bos Tim; De Vries Peter;
Brasel Ken; Gliniak Brian; Hollingsworth L T; Picha Kathleen S; McKenna
Hilary J; et al
AUTHOR ADDRESS: Immunex Res. Dev. Corp., 51 University St., Seattle, WA
98101**USA
JOURNAL: Cell 75 (6):p1157-1167 1993
ISSN: 0092-8674
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

13/3/16 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

10520866 EMBASE No: 1999431983
Ex vivo generation of CD34sup + cells from CD34sup - hematopoietic cells
Nakamura Y.; Ando K.; Chargui J.; Kawada H.; Sato T.; Tsuji T.; Hotta T.;
Kato S.
Dr. K. Ando, Department of Hematology, Tokai University School of
Medicine, Isehara, Kanagawa 259-1183 Japan
Blood (BLOOD) (United States) 1999, 94/12 (4053-4059)
CODEN: BLOOA ISSN: 0006-4971
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 21

13/3/17 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

05751254 EMBASE No: 1994164622
Molecular cloning of a novel receptor tyrosine kinase gene, STK, derived
from enriched hematopoietic stem cells
Iwama A.; Okano K.; Sudo T.; Matsuda Y.; Suda T.
Department of Cell Differentiation, Molecular Embryology/Genetics Inst.,
Kumamoto Univ. School of Medicine, 2-2-1 Honjo, Kumamoto 860 Japan
Blood (BLOOD) (United States) 1994, 83/11 (3160-3169)
CODEN: BLOOA ISSN: 0006-4971
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

13/3/18 (Item 3 from file: 73)
DIALOG(R) File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

05636203 EMBASE No: 1994041406
STK-1, the **human** homolog of Flk-2/Flt-3, is selectively expressed in CD34sup + **human** bone marrow cells and is involved in the proliferation of early progenitor/stem cells
Small D.; Levenstein M.; Kim E.; Carow C.; Amin S.; Rockwell P.; Witte L.; Burrow C.; Ratajczak M.Z.; Gewirtz A.M.; Civin C.I.
Department of Pediatrics, Oncology Center, Johns Hopkins Univ. Sch. of Medicine, 600 North Wolfe Street, Baltimore, MD 21287 United States
Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1994, 91/2 (459-463)
CODEN: PNASA ISSN: 0027-8424
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

13/3/19 (Item 1 from file: 399)
DIALOG(R) File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

134085068 CA: 134(7)85068m JOURNAL
Murine stromal cell line HESS-5 maintains reconstituting ability of ex vivo-generated hematopoietic stem cells from human bone marrow and cytokine-mobilized peripheral blood
AUTHOR(S): Shimakura, Yasuhito; Kawada, Hiroshi; Ando, Kiyoshi; Sato, Tadayuki; Nakamura, Yoshihiko; Tsuji, Takashi; Kato, Shunichi; Hotta, Tomomitsu
LOCATION: Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193
JOURNAL: Stem Cells (Miamisburg, Ohio) DATE: 2000 VOLUME: 18 NUMBER: 3
PAGES: 183-189 CODEN: STCEEJ ISSN: 1066-5099 LANGUAGE: English
PUBLISHER: AlphaMed Press

13/3/20 (Item 2 from file: 399)
DIALOG(R) File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

131196608 CA: 131(15)196608v JOURNAL
Ex vivo expansion of human cord blood stem cells and its application to gene therapy
AUTHOR(S): Ando, Kiyoshi; Kawada, Hiroshi; Shimizu, Takashi; Tsuji, Takashi; Nakamura, Yoshihiko; Kimura, Minoru; Miyatake, Hiroko; Shimakura, Yasuhito; Inokuchi, Sadaki; Kato, Shunichi; Hotta, Tomomitsu
LOCATION: Research Center for Genetic Engineering and Cell Transplantation, Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193
JOURNAL: Int. Congr. Ser. DATE: 1999 VOLUME: 1175 NUMBER: Tissue Engineering for Therapeutic Use 3 PAGES: 1-14 CODEN: EXMDA4 ISSN: 0531-5131 LANGUAGE: English PUBLISHER: Elsevier Science B.V.
?

Set	Items	Description
S1	279	FLK(W)2
S2	43	FLK(W)2(10N) (HUMAN)
S3	24	RD S2 (unique items)
S4	3794	FLT3
S5	20	S4 AND PY<1993
S6	7	RD S5 (unique items)
S7	279	FLK(W)2
S8	4	S7 AND PY<1993
S9	1	RD S8 (unique items)
S10	9	S7 AND REVIEW?
S11	9	RD S10 (unique items)
S12	37	S7 AND (HUMAN AND MURINE)
S13	20	RD S12 (unique items)
?		

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:53:00 ; Search time 34.4826 Seconds
(without alignments)
2765.606 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQRSDRLLLVLSV.....RGLRAQSPQVQVIHRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 73.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5264	100.0	992	A39931	protein-tyrosine k
2	5102	96.9	1000	S18827	Flt3 protein - mou
3	4408.5	83.7	993	A36873	protein-tyrosine k
4	1258.5	23.9	980	TVCTMD	macrophage colony-
5	1247	23.7	941	TVMTVD	protein-tyrosine k
6	1232.5	23.4	978	A49814	protein-tyrosine k
7	1223	23.2	975	TVMSKT	protein-tyrosine k
8	1221.5	23.2	972	TVHUMD	macrophage colony-
9	1220	23.2	954	I51703	c-kit-related kina
10	1215	23.1	977	I45877	protein-tyrosine k
11	1210	23.0	978	S16385	macrophage colony-
12	1198.5	22.8	976	TVMSMD	macrophage colony-
13	1195	22.7	976	TVHUKT	protein-tyrosine k
14	1188.5	22.6	975	T30816	macrophage colony-
15	1181	22.4	960	JN0677	protein-tyrosine k
16	1157.5	22.0	1088	1PFRGA	platelet-derived g
17	1152.5	21.9	1089	1PFHUGA	platelet-derived g
18	1132	21.5	1087	I51552	platelet-derived g
19	1123.5	21.3	1089	I53727	platelet-derived g
20	1098	20.9	1098	1PFMSRB	platelet-derived g
21	1078	20.5	1106	1PFHUGB	platelet-derived g
22	1060	20.1	1048	T30815	platelet-derived g
23	998.5	19.0	1338	S09982	protein-tyrosine k
24	984.5	18.7	1336	I60598	Fit-1 tyrosine kin
25	983.5	18.7	1333	I78875	receptor tyrosine
26	980	18.6	1379	JC4954	vascular endotheli
27	970	18.4	1330	I549010	embryonic receptor
28	967.5	18.4	790	1FOWH2	gag-kit polyprotei
29	965	18.3	1348	I551656	vascular endotheli

ALIGNMENTS

RESULT 1

A39931

protein-tyrosine kinase (EC 2.7.1.112) flk-2, hematopoietic - mouse

C;Species: Mus musculus (house mouse)

C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 04-Feb-2000

C;Accession: A39931

R;Matthews, W.; Jordan, C.T.; Wiegand, G.W.; Pardoll, D.; Lemischka, I.R.

Cell 65, 1143-1152, 1991

A;Title: A receptor tyrosine kinase specific to hematopoietic stem and progenitor cel:

A;Reference number: A39931; MUID:91292518; PMID:1648448

A;Accession: A39931

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-992 <MAT>

C;Cross-references: GB:M64689; NID:g193327; PIDN:AAA37634.1; PID:g193328

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein

F;609-953/Domain: protein kinase homology <KIN>

F;617-625/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 5264; DB 2; Length 992;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRLLLVLSVMILETVTNQDLPVVKVLISHENNGSSACKPSSYRMVRS 60

Db 1 MRALAQRSDRLLLVLSVMILETVTNQDLPVVKVLISHENNGSSACKPSSYRMVRS 60

Qy 61 PEDLQCTPRROSEGTVEAATVEAESGSITLQVQLATPGDLSCLMVFVKHSLGCQPHFD 120

Db 61 PEDLQCTPRROSEGTVEAATVEAESGSITLQVQLATPGDLSCLMVFVKHSLGCQPHFD 120

Qy 121 LQNRGIVSMALINVTETQAGEYLLHIQSERANYTVLFTVNRDITQYLVRPFRQWENQ 180

Db 121 LQNRGIVSMALINVTETQAGEYLLHIQSERANYTVLFTVNRDITQYLVRPFRQWENQ 180

Qy 181 DALLCISGVPETVEVWLCSSHRESCKEEGPAVVRKEKVLHELFGTDIRCCARNALGR 240

Db 181 DALLCISGVPETVEVWLCSSHRESCKEEGPAVVRKEKVLHELFGTDIRCCARNALGR 240

Qy 241 ECTKLTFTDLNQAPOSTLPQLFKVGEPLIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300

Db 241 ECTKLTFTDLNQAPOSTLPQLFKVGEPLIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300

Qy 301 MSTYSTNRTMIRILIAFVSSVGRNDTGYTTCSSSKHPQSALVTILEKGFINATSSQEEY 360

Db 301 MSTYSTNRTMIRILIAFVSSVGRNDTGYTTCSSSKHPQSALVTILEKGFINATSSQEEY 360

Qy 361 BIDPYKEKCFSVRFKAYPRIRCTWIFPSQAFCEQGLEGGYSISKFCDHKNKPGVIFY 420

Db 361 BIDPYKEKCFSVRFKAYPRIRCTWIFPSQAFCEQGLEGGYSISKFCDHKNKPGVIFY 420

QY 421 AENDDAQFTKMTFTLNIRKPKQVLNANASQSCSDGYPLPSWTWKCDKSPNCTEIEIP 480
DB 421 AENDDAQFTKMTFTLNIRKPKQVLNANASQSCSDGYPLPSWTWKCDKSPNCTEIEIP 480
QY 481 EGVNKKANRKFQGVQWSSSTLNMSBAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540
DB 481 EGVNKKANRKFQGVQWSSSTLNMSBAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540
QY 541 DNISFYATTIGLCPFFIVLVILVILCHYKQFRYESQLOQMIOVTPGLDNEYFYVDFRDYEY 600
DB 541 DNISFYATTIGLCPFFIVLVILVILCHYKQFRYESQLOQMIOVTPGLDNEYFYVDFRDYEY 600
QY 601 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISKGTGVSIOQAVKMLKEKADSCKEALM 660
DB 601 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISKGTGVSIOQAVKMLKEKADSCKEALM 660
QY 661 SELKMMTHLGHNDINVLNLAGCTLSGPVYLIFCYCCYGDLLNLYRSKREKPHRTWTEIFK 720
DB 661 SELKMMTHLGHNDINVLNLAGCTLSGPVYLIFCYCCYGDLLNLYRSKREKPHRTWTEIFK 720
QY 721 EHNFSYPTFOAHSNSMPCSRREVQHPDQLDLSGFGNGSIHSEDEIEYENQKRLAESEE 780
DB 721 EHNFSYPTFOAHSNSMPCSRREVQHPDQLDLSGFGNGSIHSEDEIEYENQKRLAESEE 780
QY 781 EDNLNLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
DB 781 EDNLNLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVVDAN 900
DB 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVVDAN 900
QY 901 FYKLIOGKFMQEPFYATGEGIYFVMSQWAFDSKRPSPNLTSLFGCLQAEAEACIRT 960
DB 901 FYKLIOGKFMQEPFYATGEGIYFVMSQWAFDSKRPSPNLTSLFGCLQAEAEACIRT 960
QY 961 SIHLPKQAAPQORGGLRAQSPQOVKIHRS 992
DB 961 SIHLPKQAAPQORGGLRAQSPQOVKIHRS 992
RESULT 2
Flt3 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
C:Accession: S18827
R:Rosnet, O.; Marchetto, S.; deLapeyriere, O.; Birnbaum, D.
A:Title: Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the PDGFR/CSF1 Oncogene 6, 1641-1650, 1991
A:Reference number: S18827; MUID:92019834; PMID:1656368
A:Accession: S18827
A:Molecule type: mRNA
A:Residues: 1-1000 <ROS>
A:Cross-references: EMBL:X59398; NID:G50978; PIDN:CAA42041.1; PID:G50979
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C:Keywords: Atf
F:609-953/Domain: protein kinase homology <KIN>
F:617-625/Region: protein kinase ATP-binding motif
Query Match 96.7%; Score 5102; DB 2; Length 1000;
Best Local Similarity 96.7%; Pred. No. 9.2e-254;
Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;
QY 1 MRALAQSDRRLLLVLSWMILETVNQDLPIVKVLI SHENNGSAGKPPSSYRMVGRS 60
DB 1 MRALAQSDRRLLLVLSWMILETVNQDLPIVKVLI SHENNGSAGKPPSSYRMVGRS 60
QY 61 PEDLOCTPRQSGTYEATVEVAESGTSITQVOLTATPGDLSCLWVFKHSSLCQCPHFD 120
DB 61 PEDLOCTPRQSGTYEATVEVAESGTSITQVOLTATPGDLSCLWVFKHSSLCQCPHFD 120
QY 121 LQNGSIVSMALNVTTQAGEYLLHIQSEAAANYTLVFTNVVRDTQLYVLRPYFRKMENQ 180

DB 121 LQNGSIVSMALNVTTQAGEYLLHIQSEAAANYTLVFTNVVRDTQLYVLRPYFRKMENQ 180
QY 181 DALLCISEGPEPTVEVWLCSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISEGPEPTVEVWLCSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLFITDLNQAPQSTLPQLFLKVGEBPLWIRCKAIHVNHGFGLTWELEDKALBEGSYFE 300
DB 241 ESKYLFITDLNQAPQSTLPQLFLKVGEBPLWIRCKAIHVNHGFGLTWELEDKALBEGSYFE 300
QY 301 MSTYSTNRTMIRILLAPVSSVGRNDTCYTCSSSKHPQSALVTILEKGFINATSSQBEY 360
DB 301 MSTYSTNRTMIRILLAPVSSVGRNDTCYTCSSSKHPQSALVTILEKGFINATSSQBEY 360
QY 361 EIDPYEKFCSPVRKAYPRIRCTWIFSOASFPCEORGLDGYISKFCDHKNKPGEYIFY 420
DB 361 EIDPYEKFCSPVRKAYPRIRCTWIFSOASFPCEORGLDGYISKFCDHKNKPGEYIFY 420
QY 421 AENDDAQFTKMTFTLNIRKPKQVLNANASQSCSDGYPLPSWTWKCDKSPNCTEIEIP 480
DB 421 AENDDAQFTKMTFTLNIRKPKQVLNANASQSCSDGYPLPSWTWKCDKSPNCTEIEIP 480
QY 481 EGVNKKANRKFQGVQWSSSTLNMSBAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540
DB 481 EGVNKKANRKFQGVQWSSSTLNMSBAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540
QY 541 DNISFYATTIGLCPFFIVLVILVILCHYKQFRYESQLOQMIOVTPGLDNEYFYVDFRDYEY 600
DB 541 DNISFYATTIGLCPFFIVLVILVILCHYKQFRYESQLOQMIOVTPGLDNEYFYVDFRDYEY 600
QY 601 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISKGTGVSIOQAVKMLKEKADSCKEALM 660
DB 601 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISKGTGVSIOQAVKMLKEKADSCKEALM 660
QY 661 SELKMMTHLGHNDINVLNLAGCTLSGPVYLIFCYCCYGDLLNLYRSKREKPHRTWTEIFK 720
DB 661 SELKMMTHLGHNDINVLNLAGCTLSGPVYLIFCYCCYGDLLNLYRSKREKPHRTWTEIFK 720
QY 721 EHNFSYPTFOAHSNSMPCSRREVQHPDQLDLSGFGNGSIHSEDEIEYENQKRLAESEE 780
DB 721 EHNFSYPTFOAHSNSMPCSRREVQHPDQLDLSGFGNGSIHSEDEIEYENQKRLAESEE 780
QY 781 EDNLNLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
DB 781 EDNLNLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVVDAN 900
DB 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVVDAN 900
QY 901 FYKLIOGKFMQEPFYATGEGIYFVMSQWAFDSKRPSPNLTSLFGCLQAEAEACIRT 960
DB 901 FYKLIOGKFMQEPFYATGEGIYFVMSQWAFDSKRPSPNLTSLFGCLQAEAEACIRT 960
QY 961 -----SIHLPKQAAPQORGGLRAQSPQOVKIHRS 992
DB 961 MGNVPEHPHSIYQNRRLPSREAGS-EPPSPQAQVQKIHRS 1000
RESULT 3
A36873
protein-tyrosine kinase (EC 2.7.1.112) STK-1 precursor - human
N:Alternate names: stem cell tyrosine kinase 1
C:Species: Homo sapiens (man)
C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 04-Feb-2000
C:Accession: A36873
R:Small, D.; Levenstein, M.; Kim, E.; Carow, C.; Amin, S.; Rockwell, P.; Witte, L.; Bu
Proc. Natl. Acad. Sci. U.S.A. 91, 459-463, 1994
A:Title: STK-1, the human homolog of Flk-2/Fit-3, is selectively expressed in CD34(+) A;Reference number: A36873; MUID:94119906; PMID:7507245
A:Accession: A36873
A>Status: preliminary


```

Db 282 NAWGNHSAVMFVRVESAYLNLTSEQSLLOEVTVEKVDLQVKVEAYPGLESFNNWTYLG 341
Qy 386 FSQASFPCEQGLEDDGYSISKPCD----HNKPGGEYFYAENDDAQTKMFTLNIRKKPQ 441
Db 342 FSDYQDKLDFVTIKDTYRTYSTLSPLRKKSEAGRYSLARNAGGQNALTELTIRYPPE 401
Qy 442 VLANASASQAS----CSSDGYPLPSWTWKCKSDKSPNCTEE--IPGVMNKKANRKYVG 494
Db 402 VRVTMTLINGSDTLLCEASGYQPSVTVQCRSHTRDCESAGLVLEDHSHSEVLVSQVPPH 461
Qy 495 QWSSSTLNMSSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFFIQDNISFYATIGLC-- 552
Db 462 EVIVHSLAIGTLEHNRYECRAFNSVGNSSQTFWPISIGAHTPLPDELFTPVLLTQMS 521
Qy 553 -LPFIVVLVILCHYKQKQRYESQLOMQVGTGLDNEFYFVDFRDYEDLKWEPREN 611
Db 522 IMALLLLLLLLLYKQKPKYQVRWKIIE--SYEGNSYTFIDPTQLPYNEKWEFPPNNL 579
Qy 612 EFGKVLGSGAFGRVMNATAYGISKTGVSIOAVKMLKEKADSCKEALMSLKMTHLGH 671
Db 580 QFGKTLGAGAFGVKVEATAEGLKEDAVLVKAVKMLKSTAHADKEALMSLKMTHLGH 639
Qy 672 HDNIVNLLGACTLSGPPVLYIFCYCYGDLNLYRSKRE-----KF 711
Db 640 HENIVNLLGACTHGGPVLVITEYCCYGDLLNLRQAEMALGPSLSVGQDPEAGAGYKNI 699
Qy 712 HRTWTEIFKEHNFSSYPTFOAHNSNMPGSRREVQLHPDLQSLGFGNSIHSEDEIEYEN 771
Db 700 HLEKYYVRDRDGSF-----SQGVDTYVEMRPVSTSSNDSFSEEDL---- 740
Qy 772 QKRLAEEDLNLVTFEDLLCFAYQVAKGMEFEKFCVHRDLAARNVLVTHGKVKVIC 831
Db 741 -----GKEDGRPLERDLHFSQVQAQMAFLASKNCIHRDVAARNVLLTSRVAKIG 793
Qy 832 DFLGARDILSDSSVYVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNP 891
Db 794 DFLGARDIMDSNYIVKGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNP 853
Qy 892 YPGIPVDANFYKLIQSGFKMEQPYATEGIFYVMSQWAFDSRKPSPNLTSLFGCOLA 951
Db 854 YPGILVNSFYKLVKQGYQAQAFAPAKNIYSINQACWALEFTRPTFQQICSL--QKQ 911
Qy 952 EABEACIRTSIHLPKQAAPQ-----RGLRAQSPQKQ 984
Db 912 AQEDRRVNTNLPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 953

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RESULT 5
TVNMVD
C:Species: feline sarcoma virus
A:Note: host Felis sp. (cat)
C:Date: 27-Nov-1985 #sequence_revision 31-Dec-1991 #text_change 13-Jun-1997
C:Accession: A00654
R:Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 85-89, 1984.
A:Title: Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected homology with the src gene.
A:Reference number: A00654; MUID:84119469; PMID:6582485
A:Accession: A00654
A:Molecule type: DNA
A:Residues: 1-941 <HAM>
C:Comment: This protein is synthesized as a gag-fms polyprotein.
C:Genetics:
A:Gene: fms
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
otein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-941/Product: protein-tyrosine kinase fms #status predicted <MAT>
F;24-509/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>

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F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-484/Domain: immunoglobulin homology <IMM5>
F;510-534/Domain: transmembrane #status predicted <TMM>
F;535-941/Domain: intracellular #status predicted <INT>
F;577-915/Domain: protein kinase ATP-binding motif
F;585-593/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted
F;45,73,94,153,275,286,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent)
F;613,630,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

```

```

Query Match 23.7% Score 1247; DB 1; Length 941;
Best Local Similarity 33.2%; Pred. No. 1.6e-56;
Matches 325; Conservative 162; Mismatches 347; Indels 144; Gaps 31;

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```

Qy 75 TVYEAAATVEAESSITLOVLATPGDLSCL-----W-----VFKHSSLCQPHFLQNRG 125
Db 13 TAMHAQGVPIQPSGPELVVEPTVTTLRCVGNCSVEWDGPISPHNLNLDLPSSI---- 68
Qy 126 IVSMAILNVTQTAGEYLLHI-----QSERANYTLFTVNVDRDTQLYVL--RRPY----- 173
Db 69 ---LTTNATFQNTGT--HCTEPCNPRGNAT1-----HLVYKDPARPWKVLAQE 114
Qy 174 FRKMNQDALL-CISEGVPEPTVEWLVLCSSHRESCKEKGPAVVRKEEVLHFLFGTDI-- 230
Db 115 VTVLEGQDALLPCL--LTDPALE-----AGSVLRVRGRPVLRQTNYSFSPWHGFTIHK 166
Qy 231 -----RCCARNALGRECTKL-----FTIDLNAQPOSTL--POLFLKV--GEPLWIRCK 274
Db 167 AKFTIENHYQCSAR--VDGRTVTSMGIMLVKQKDISGSPATLLEPAELVRIOGEAAQIVCS 225
Qy 275 AIHVNHGFGLTWELEDKALEBGSYFEMSTYNTNRMILLAFVSSVGRNDNTGYTCSSS 334
Db 226 ASNDVNPFLSRHGDTKL-----TISQGDPHDNRVQ--KVLTLNLDHVSFQDAGNVSCTAT 281
Qy 335 K---HPQSALVTILEKGFINATSSQE--EYEDIPYEFKFCFSVRFKAYPRIC--TWI---- 385
Db 282 NAWGNHSAVMFVRVESAYSNLTSEQSLLOEVTVEKVDLQVKVEAYPGLESFNNWTYLG 341
Qy 386 FSQASFPCEQGLEDDGYSISKPCD----HNKPGGEYFYAENDDAQTKMFTLNIRKKPQ 441
Db 342 FSDYQDKLDFVTIKDTYRTYSTLSPLRKKSEAGRYSLARNAGGQNALTELTIRYPPE 401
Qy 442 VLANASASQAS----CSSDGYPLPSWTWKCKSDKSPNCTEE--IPGVMNKKANRKYVG 494
Db 402 VRVTMTLINGSDTLLCEASGYQPSVTVQCRSHTRDCESAGLVLEDHSHSEVLVSQVPPH 461
Qy 495 QWSSSTLNMSSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFFIQDNISFYATIGLC-- 552
Db 462 EVIVHSLAIGTLEHNRYECRAFNSVGNSSQTFWPISIGAHTPLPDELFTPVLLTQMS 521
Qy 553 -LPFIVVLVILCHYKQKQRYESQLOMQVGTGLDNEFYFVDFRDYEDLKWEPREN 611
Db 522 IMALLLLLLLLLYKQKPKYQVRWKIIE--SYEGNSYTFIDPTQLPYNEKWEFPPNNL 579
Qy 612 EFGKVLGSGAFGRVMNATAYGISKTGVSIOAVKMLKEKADSCKEALMSLKMTHLGH 671
Db 580 QFGKTLGAGAFGVKVEATAEGLKEDAVLVKAVKMLKSTAHADKEALMSLKMTHLGH 639
Qy 672 HDNIVNLLGACTLSGPPVLYIFCYCYGDLNLYRSKRE-----KF 711
Db 640 HENIVNLLGACTHGGPVLVITEYCCYGDLLNLRQAEMALGPSLSVGQDPEAGAGYKNI 699
Qy 712 HRTWTEIFKEHNFSSYPTFOAHNSNMPGSRREVQLHPDLQSLGFGNSIHSEDEIEYEN 771
Db 700 HLEKYYVRDRDGSF-----SQGVDTYVEMRPVSTSSNDSFSEEDL---- 740
Qy 772 QKRLAEEDLNLVTFEDLLCFAYQVAKGMEFEKFCVHRDLAARNVLVTHGKVKVIC 831
Db 741 -----GKEDGRPLERDLHFSQVQAQMAFLASKNCIHRDVAARNVLLTSRVAKIG 793
Qy 832 DFLGARDILSDSSVYVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNP 891
Db 794 DFLGARDIMDSNYIVKGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNP 853
Qy 892 YPGIPVDANFYKLIQSGFKMEQPYATEGIFYVMSQWAFDSRKPSPNLTSLFGCOLA 951
Db 854 YPGILVNSFYKLVKQGYQAQAFAPAKNIYSINQACWALEFTRPTFQQICSL--QKQ 911
Qy 952 EABEACIRTSIHLPKQAAPQ-----RGLRAQSPQKQ 984
Db 912 AQEDRRVNTNLPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 953

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Db 794 DFLGARDIMDSNYIKGNARLPVKWAPESIFDCVYTVQSDVMSYGLLWEIFSLGNP 853
Qy 892 YPGIPVDANFYKLIQSGFKWQEPFYATEGYFYVMQSWAFDSKRSPFNLTSLFLGCOLA 951
Db 854 YPGILVNSRYKLVKQGYQMAQAFAPKNYISIMQACWALEPFRPTFQOICSL--OKQ 911
Qy 952 EABEACIRTSIHLPKQAA 969
Db 912 AQDRRVPNYTNLPSSSS 929
RESULT 6
A9814
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A49814; S49088
R:Tsujimura, T.; Hirota, S.; Nomura, S.; Niwa, Y.; Yamazaki, M.; Tono, T.; Morii, E.; Kikuchi, T.; Blood 78, 1942-1946, 1991
A>Title: Characterization of a mutant allele of rats: a 12-base deletion in tyrosine kinase
A:Reference number: A49814; PMID:92003944; PMID:1912577
A:Accession: A49814
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-978 <TSU>
A:Cross-references: GB:D12524; NID:G220707; PIDN:BAA02094.1; PID:G220708
R:Tsujimura, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.
A:Description: Two isoforms of rat c-kit receptor tyrosine kinase.
A:Reference number: S49088
A:Accession: S49088
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511,516-978 <TS>
A:Cross-references: EMBL:X62491; NID:G509135; PIDN:CAA44354.1; PID:G509136
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; phosphotransferase; tyrosine-specific protein kinase
F:129-188/Domain: immunoglobulin homology <IM>
F:589-932/Domain: protein kinase homology <KIN>
F:597-605/Region: protein kinase ATP-binding motif

Query Match 23.4%; Score 1232.5; DB 1; Length 978;
Best Local Similarity 32.2%; Pred. No. 9.2e-56;
Matches 323; Conservative 176; Mismatches 340; Indels 165; Gaps 37;

Qy 36 CVLISHENNGSAGKPSYRMVRGSPEDLOCTPRQSGTYVEAATVEAEGSITLQVQ 95
Db 12 CVLLVLLRGQTGTSQPSA-----SPGEPSPSTQPAQSELIVEAGD-TIRLT 57
Qy 96 LATPGDLSCLVFKHSLGCGPHFDLQNRGIVSMALNV-TETQAGEYLLHIQSERANYT 154
Db 58 CTDPAFVK-WTFE-----ILDVRIENKQSWIR-EKAEATH 92
Qy 155 VLFT-----VNRVD-TQLVYLRPFYFRKMNQDALLCISSEVPPTV-EWVLC 200
Db 93 GKTYCTGSGLSRSIYFVDPDPAVLFLVGLPLFGKENDALVRC---PLTDPQVSNVSLI 149
Qy 201 SSHRESC-----KEEGPAVVRKEKVLHFLGTDIRCARNALGRECTKLFTIDNQ 252
Db 150 ECDGKSLPTDLKFVNPBKAGTITKNVRAVHRLC---IRCAAQREGKWRSDKFTLVRA 206
Qy 253 A-----POSTLPQL--FLKVEPLWIRKALVNHVHGLTW-----ELEDKALEE 295
Db 207 AIKAIPVSVSPETSHLLKEGDTFTVICTIKDVSTVSDMMIKLPQPSKAQVKNRNSWHQ 266
Qy 296 GSYFEMSTYSTNRTMIRILLAFVSGNRDGTGYTCSSSKHPSQALVT---ILEKGFIN 352
Db 267 GDF-----NYERQETLT-----ISSARVDSGVFNCVANNFTGSGANVTTLKLVKEGFIN 316
Qy 353 --ATSQEEYEIDPYEKFCSVRFKAYPR-IRCTWIFSOASFQCEORGLE-----DGYSIS 405
Db 317 IFFVKNITVFTDG-ENVDLVVEFEAYKPEHQOIMYMRIT--PTNRGDEVKSDNQSN 373

Qy 406 KFCDH-----KNKPGEYIFYAENDDAQFTKMTFLNIRKQPVLV--NASASQACSSD 456
Db 374 RYVNELRLTRLKGTEGGTYTLVNSDVSAVTPDDVYVNTKPEILTYDLRMNLRQCVA 433
Qy 457 GYPLPSWTWKCKSDKSNCTEIEIPB-GVWNKAKRKVQGWQVSSSTLWMSBAGLLVKC 515
Db 434 GFPEPTIDWYFCTGAQRCTVPVPPVDVQIQNASVSPFGKLVQSSIDSVPFRHNGTVEC 493
Qy 516 CAYNSMGTSCTEFLNSPGPPFF-----IQDN-----ISFYATIGLCPLPFWLVIV 561
Db 494 KASNAVGS--SAFFN-----PAFKGNSKEQIOPHTLFTPLLIGFVVTAGL-----MGIIVM 543
Qy 562 LICHYKKQFRYESQLQMI-QVTGFLDNEYFYVDFRDYEDLKWEPFRENLEFGKVLGSG 620
Db 544 VLAYKYLQKPMYEQWKVBEING---NNYVVIDPTQLPYDHKWEFPRNRLSFGKTLGAG 600
Qy 621 AFGVMNATAYGISKTGVISIOVAVNMLKEKADSKCEKALMSSELKMTLGHHDNIVNLG 680
Db 601 AFGKVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSSELKVLVSLGNHMINVLG 660
Qy 681 ACTLSGPPVILIFYCCYCGDLNLYLSRKEKFRHTWTEIFKEHNFSSYPTFOAHSSNMPG 740
Db 661 ACTVGGPTLVITYCCYCGDLNLYLRKRKDSF--IFSKQEEQADAALYKNLLHSHKSSCDS 718
Qy 741 SREVLHPPLDQLSGFN-----GNSIHSEDEIEYENQKRLAEDEEDLNVLTFEDL 791
Db 719 SNEY-----MDMKGVSVVVTKTDKRSARIDSIERDVTVPAINEDDELALDL---EDL 770
Qy 792 LCFAYQVAKGMELEFKSCVHRDLAARNVLVTHGKVKICDPLGLADILSDSSVYVRGNA 851
Db 771 LSPSYQVAKGMFLASKNCIHRDLAARNILLTHGRTIKICDPLGLADIRNDSNYVVKGNA 830
Qy 852 RLPVKWAPESLFEIGYTIKSDVMSYGLLWEIFSLGVNYPGIPVDANFYKLIQSGFKM 911
Db 831 RLPVKWAPESIFNCVYTFESDVMSYGLFWELFSLGSPYGPMPVDSKFKMKKEGFRM 890
Qy 912 EQPYAYTEGIFYVMQSWAFDSKRSPFNLTSLFLGCOLAAEE 955
Db 891 LSPHAPAMYTEVMKTCWDADPLKRPTEKQVVLIEKQISDSSK 934
RESULT 7
TVMSKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - mouse
N:Alternate names: tyrosine kinase receptor C-kit
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 31-Mar-2000
C:Accession: S00474; B44876; I49596
R:Qiu, P.; Rav, P.; Brown, K.; Barker, P.E.; Jhanwar, S.; Ruddle, F.H.; Besmer, P.
EMBO J. 7, 1003-1011, 1988
A>Title: Primary structure of c-kit: relationship with the CSP-1/PDGF receptor kinase
A:Reference number: S00474; PMID:89296403; PMID:2456920
A:Accession: S00474
A:Molecule type: mRNA
A:Residues: 1-975 <QIU>
A:Cross-references: GB:Y00864; NID:G50423; PIDN:CAA68772.1; PID:G50424
R:Rossi, P.; Marziani, G.; Albanesi, C.; Charlesworth, A.; Geremia, R.; Sorrentino, V.
Dev. Biol. 152, 203-207, 1992
A>Title: A novel c-kit transcript, potentially encoding a truncated receptor, original
A:Reference number: A44876; PMID:92331813; PMID:1378413
A:Accession: B44876
A:Molecule type: DNA
A:Residues: 771-814 <ROS>
A>Note: sequence extracted from NCI backbone (NCBIN:108837, NCBI:108840)
R:Yasuda, H.; Galli, S.J.; Geisler, E.N.
Biochem. Biophys. Res. Commun. 191, 893-901, 1993
A>Title: Cloning and functional analysis of the mouse c-kit promoter.
A:Reference number: 149596; PMID:93221533; PMID:7682073
A:Accession: I49596
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>

A:Accession: I59083
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 874-972 <RE3>
 A:Cross-references: GB:M1193; NID:gl82521; PIDN:AAA35834.1; PID:gl82522
 R:Rienhuus, A.W.; Bunn, H.F.; Turner, P.H.; Gopal, T.V.; Naeh, W.G.; O'Brien, S.
 Cell 42, 421-428, 1985
 A:Title: Expression of the human c-fms proto-oncogene in hematopoietic cells and its del
 A:Reference number: I52772; MUID:85282599; PMID:4028159
 A:Accession: I52772
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-295 <RE4>
 A:Cross-references: GB:M11067; NID:gl82674; PIDN:AAA35848.1; PID:g442423
 C:Genetics:
 A:Gene: GDB:CSF1R; FMS
 A:Cross-references: GDB:120600; OMIM:164770
 A:Map position: 5q33.2-5q33.3
 A:Introns: 17/1; 103/1; 198/1; 243/3; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1; 6
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
 C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
 fic protein kinase
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-972/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
 F:24-512/Domain: extracellular #status predicted <EXT>
 F:35-86/Domain: immunoglobulin homology <IMM1>
 F:120-179/Domain: immunoglobulin homology <IMM2>
 F:217-280/Domain: immunoglobulin homology <IMM3>
 F:316-383/Domain: immunoglobulin homology <IMM4>
 F:412-487/Domain: immunoglobulin homology <IMM5>
 F:513-537/Domain: transmembrane #status predicted <TM>
 F:538-972/Domain: intracellular #status predicted <INT>
 F:580-917/Domain: protein kinase homology <KIN>
 F:588-596/Region: protein kinase ATP-binding motif
 F:42-84,127-177,224-278,419-485/disulfide bonds: #status predicted
 F:45,73,153,240,275,302,335,412,428,480/Binding site: carbohydrate (Aen) (covalent)
 F:616,633,778/Active site: Lys, Glu, Asp #status predicted
 F:783,796/Binding site: magnesium (Aen, Asp) #status predicted

Query Match 23.2%; Score 1221.5; DB 1; Length 972;
 Best Local Similarity 32.0%; Pred. No. 3.3e-55;
 Matches 330; Conservative 152; Mismatches 331; Indels 201; Gaps 33;

QY 76 VYBAATVEAESGSIITQVQLATPGDLSCVWFKHSLGQOPHDLQNRGIVSMAIL--- 132
 DB 22 VIEPSVPELVKCAT--VTLRCVNGSVWDGPPS-----PHTLYSDG--SSSILSTN 72
 QY 133 NVTTQAGEYLLHIQSRANYTVLFTVNVVDTQLYVLRPY-----FRKMNODALL-C 185
 DB 73 NATFQNTGTVRCTEPGDPLGSAAILHYVKDP-----ARPWNVLAQEVVVFEDQALLPC 127
 QY 186 ISEGVPEPTVEWVLCSSHRSCKEKGPAVVRKEK-----VLHE---LP 226
 DB 128 L---LTDPLV-----EAGVSLVRVRGRPLMRHTNYSFSPWGHFTIHRAFIQ 171
 QY 227 GTDIRCARNALGRECTKLTIDLNOAPOSTLP-----OLFLKVGCEPLWIRCKAI 276
 DB 172 SDQYQCSALMG-GR---KWSISIRLKVKQVIFPGPPALTLPABLVRGEEAAQIVCSAS 227
 QY 277 HVNHGFLGTWELEDKALEEGSYFEMSTYSTNRTWIRILLAFVSSVGRNDTGYYTCSS-- 334
 DB 228 SDVNVFDFVLQHNKTL--AIPOQSDFNHNRQ-KVLTNLNDQVDFQHAGNYSVCVASNV 283
 QY 335 --KHPSQALVTILEKGFNATSQE-EYELDPYKFCFVRFKAYPRIR-CTWIFQAS 390
 DB 284 QGKH-STSMFPRVVEAYLNLSSQNLQIEVTVGEGNLKVMVEAYFGLQFNNTY----- 338
 QY 391 FPCQRLGEDGYSISKFCDHKNKP-----GEVIFVAEN 423
 DB 339 -----LGPSPDHOPEPEPLANATTKOTYRHTFTLSLPLKPSSEAGRYSFILARN 385
 QY 424 DDAQFTKNFTINIRKPKQV-----LANASASQACSSDGYPLPSTWTKKCDKSPNCTEE 478

DB 386 PGGWRAITFELTLRYPPPEVSVIWTFFINGSGT-LICAASGYPPQPNVTLQCSGHTDRCD 444
 QY 479 IPEGVWN---KKANRKVFGQWVSSSTLNMSSEAGLLVKCCAYNSMGTSCTETFLNSPG 534
 DB 445 QVLQVWDDPYPELVLSQEPFHKTIVTQSLLTVETLEHNTYECRAHNSVGSWAFIPISAG 504
 QY 535 PFFPIQNISFYATIGLC---LPIVVVLVILCHIKYKQFPYESQLOMIQVTPGLDNEFF 591
 DB 505 ATHPPDEFLTPVAVACMSIMALLLLLLLYLKQPKYQVRWKIIE--SYEGNSYT 562
 QY 592 YVDPDYEDLKWFEFFRENLEFGKVLGSGAGRVNMTATYGIKGTGVSIQVAVKMLKEKA 651
 DB 563 FIDPTQLPYNEKEFFPPNNLQFGKTLGAGAFKGVVEATAFGLGKEDAVLKVAVKMLKSTA 622
 QY 652 DSEKEALMSSELKMTMHLGHHDNIVNLGACTLSPVYVLIFFEYCYGDLNLYLRSKREKF 711
 DB 623 HADEKEALMSSELKMTMHLGHHDNIVNLGACTHGGPVLVITEYCYGDLNLYLRSKREKF 680
 QY 712 HRTWTEIFKHNFSYPTFOAHNSNMPGSGREVOLHPLDQLDLSGFGNMSIHSDE---- 766
 DB 681 -----AMLGP---SLSPQDPEGGVDYKNIHLEKRYVRD 712
 QY 767 -----LEYENQKELAE--EEDLNVLTFEDLLCFAYOVAKGMEFLSPK 808
 DB 713 SGFSSQGVDTYVEMRPYSTSNDOSFSDLDKEDGRPLELRLDLHFSQVAGMAFLASK 772
 QY 809 SCVRDLAARNVLTHGVKVKICDFGLARDILSDSSVYVRGNARLPVKWMAPESEFEGY 868
 DB 773 NCHRDVAARNVLTNGHVAKIGDFGLARDIMDNSYIVKGNARLPVKWMAPESEFDCVY 832
 QY 869 TIKSDVMSYGILLWEIFSLGPNYPGIPVDANFYKLIQSGFKMEQPPFYATEGIYFVMQSC 928
 DB 833 TVQSDVMSYGILLWEIFSLGPNYPGILVNSKFYKLVKDYQMAQPAFAPKNIYSIMQAC 892
 QY 929 WAFDRSRKRPFPNLTSLFLGCOLAERACITSTHLPKQAAPOQRGGLRAQSPQ 982
 DB 893 WALEPHTHRTPTQQICSLF--QEQAQEDRRERDYNLFPSS---RSGSGSSSSE 941

RESULT 9

I51703
 c-kit-related kinase 1 (XKRk1) - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
 C:Accession: I51703
 R:Baker, C.V.; Sharpe, C.R.; Torpey, N.P.; Heasman, J.; Wylie, C.C.
 Mech. Dev. 50, 217-228, 1995
 A:Title: A Xenopus c-kit-related receptor tyrosine kinase expressed in migrating stem
 A:Reference number: I51703; MUID:95344996; PMID:7619732
 A:Accession: I51703
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-954 <BAK>
 A:Cross-references: EMBL:Z48770; NID:g763033; PIDN:CAA88688.1; PID:g763034
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolo
 C:Keywords: Atp
 F:575-915/Domain: protein kinase homology <KIN>
 F:583-591/Region: protein kinase ATP-binding motif

Query Match 23.2%; Score 1220; DB 2; Length 954;
 Best Local Similarity 32.0%; Pred. No. 3.9e-55;
 Matches 315; Conservative 160; Mismatches 321; Indels 188; Gaps 35;

QY 77 YEATVEAESGSIITQVQLATPGDLSC-----LWVFKHSLGQOPHDLQNRGIVSMA 130
 DB 15 YTGDAVPKINDGEDRVTVNVGDKVSLCERDAHLVTLAFQKSLMKKPR-DLKSRLP---- 68
 QY 131 ILNVET-----QAGEYLLHIQSRANYTVLFTVNVVDTQLYVLRPRYFRKME 178
 DB 69 -LNNSETDQFVILKADLRHIGRYICTWTQNTSV--SLFVKDPAFPFLDIPFDVTE 125
 QY 179 NODAL-LCISGEVPEPTVEWVLCSSHRSCKEKGPAVVRKEKVLHLEFGTDIRC----- 232

Db 126 GADTVGMPF---TDPMDIAI-----EK- -DGSPLPE-----NFTFTDIEAGITIK 169
Qy 233 -----CARNALGR-ECTKLTFTIDLNOAQSTLPOLEL-----KVEPLWIRC 273
Db 170 TVOLAFDSCVCGNKGSTGKSTSTSIHVKKPKK-VPTVFLSKSRQLVKTGEPEVTC 228
Qy 274 KAIHVNHGFLTW-ELEDKALEGSEFENSTYSTRMTIRILLAFVSSVGRNDTGYTCS 332
Db 229 AVLDFSTVKAQWLDVKEGVTQANFRSSNVFSYNLTLS-----DGVPSERFTTCQ 282
Qy 333 SSKHPSQ---SALVTILEKGFINATSOE-EYEIDPYEKFCFSVRKAYPR-IRCTWIFS 387
Db 283 AENAIGQVNAITFLDIVGVNLTVALENTTISVAGNDLVKLVYDAYPHPDGVMYTF 342
Qy 388 QASFPCEQRLGEGYSIKFCDHKN-----KPEYIFYAENDDAQTKWF 432
Db 343 NETL-----LNTSHYVATK---DEGNRYVSELHLIRLKGTEKGVYFTYTNSSDDASVSF 396
Qy 433 TLRIRKPOVLANASQAS--CSDGYPPLSWTKKCDKSPNCTEEIEPEGVNNKK--A 488
Db 397 NIOVKTRPEILIAERTSEGTLCQVATGFPVPAIOWYFCPSGEORCTDYPLSPVNEKFIQ 456
Qy 489 NRKVFQWSSSTLANSEAGKGLLVKCCAYNSMGTS-----CETIFLNSPGP 535
Db 457 ENSSLGRIVVESTIDVNDLKNKGTVCVASNEVESAYSVFPAIKEKLRHTLTFT----- 511
Qy 536 FPIQDNISFYATIGLCLPIVVLIVLICHYKKQRYESOLQMI-QVTGPLDNEYFYVD 594
Db 512 -PLL---IGFIAAGL---MCTAVAVLMYKYLQKPKYEIQWVBEING---NNYVYID 560
Qy 595 FRDYEYDLKWEFPRENLEFGKVLGSGAFGRVMNATAYGSKTGVSIQVAVMLKEKADSC 654
Db 561 PTQLPVDNKNWEPFRDLFCGKILKAGAFKGVVEATAYGLLKEDSRITVAVKMLKPSAHT 620
Qy 655 EKPALMSLQWTHLGHNDINVLNLAGACTLSGPVYLIFCYCCYDGLNLYRSKREKPHRT 714
Db 621 EREALMSLVLYLGHKHNVLNLAGACTVGGPTLVITEYCCYDGLNLYLRKRDSP--- 677
Qy 715 WTIFPKHNPSSYPTQAMSNSSMPGSRVOLHPPDLQSLGFGNSHSEDEIEYENQK- 773
Db 678 -----ICPKPEDNS-----EAALYKYL-----LNTRDMGCEGMSYIDMKP 713
Qy 774 -----RLAEEEEEDLNLTFTDLCFAYQVAKGMEFLFKSC 810
Db 714 AVSYVVPKTKDRSGSGFGDQDVSVSIPEDDL-ALDTEDLNFSQVAGMFLASKNC 772
Qy 811 VHRDLAARNVLVTHGKVVKICDFGLARDILSDSSYVVRGNARLPVKWMAPESEFEGYTI 870
Db 773 IHRDLAARNILLTHGRITTKICDFGLARDIRNDSYVVKGNARLPVKWMAPESEFHCYVTF 832
Qy 871 KSDVWSYGILLWEIFSLGVNYPYFGIPVDANFYKLIQSGFKMEOPFYATEGIYFVMSQWA 930
Db 833 ESDVWSYGILLWEIFSLGSPYPRIPVDSEFKYKIKDGYRMSPECAPLEMYEIMRSCWN 892
Qy 931 FDKRPSFNLTSFLGCOLAAE 954
Db 893 SDPLKRTFKQIVQVMEQQLSDSK 916

RESULT 10
145877

protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - aurochs

C:Species: Bos primigenius (aurochs)

C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Apr-2000

C:Accession: I45877

R:Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.

Gene 141, 305-306, 1994

A:Title: Sequence of a bovine c-kit proto-oncogene cDNA.

A:Reference number: I45877; MUID:94215924; PMID:7512939

A:Accession: I45877

A>Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-977 <KUB>

A:Cross-references: GB:D16680; NID:9516659; PIDN:BAA04084.1; PID:g516660
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolog
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:329-395/Domain: immunoglobulin homology <IMM>
F:588-932/Domain: protein kinase homology <KIN>

Query Match 23.1%; Score 1215; DB 2; Length 977;
Best Local Similarity 32.8%; Pred. No. 7.2e-55;
Matches 304; Conservative 141; Mismatches 298; Indels 184; Gaps 28;
Qy 134 VTE-----TQAGEYLLHIQSERANYTLFTVNRDQ-LYVLRPPYFRMENQDALLCI-- 186
Db 83 ITEKAEATNTGNTYC---TNKGGLSSSIYVVRDPEKFLIDLPLYGKEENDTLVRCPLT 139
Qy 187 -----SEGVEP-TVEVWLCSSHRESCKEKPAPVRKEEVLHFGTDIRC-- 232
Db 140 DPEVTNVLTCGSGKPLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLH 185
Qy 233 CARNALGRE-CTKLTFTIDLNOAQPS-----TLPLQLFKVGEPLWIRCATHVNHGFLT 285
Db 186 CSANQRGKSMLSKKFTLKVPAAIKAVPVSVSKTSYLLREGEBAFVTCLIKDVSSVSDSM 245
Qy 286 WELEDKALEGSEFENSTYSTRMTIRILLAFVSSVGRNDTGYTCSKSPHPSOALVTI 345
Db 246 WIKENSQOTKATKKNSHQGFYSYLRQERLTITISSARVNDSGVFEMCYANNTFGSANVT 305
Qy 346 LE---KGFINA-TSSQEEYEIDPYEKFCFSVRKAYPR-IRCTWIFSQASFPCEQRLG 400
Db 306 LEVVDGKFINIFPMNTTVFVNDGENVDLVVEYBAYPKPVHROWIYMNRT----- 355
Qy 401 GYSISKPCDHK-----NKPGYIFYAENDDAQTKMFTLINIRKK 439
Db 356 --STDKWDYDPKSESNIRYVNEHLHLRLKGTGGYTFHVSNSDVNSSTFVNVYNTK 413
Qy 440 PQVLANASA--SOACSSSDGYPLPSWTWKCKSDKSPNCTEEI-PEGVNNKCANRKVFQW 496
Db 414 PEILTHDRLVNGMLQCVAAAGFPETIDWYFCPGTEQRCSPVGPVDPVQIQNSSVSPFGKL 473
Qy 497 VSSSTLNMSSAGKLLVKKCCAYNSMGTS-----CETIFLNSGPPFPFI 539
Db 474 VVYSTIDDSFTKNGTVECRAYNDVGKSSASFNPAFKGNSKEQIHAHTLTFT-----PLL 527
Qy 540 QDNISFYATIGLCLPIVVLIVLICHYKKQRYESOLQMI-QVTGPLDNEYFYVDPRDY 598
Db 528 ---IGFVIAAGLMCIFWML-----TYKYLQKPMYEVQWKVVEING---NNYVIDPTQL 577
Qy 599 EYDLKWEFPRENLEFGKVLGSGAFGRVMNATAYGSKTGVSIQVAVKMLKEKADSCKEA 658
Db 578 PYDHKWEFPNRNLSFGKTLGAGAFKGVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREA 637
Qy 659 LMSLQWTHLGHNDINVLNLAGACTLSGPVYLIFCYCCYDGLNLYRSKREKPHRTWTEI 718
Db 638 LMSLQVLSYLGHNMTVNLGACTIGGPTLVITEYCCYDGLNLYLRKRDSP----- 690
Qy 719 FKEHNPSSYPTQAMSNSSMPGSRVOLHPPDLQSLGFGNSHSEDEI-----EYENQ 772
Db 691 -----ICSKQEDHAEVALYK-----NLLHKSSESCNDSTNEYMDM 725
Qy 773 K-----RLAEEEEEDLN-----VLTFEDLLCFAYQVAKGMEFL 806
Db 726 KPGVSYVVPKTKDRSARIGSVIERDVTPTAIMEDEDLALDLELLSFSYQVAKGMFLA 785
Qy 807 FKSCVHRDLAARNVLVTHGKVVKICDFGLARDILSDSSYVVRGNARLPVKWMAPESEFEG 866
Db 786 SKNCIHRDLAARNILLTHGRITTKICDFGLARDIRNDSYVVKGNARLPVKWMAPESEFNC 845
Qy 867 IYTIKSDVWSYGILLWEIFSLGVNYPYFGIPVDANFYKLIQSGFKMEOPFYATEGIYFV 926
Db 846 YTFESDWSYGILLWEIFSLGSPYPRIPVDSEFKYKIKDGYRMSPECAPLEMYEIMRSCWN 905
Qy 927 SCWAFDSRKRPSPFNLTSLGCOLAAE 953
Db 906 TCWDADPLKRTFKQIVQVMEQQLSISES 932

RESULT 11
S16385
macrophage colony-stimulating factor 1 receptor precursor - rat
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) CSF-1R
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Jun-2000
A:Accession: I60321; S16385
R:Borycki, A.G.; Guillier, M.; Leibovitch, M.P.; Leibovitch, S.A.
Growth Factors 6, 209-218, 1992
A:Title: Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence analysis and
A:Reference number: I60321; MUID:93001225; PMID:1389227
A:Accession: I60321
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-978 <RES>
A:Cross-references: EMBL:X61479; NID:957543; PIDN:CAA43706.1; PID:957544
A:Note: in Genbank entry RRCSE1, release 113.0, the source is designated as Rattus rattu
A:Note: submitted to the EMBL Data Library, August 1991
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; kinase-rela
protein; tyrosine-specific protein kinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-978/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F:20-515/Domain: extracellular #status predicted <EXT>
F:35-86/Domain: immunoglobulin homology <IMM1>
F:120-179/Domain: immunoglobulin homology <IMM2>
F:217-280/Domain: immunoglobulin homology <IMM3>
F:316-381/Domain: immunoglobulin homology <IMM4>
F:410-485/Domain: immunoglobulin homology <IMM5>
F:516-535/Domain: transmembrane #status predicted <TM>
F:536-978/Domain: intracellular #status predicted <INT>
F:578-915/Domain: protein kinase homology <KIN>
F:586-594/Region: protein kinase ATP-binding motif
F:42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
F:45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status
F:614,631,776/Active site: Lys, Glu, Asp #status predicted
F:781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 23.0%; Score 1210; DB 2; Length 978;
Best Local Similarity 33.5%; Pred. No. 1.3e-54;
Matches 318; Conservative 147; Mismatches 329; Indels 154; Gaps 31;

QY 78 EAATVEAEGSITLQVLTATPGLSLVFKHSLGQCPHDLQNGIVSMALNVTET 137
DB 36 ETVTLCRCVSGSWEVD-----GPISPYTLDPSPGS-----TLTRNATFK 77
QY 138 QAGEY-LLHQSEBANYTLFTVNVRTQLV-----LRRPYFRKMNQDALL-CIS 187
DB 78 NTGYRTELEDNPAGSTTI-----HLVYKDPANSWNLLAQEVTVVEGQEAFLPCL- 128
QY 188 EGVPEPTVEWVLCSSHRESCKEPPAVRK-----BEKVLHBLFGTDIRCC 233
DB 129 --ITDPALK-----DSVSLMREGGRQVLRTVTFPSAWRGFIIRKAKVL-----DSNTVVC 177
QY 234 ARNALGRECTKL-FTIDLN-----QAPQSTL-PQLFLKV-GEPLIRCKAIAHNNHGFGLTW 286
DB 178 KTWVNGRESTSTGLWKNVRVHPPEPQIKLEPSKLVRIRGAAQIVCSATNAEYGFNVIL 237
QY 287 ELEDKALE--EGSPFEMSTSTNTMTIRILLAPFVSSVGRNDTGYTC-SSSKHPSQSALV 343
DB 238 KRGTKLEIPLNSDFQNYKKVRL-----SLNAVDQAGYSCVANSVNGVTRITAM 291
QY 344 T--ILEKGFINATSQE-EYEIDPYEKFCFSVRFKAYPRIR-CTWIRFSQASFPCEQGLE 399
DB 292 NFQVVEAYNLNLTSEQSLQVSGDSLLTVHADAYPSIOHYNWTVLGPFFE-DQRKLE 350
QY 400 -----DGVSIKFCDH--KNKPEGEYIFAEENDDAQTKMTNLIRKPPVLANASASQ 450
DB 351 FITQATRYRTFKLFLNRVKASEAGQFLMAQKNAGMNNLTFFELTRYPPPEVSVTWMPVN 410
QY 451 AS-----CSSDGYPLPSWTWKCKSDKSPNCTEIEPGVWN-----KKNRKPVGQWSSSTL 502

Db 411 GSDVLCDSVSGYPQPSVTWMECRGHTDRCDQAALQVWNDTHPEVLSQKPFDPKVIQSOL 470
QY 503 NMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPFFFIQDNISFYATIGLC---LPIIVVL 559
DB 471 PIGTLKHNTYFCKTHNSVGNSSQYFRAVSLGQSQQLPDESIFTVPVWVACMSVMSLLVLL 530
QY 560 IVLICHYKKGFRYESQLQMIQ-VTGPLDNEYFYVDREYEDLKWEPRENLEFGKVLG 618
DB 531 LLLLYKYKQPKYQVRWKILERYEG---NSYTFDPTQLPYNEKWEPPRNLLQFGKTLG 587
QY 619 SCAGFVNNATAYGISKTVGSIQAVKMLKEKADSCKEALMSELKMMTHLGHHDINVL 678
DB 598 AGAPGVVEATAFGLGKEDAVLKVAVKMLKSTAHADAKEALMSELKIMSHLGCHENIVNL 647
QY 679 LGACTLSGPVYLIFEYCCYGDLLNLYLRKRE-----KFHRTWTEI 718
DB 648 LGACTHGGFVLIVITEYCCYGDLLNLYLRKRE-----KFHRTWTEI 707
QY 719 FKEHNFSSYPTFOAHSNSSMPGSRVQLHPPDLQSLGFGNHSIHSEDETEYENQKRLAE 778
DB 708 RDSGFS-----SQGVDTYVENRVPVSTSSDSFFKQD-----L 740
QY 779 BEEDNLVLTFFDLCCFAYQVAKGMEFLBPKSCVHRDLAARNVLTGHVKYKICDFGLARD 838
DB 741 DKEPSRPLELDLHFFSQVAGMAFLASKNCIHRDVAARNVLTSGHVAKIGDFGLARD 800
QY 839 ILSDSYVVRGNARLPVKMAPESLFEIGIYTKSDVMSYGLLWEIFSLGVNYPGIPVD 898
DB 801 IMNDSYVVRGNARLPVKMAPESILYCVYTVQSDVMSYGLLWEIFSLGLNYPGILVN 860
QY 899 ANFYKLIOGFGMEOPFYATEGIYFMOSCAWAFDSKSPSPNLSFTL 946
DB 861 NKFYKLVDGYQMAQPVFAPKNIYSIMOSCDLEPRTPTFOQICFL 908

RESULT 12

TVM5MD

macrophage colony-stimulating factor 1 receptor precursor - mouse

N:Contains: protein-tyrosine kinase (EC 2.7.1.112) csflr/fms

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000

A:Accession: S01880

R:Rothwell, V.M.; Rohrschneider, L.R.

Oncogene Res. 1, 311-324, 1987

A:Title: Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.

A:Reference number: S01880; MUID:88217329; PMID:2966922

A:Accession: S01880

A:Molecule type: mRNA

A:Residues: 1-976 <ROT>

A:Cross-references: EMBL:X06368

C:Genetics:

A:Gene: fms

C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolo

C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote

fic protein kinase

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-976/Product: macrophage colony-stimulating factor 1 receptor #status predicted <EXT>

F:20-515/Domain: extracellular #status predicted <EXT>

F:35-86/Domain: immunoglobulin homology <IMM1>

F:120-179/Domain: immunoglobulin homology <IMM2>

F:217-280/Domain: immunoglobulin homology <IMM3>

F:316-381/Domain: immunoglobulin homology <IMM4>

F:410-485/Domain: immunoglobulin homology <IMM5>

F:516-535/Domain: transmembrane #status predicted <TM>

F:536-976/Domain: intracellular #status predicted <INT>

F:578-914/Domain: protein kinase homology <KIN>

F:586-594/Region: protein kinase ATP-binding motif

F:42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted

F:45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #stat

F:614,631,776/Active site: Lys, Glu, Asp #status predicted

F:781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match	22.8%;	Score 1198.5;	DB 1;	Length 976;
Best Local Similarity	34.1%;	Pred. No. 5e-54;		
Matches 317;	Conservative 148;	Mismatches 347;	Indels 117;	Gaps
Qy	78	EAATVEAESGSIITLQVOLTATPDGLSCLAVFKHSSIGCCPHFDLQNRGIVSMALINTVET	137	
Db	36	ETVTLRCVSGSWEVD-----GPISFIWTLDPESPES-----TITTSNATFK	77	
Qy	138	QAGEY-LLHITQSERANYTVLFTVNVNDDTQLYV-----LRPPYFRKMNODALL-CIS	187	
Db	78	NTGTYRCTELEDPMAGSTTI-----HLVYKDPAPHSNLLAQAEVTVVGEAVLPCLI-	128	
Qy	188	EGVPEPTVEVLCSHRESCKECPAVWRKEEVLHELFGTDIR-----CCARNA	237	
Db	129	--ITDPALK-----DSVSLMRGEGQVLRKTVYFSPMRGSIIRKAKVLDSNTYVCKTMV	181	
Qy	238	LGRECTKL-FTIDLN---CAPOSTLI-POLFVKV-CEPLWIRKCAIHNVHGFLTWELED	290	
Db	182	NGRESITGWLKVNVRVHPFPQIKLEPSKLVIRGEAAQIVCSATNAEVGFNVILKRGD	241	
Qy	291	KALE--EGSVFEMSTYSTNRKTMIRILLAFVSVGRNDTGYVTC-SSSKHPSOALVT--I	345	
Db	242	TKLEIPLNSDFQDNYKKVRAL-----SLNAVDFQAGIYSCVASNDVGTETATNMFOV	295	
Qy	346	LEKGPINATSOB-EYEIDPYEKFCFSVRFKAYPRIR-CTWIFSOASFPCEORGLE----	399	
Db	296	VESAYLMLTSEQSLLOEVSVDGLIITVHADAYPSIOHYNWTVLGGPFFB-DQRKLEFITQ	354	
Qy	400	---DGVSIKFCDBH--KNKPGEYIFAENDDAQFTKMFILNIRKKQVILANASASOAS--	452	
Db	355	RAIYRYTFKLPLNRVASEAGQYFLMAQNKAGWNNTLFELTLRYPEVSVTWMPVNGSDV	414	
Qy	453	--CSSDGYPLPSWTWKCKSDKSNCNTEETPEGVWN-----KANRKFVGQWVSSSTLNME	506	
Db	415	LFCDSVGPQPSVTWMECRGHTDRCDQEAQALHLWNDTHPEVLVSQKPFDFKVIITQSQ	474	
Qy	507	AGKGLLVKCCAYNSMGTSCTETIFLNSPGPPPTQDNISFVATIGLC--LPFTVLVLVI	563	
Db	475	LKNMTYFCKTHNSVGNSSQYFRAVSLGQSKQLPDBESLFTPVVACMSVMSLLVLLLL	534	
Qy	564	CHKYKQFRIESLOMITQ-VTGPLDNEYFYVDPRDYEYDLKMEFFPRENLEFGKVLGSGAF	622	
Db	535	LYKYKQKPKYQVRWKIITERVEG--NSYTFIDTQLPYNEKMEFFPRNNLOFGKTLGAGAF	591	
Qy	623	GRVNNATAYGISKTGVSIQVAVKMLEKADSCKEALMSELQWTHLGHNDINVLNLGAC	682	
Db	592	GKVVEATAFGLGKEDAVLKVAVKMLKSTAHADKEALMSELKIMSLGQHEINVLNLGAC	651	
Qy	683	TLSPGFVLIIPFYCCYCGDLLNLYRSKREKPHRTWTEIFKEHNFSYPTFOAHNSNMPGSR	742	
Db	652	THGGFVLVYTEYCCYCGDHLNFLRKAEAMGP-----SLSPQDSEGDSSSYKNIH	701	
Qy	743	EVQLHPPLDLQSGFNGNSIHSEDEIYEYENQKRLAEBEEDLN-----VLTFEDLLCFAYQ	797	
Db	702	LEKKYVRDD--SGFSSQGVDTYVEMRPVSTSSSDSFFFKQDLCKEHSRPLELMDLLHFS	759	
Qy	798	VAKGMELEFKSCVHRDLAARNVLVTHGKVKIKCDGLARDILSDSSYVVRGNARLIPVKW	857	
Db	760	VAQGMATFLASKNICIHRDVAARNVLLTSGHAVKIGDGFGLARDINMDSNYVVKGNA-LP	818	
Qy	858	MAPSEFEGYITTKSDVMSYGILLMTWIFSLGVNPPYGPIDVANFYKLIQSGFKEQFPFYA	917	
Db	819	MAPESI FDCVITVQSDVMSYGILLWEIPLSLGLNPYFGIHNVNKFYKLVKDGQYMAQPVFA	878	
Qy	918	TEGIFYVMSQWAPDSRKRPSPFNLTSLFL	946	
Db	879	PKNIYSIMQSCWDLPEPRPTFOQICFL	907	

RESULT 13

РЕЗУЛ
Т В И Д У К Т

protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human N; Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-kit


```
Db 445 RPTCNGNNTGLPKQNHQAL-TVEQREYGAVEVESVFTVGLSNHMTVECAFLNVGV 503
Qy 524 SCTIFLNSGPPFFIODNISFYATIGLC--LPFIVLVILVILCHYKKQRYESOLQMIQ 581
Db 504 SDDTFVE-----VSDKLTSTLGAAGVLAIFLLLLVLLYKKQRFERWKIIE 556
Qy 582 VTGFLONEFYVDFRDYEDYDKWFFRENLEFGKVLGSGAGFRVWMTATAYGISK-TGVSI 640
Db 557 ARE--GNNYTFIDPTOLPYNEKEWFFPKLKLKVLGAGAGKVVATEAFLGEDKNTL 614
Qy 641 QVAVKMLKEKADCEKALMSLKHMTLGHNDHNVNLLGACTLSGPGVYLIFEYCCYGD 700
Db 615 RVAVKMLKANAHSDERBALMSLKILSHLGHQNVNLLGACTYGGPVLVITEYCSLGD 674
Qy 701 LNVLSRKREKFRHTWTEIFKEHNFSSVPTQAHSN-----SSMFGSR 742
Db 675 LNFLOKAEFTFVNLVMI-----PEIMENSNDYKNCQKMYRSGSISSTSSST 725
Qy 743 EVOLHPPDLQSLGFGNGSIHSEDEIEYENOKRLAEBEEDLNVLTFFEDLLCFAYQVAKGM 802
Db 726 YLEWRP-----SQSHIEASGRKSLCEDNGD--WPLDIDLLRFSLOVAGL 770
Qy 803 EFLEFKSVHRDLAARNVLVTHGKVKICDFGLARDILSDSSVYVVRGNARLPVKWMAPE 862
Db 771 DFLASRNCIHRDVAARNVLLTDKRVAKICDFGLARDIMWDSNYVVKGNARLPVKWMAPE 830
Qy 863 LPEGITIKSDVMSYGLLWEIFSLGVNPPGIPVDANFVKLIQSGFKMBOPFYATEGIY 922
Db 831 IFPCVTVOSDVMSYGLLWEIFSLGSPSPSMAVDSRFYKWKRGYOMQOPDFALPEIY 890
Qy 923 FVMQSWAFDSRKRPPNLTSLFGCLQA--EABEACIRTSIHLPKQAAPQORGLRAQS 980
Db 891 MIMKMCWNLPTERTPTFMSISQMINRLLGQDBQEKLIYRNVQ-PEQVAB-----GEACDE 945
Qy 981 PQR 983
Db 946 PKR 948

RESULT 15
JN0677
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken
N:Alternate names: tyrosine kinase receptor kit
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JN0677
R:Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Naito, M.; Sakurai, M
Gene 128, 257-261, 1993
A:Title: Cloning and expression of the chicken c-kit proto-oncogene.
A:Reference number: JN0677; PMID:93292995; PMID:7685729
A:Accession: JN0677
A:Molecule type: mRNA
A:Residues: 1-960 <SAS>
A:Cross-references: DDBJ:DJ12225; NID:G303532; PIDN:BAA02506.1; PID:G303533
A:Experimental source: brain
A:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
protein kinase
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-960/Product: tyrosine kinase receptor #status predicted <MAT>
F:314-380/Domain: immunoglobulin homology <IMM>
F:573-916/Domain: protein kinase homology <KIN>
F:581-589/Region: protein kinase ATP-binding motif
F:76,135,149,269,286,306,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)
Query Match 22.4%; Score 1181; DB 1; Length 960;
Best Local Similarity 31.8%; Pred. No. 3.9e-53;
Matches 310; Conservative 159; Mismatches 356; Indels 150; Gaps 30;

Qy 45 GSSAGKPSVYRMVSGSPEDLCQTPRROSEGTVEAAVEAASGSILOVLQATPGDLSC 104
Db 24 GSVPHBESSLVVNGELRLKCN-----EGPVTWNFQNSPSAKR 65
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Search completed: May 24, 2003, 17:00:32

Job time : 41.4826 secs

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Qy 105 L-----WVFKHSSLCQPHFDLQNRGIVSMALNVMTQAGEYLLHIQSERANYTVLFTV 159
Db 66 ISNEKEWHTKTNATIRDCRYECKSKG-----SIVN-----SFVV 99
Qy 160 NVRTQLYVLRPRYFRKMNODALLCISEBVPBPPTVWVLCSSHRESCKEGPAAVRKEE 219
Db 100 FVKDPNVLFVLSLIYKGEDSDILLVCPLTDPD-VLNFTRKRCCKGKPLPKMNTFIPNPK 158
Qy 220 ---KVLHELFGTDIRCCAR-NALGRECTKLTIDLQAP-QSTLPOL-----FLKVG 266
Db 159 GIITKNVQSRFGKGCYQCLAKHNGVEKISEHIP---LNVRPVHKALFVITLSKSYELLKEG 215
Qy 267 EPLMIRKCAIHVNHGFGILTWELEDKALEEGSYFEMSTYSTNRTMIRIILLAFVSSVGRNDT 326
Db 216 BEPEVTCIITDVSVRKASWISYKSAIVTSKRNLDGYERK---LTLMIRSIVGVNDS 271
Qy 327 GYITCSSKHP--SQSALVTI--LEKFINATSQE-EYEDPYEKFCFSVRFKAYPRIR 381
Db 272 GEFTC-QAENPFPGKTNATVTLKALAGFVRLFATWNTTIDINAGQNGNLTVYEYAPK-- 328
Qy 382 CTWIFSOASPECEQGLEGGYSISKFDHKNK-----PGEYIF 419
Db 329 -----PKEEVMMYMETLQNSDHYVYKFTKTVGNNSYTSSELHLRLKTEGGIYTF 378
Qy 420 YAENDDAQFTKQFTLNIRKKPOVLANASQ--ASCSSDGYPLPSWTWKCKSDKSPNCTE 477
Db 379 FVNSDASSSVTFVYVYKTRPEILTLMDLNDIILQCVATGPPATIIYWFPGTEQRLD 438
Qy 478 E--IPEGVWNKKANRY--FGWVSSSTLMSBAGLLVKCCAYNSMGTSCEITFLNS 532
Db 439 SPTISPMDVKVSYTNSVPSPERILVESTVNAS-MFKSTGTICCEASSNGDK-SSVFFNF 496
Qy 533 PGPPFFIOMNISFYA-----TIGLCLPFIWLVILVILCHYKKQRYESOLQMI-QVTG 584
Db 497 A-----IKEQIRTHLTPLLIAPGVAAGLMCIIMVILVYIYLOPKPYEQVQKVEEING 551
Qy 585 PLONEYFVDFRDYEDYDKWFFRENLEFGKVLGSGAGFRVWMTATAYGISKTGVSIOVAV 644
Db 552 ---NNYVYIDPTQLPYDHKWEFFPRNRLSFGKTLGAGAGKVVATEAYGLFKSDAAMTVAV 608
Qy 645 KMLKEKADSCKEALMSLKHMTLGHNDHNVNLLGACTLSGPGVYLIFEYCCYGDLLNVL 704
Db 609 KMLKPSAHLTEREALMSLKHMTLGHNDHNVNLLGACTIGGPTLVITEYCCYGDLLNVL 668
Qy 705 RSKREKP-----HRTWTE--IPKEHNFSSVPTFOA-HSNSMPPGSGREVQHPDLSQFN 757
Db 669 RKRKDSFICPKHEBAEAAVYENLLHQAEPADAVNMYMDMKPGVSVYAVPPKADKKRPVK 728
Qy 758 GNSIHSDEIEYENOKRLAEBEEDLNVLTPEDLICFAYQVAKGMFELEFKSCVHRDLAA 817
Db 729 SGS-----YTQDDVTLSMLEDELALDVEDLLSFSYQVAKGMSFLASKNCIHRDLAA 780
Qy 818 RNVLVTHGKVVKICDFGLARDILSDSSVYVVRGNARLPVKWMAPELSPGEGIYTIKSDVMSY 877
Db 781 RNILLTHGRITKICDFGLARDIRNDSNVVVKGNARLPVKWMAPESEIFNCVVTTFESDVMSY 840
Qy 878 GILLWEIFSLGVNPPGIPVDANFVKLIQSGFKMBOPFYATEGIYFVMQSWAFDSRPRP 937
Db 841 GILLWEIFSLGSPSPGMPVDSKFKYMKIEGYRMFSPESCPPEMYDIMKSCWDADPLQRP 900
Qy 938 SFPNLTSLFGCLQAE 952
Db 901 TFKOIVOLIEQQLSD 915
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:38:45 ; Search time 17.9909 Seconds
(without alignments)
2286.959 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MHALAQRSDRRLLLVLSV.....RGLRAQSPQKVIHRERS 992

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5264	100.0	992	1 FLT3 MOUSE	Q00342 mus musculu
2	4429.5	84.1	993	1 FLT3 HUMAN	P36888 homo sapien
3	1258.5	23.9	980	1 KFSM FELCA	P13369 felis silve
4	1249.5	23.7	978	1 KFSM FSVMD	P00545 feline sarc
5	1223	23.2	975	1 KIT MOUSE	P05532 mus musculu
6	1222.5	23.2	978	1 KIT CAPIH	Q28317 capra hircu
7	1221.5	23.2	972	1 KFSM HUMAN	P07333 homo sapien
8	1219	23.2	977	1 KFSM MOUSE	P09581 mus musculu
9	1215	23.1	977	1 KIT BOVIN	P43481 bos taurus
10	1210	23.0	978	1 KFSM RAT	Q00495 rattus norv
11	1207	22.9	975	1 KIT CANFA	O97799 canis fami
12	1196	22.7	976	1 KIT HUMAN	P10721 homo sapien
13	1181	22.4	960	1 KIT CHICK	Q08156 gallus gall
14	1178.5	22.4	978	1 KIT FELCA	Q28889 felis silve
15	1157.5	22.0	1088	1 PGDS RAT	P120786 rattus norv
16	1152.5	21.9	1089	1 PGDS HUMAN	P16234 homo sapien
17	1142.5	21.7	1089	1 PGDS MOUSE	P26618 mus musculu
18	1132	21.5	1087	1 PGDS XENLA	P26619 xenopus lae
19	1098	20.9	1098	1 PGDR MOUSE	P05622 mus musculu
20	1078	20.5	1106	1 PGDR HUMAN	P09619 homo sapien
21	998.5	19.0	1338	1 VGR1 HUMAN	P17948 h vasculat
22	984.5	18.7	1336	1 VGR1 RAT	P53767 rattus norv
23	983.5	18.7	1333	1 VGR1 MOUSE	P35969 mus musculu
24	967.5	18.4	370	1 KIT FSVHZ	P04048 feline sarc
25	965	18.3	1348	1 VGR2 COTJA	P52583 coturnix co
26	961.5	18.3	1356	1 VGR2 HUMAN	P35968 homo sapien
27	954.5	18.1	1298	1 VGR3 HUMAN	P35916 homo sapien
28	952	18.1	1363	1 VGR3 MOUSE	P35917 mus musculu
29	934	17.7	1343	1 VGR2 RAT	Q08775 rattus norv
30	926.5	17.6	1367	1 VGR2 MOUSE	P35918 mus musculu
31	818	15.5	813	1 FGR2 XENLA	Q03364 xenopus lae
32	810.5	15.4	823	1 CEK3 CHICK	P18461 gallus gall
33	791	15.0	821	1 FGR2 HUMAN	P21802 homo sapien

RESULT 1
FLT3_MOUSE
ID FLT3_MOUSE STANDARD; PRT; 992 AA.
AC Q00342;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE FL cytokine receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor flk-2) (Fetal liver kinase 2) (Tyrosine-protein kinase FLT3).
GN FLT3 OR FLT-3 OR FLK-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91292518; PubMed=1648448;
RA Matthews W., Jordan C.I., Wiegand G.W., Pardoll D., Lemischka I.R.;
RT "A receptor tyrosine kinase specific to hematopoietic stem and progenitor cell-enriched populations.";
RL Cell 65:1143-1152(1991).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=92019834; PubMed=1656368;
RA Rosnet O., Marchetto S., Delapeyriere O., Birnbaum D.;
RT "Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the PDGFR/CSFIR family.";
RL Oncogene 6:1641-1650(1991).
RN [3]

RP CHARACTERIZATION.
RX MEDLINE=93205405; PubMed=8384358;
RA Maroc N., Rottapel R., Rosnet O., Marchetto S., Lavezzi C., Mannoni P., Birnbaum D., Dubreuil P.;
RT "Biochemical characterization and analysis of the transforming potential of the FLT3/FLK2 receptor tyrosine kinase.";
RL Oncogene 8:909-918(1993).
CC -!- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: HEMATOPOIETIC STEM AND PROGENITOR CELL-ENRICHED POPULATIONS. FOUND IN BRAIN, PLACENTA AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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DR EMBL; M64689; AAA37634.1; --
 DR EMBL; X59398; CAA42041.1; --
 DR PIR; A39931; A39931.
 DR HSP; P11362; IFGK.
 DR MGD; MGI:195559; Flt3.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR Signal; Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 992 FL CYTOKINE RECEPTOR.
 FT DOMAIN 28 544 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 545 564 POTENTIAL.
 FT DOMAIN 565 992 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 611 946 PROTEIN KINASE.
 FT NP_BIND 617 625 ATP (BY SIMILARITY).
 FT BINDING 645 645 ATP (BY SIMILARITY).
 FT ACT_SITE 814 814 BY SIMILARITY.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 503 503 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 150 150 R -> A (IN REF. 2).
 FT CONFLICT 242 242 C -> S (IN REF. 2).
 FT CONFLICT 726 726 S -> F (IN REF. 2).
 FT CONFLICT 957 979 CIRTSTHLPKQAAPOQRGGRLAQ -> MYQNMGNGVPEHPS
 FT CONFLICT 983 983 IYQNRPLSEAGEPP (IN REF. 2).
 FT CONFLICT 983 983 R -> A (IN REF. 2).
 FT SEQUENCE 992 AA; 112639 MW; 407A087853372100 CRC64;

Query Match 100.0%; Score 5264; DB 1; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRDRRLLLVLSVWILETVNQDLPIVKCVLISHENNNGSAGKPSRYMYRGS 60
 DB 1 MRALAQRDRRLLLVLSVWILETVNQDLPIVKCVLISHENNNGSAGKPSRYMYRGS 60
 QY 61 PEDLOCTPRQSGTVYEAATVVAESGSIITLOVQATPGDLSCLWVFKHSSLCQPHFD 120
 DB 61 PEDLOCTPRQSGTVYEAATVVAESGSIITLOVQATPGDLSCLWVFKHSSLCQPHFD 120
 QY 121 LQNRGVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVRTDQLVLRPYPFRKMEQ 180
 DB 121 LQNRGVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVRTDQLVLRPYPFRKMEQ 180
 QY 181 DALLCISEGVPEPTVENVLVCSSHRESCKEGPAAVRKEEKVLHFLFTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVENVLVCSSHRESCKEGPAAVRKEEKVLHFLFTDIRCCARNALGR 240
 QY 241 ECTKFLFTIDNQAPSTLPQLFKVGEPLMIRCKAIHNVHGFGLTWELEKALBEGSYFE 300
 DB 241 ECTKFLFTIDNQAPSTLPQLFKVGEPLMIRCKAIHNVHGFGLTWELEKALBEGSYFE 300
 QY 301 MSTYGTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQEEY 360

DB 301 MSTYGTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKPCFSVRPKAYPRIRCTWIFSOASPFCEORGLDGYISKPKCDHKMKPGEYIPY 420
 DB 361 EIDPYEKPCFSVRPKAYPRIRCTWIFSOASPFCEORGLDGYISKPKCDHKMKPGEYIPY 420
 QY 421 AENDDAOFTKMTNIRKKPOVLANASQASCSGSDGVPPLSWTWKCKSDKSPNCTEETIP 480
 DB 421 AENDDAOFTKMTNIRKKPOVLANASQASCSGSDGVPPLSWTWKCKSDKSPNCTEETIP 480
 QY 481 EGVNKKANRKFVQWVSSSTLNSEAGKLLVKKCAVNSMGTSCTETIFLNSPGPPFFIQ 540
 DB 481 EGVNKKANRKFVQWVSSSTLNSEAGKLLVKKCAVNSMGTSCTETIFLNSPGPPFFIQ 540
 QY 541 DNISFYATIGLCLPFIIVLIVLICHKYKKQPRYSOLOMIQVTPGLDNEYFYVDFRDVEY 600
 DB 541 DNISFYATIGLCLPFIIVLIVLICHKYKKQPRYSOLOMIQVTPGLDNEYFYVDFRDVEY 600
 QY 601 DLKWEFPRENLEFGKVLGSGAGFGRVMNATAYGISTGVSIQVAVKMKKADSCKEALM 660
 DB 601 DLKWEFPRENLEFGKVLGSGAGFGRVMNATAYGISTGVSIQVAVKMKKADSCKEALM 660
 QY 661 SELKQWTHLGHNDINVLNLLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTETPK 720
 DB 661 SELKQWTHLGHNDINVLNLLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTETPK 720
 QY 721 EHNPSYPTFOAHNSNMPGSRVOLHPPDLQSGFNGNSIHSEDEIEYENQKRLAESEE 780
 DB 721 EHNPSYPTFOAHNSNMPGSRVOLHPPDLQSGFNGNSIHSEDEIEYENQKRLAESEE 780
 QY 781 EDNLVLTFFDLCLCFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVYKICDFGLARDIL 840
 DB 781 EDNLVLTFFDLCLCFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVYKICDFGLARDIL 840
 QY 841 SDGSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGWNVPYGPVPDAN 900
 DB 841 SDGSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGWNVPYGPVPDAN 900
 QY 901 FYKLIQSGFKMEQPFYATGFIYVWQSWAFDSRKRSPFNLTSLFGLCOLAAEAEACIRT 960
 DB 901 FYKLIQSGFKMEQPFYATGFIYVWQSWAFDSRKRSPFNLTSLFGLCOLAAEAEACIRT 960
 QY 961 SIHLPKQAAPOQRGGLRAQSPQROVKIHRERS 992
 DB 961 SIHLPKQAAPOQRGGLRAQSPQROVKIHRERS 992

RESULT 2
 FLT3_HUMAN
 ID FLT3_HUMAN STANDARD; PRT; 993 AA.
 AC P36888; Q13414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FL cytokine receptor precursor [EC 2.7.1.112] (Tyrosine-protein kinase
 receptor FLT3) (Stem cell tyrosine kinase 1) (STK-1) (CD135 antigen).
 GN FLT3 OR STK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94119906; PubMed=7507245;
 RA Small D., Levenstein M., Kim E., Carow G., Amin S., Rockwell P.,
 RA Witte L., Burrow C., Ratajczak M.Z., Gewirtz A.M., Civin C.I.;
 RT "STK-1, the human homolog of Flk-2/Flt-3, is selectively expressed in
 RT CD34+ human bone marrow cells and is involved in the proliferation of
 RT early progenitor/stem cells."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:459-463 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.


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|||||
Db 838 SDSNYVVRGNARLPVKWAPESLFEGLTYITKSDVMSYGLLWEIFSLGVNPPGIPVDAN 897
Qy 901 FYKLIOGPKWOPFFVATEGIYFMWSCAFDGRKPSFNLTSFLGCOLAEAEAC--- 957
Db 898 FYKLIONGFMDQFFVATERIYIIMOSCAFDRKRPSPNLTSFLGCOLADAEAWYQN 957
Qy 958 -----IRTSIHLPRQAAPOQRG-GLRAQSPORQVK 986
Db 958 VDRGVSECHTYQNRPPSREMDLGLLSPOAQVE 991

RESULT 3
KFMS FELCA
ID KFMS FELCA STANDARD; PRT; 980 AA.
AC P13369;
DT 01-JAN-1990 (rel. 13, Created)
DT 01-JAN-1990 (rel. 13, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
DE (EC 2.7.1.112) (Fms proto-oncogene) (c-fms).
GN CSF1R OR FMS.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8907753; PubMed=2849512;
RA Woolford J., McLaughlin A., Rohrschneider L.R.;
RT "Activation of the feline c-fms proto-oncogene: multiple alterations
RT are required to generate a fully transformed phenotype.";
RL Cell 55:965-977(1988).
CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; J03149; AAA30811.1; -.
CC PIR; A31636; TVCTWD.
CC HSSP; P11362; IFGK.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR003600; Ig_Like.
CC InterPro; IPR001824; RTKinaseIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00047; Ig; 3.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 2.
CC SMART; SM00410; IG like; 4.
CC SMART; SM00408; IGG2; 1.
CC SMART; SM00219; TyrcK; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
CC PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
CC PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
CC ProtocOncogene; Tyrosine-protein_kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 19 POTENTIAL.

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FT CHAIN 20 980 MACROPHAGE COLONY STIMULATING FACTOR I
FT RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE DOMAIN 1.
FT IG-LIKE C2-TYPE DOMAIN 2.
FT IG-LIKE C2-TYPE DOMAIN 3.
FT IG-LIKE C2-TYPE DOMAIN 4.
FT IG-LIKE C2-TYPE DOMAIN 5.
FT PROTEIN KINASE
FT ATP (BY SIMILARITY).
FT BINDING 593 593 ATP (BY SIMILARITY).
FT ACT SITE 613 613 BY SIMILARITY.
FT DISULFID 776 776 POTENTIAL.
FT DISULFID 127 177 POTENTIAL.
FT DISULFID 224 278 POTENTIAL.
FT MOD RES 417 482 POTENTIAL.
FT CARBOHYD 45 45 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 980 AA; 108506 MW; 455CF661E97CF6FF CRC64;

Query Match 23.9%; Score 1258.5; DB 1; Length 980;
Best Local Similarity 32.7%; Pred. No. 9.8e-77;
Matches 328; Conservative 168; Mismatches 353; Indels 153; Gaps 32;

Qy 75 TVYEAAATVEVAESGSIPLQVQLATPGDLSCV-----W---VFKHSSIGCOFHPDLQNR 125
Db 13 TAWHAQGPVPIQSPGELVVEPGTITLRCVNGSVEMDGPISPHWNLDLDPSPSI---- 68
Qy 126 IVSMALINVTETQAGEYLHI-----QSERANYTVLFTVNRDQTLVYL--RRPY----- 173
Db 69 ---LTTNNATFQNTGTY--HCTEPGNPQGNATI-----HLYVKDPAKPMKVLQAE 114
Qy 174 FRKMENDALL-CISEGVPPPTVEWLCSHRESKEEGPAVVRKEEVKLHELFTGDI-- 230
Db 115 VTVLEGQDALLPCL---LTPDALB-----AGVSLVRVGRVPLVQTNYSFSGHFTTHK 166
Qy 231 -----RCCARNALGRECTKL-----FTIDLNQAPQSTL-PQLFLKV-GEPLWIRCK 274
Db 167 AKFTENHVIQCSAR-VDRGRTVTSMGILWKVKQDISGPATLTLEPAELVRIQGEAAQIVCS 225
Qy 275 AIHVNHGFGLTWELEDKALEEGSYFEMSTVSTNTRMTIRILLAFVSSVGRNRTGYTCSS 334
Db 226 ASNIDVNFVSLRHGDTKL---TISQSQSDPHDNRYQ-KVLTLNLDHVSFQDAGNYSCTAT 281
Qy 335 K---HPSQSALVTILEKGFINATSSQB-EYEIDPYEFCFVSFKVAPRIRC-TWI---- 385
Db 282 NAMGNHSASWFRVBSAYLNLISEQLLOEVTVGEKVDQVQVEAYPGLSFNWYLG 341
Qy 386 FSQASFPCEQGLLEDGYISIKFCD-----HKNKPGEYIFYAENDDAQFTMFTLNRKPK 441
Db 342 FSDYQDKLDFVTIKDTYRTSTLSLPRLKRSAGRYSFLARNAGGNALTFELTLRYPPE 401
Qy 442 VLANASASQAS-----CSSDGYPLPSWTWKCKSDKSPNCTEB---IPEGVWNKANKRVFG 494
Db 402 VRVTMTLINGSDTLLCEASGYPQSPVTVVQCRSHTRDRCDESAGLVLEDHSEVLSQVFP 461
Qy 495 QWVSSSTLNMSKAGLLVKCCAYNSMGTSCETIFLNSPGFPFIQDNISFATIGLC-- 552
Db 462 EVIVHSLAIGTLEHNRTYECRAFNSVGNSSQTFWPISIGAHTQLPDELLFTVLLTCWS 521
Qy 553 -LPPIVVLIVLICHKKYKQFRYESQLQMIQVTGPLDNEYFYVDPRDVEYDLKWEPPE 611

```


CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D45168; BAA08116.1; -.
 DR HSP; P11362; 1FGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG like; 2.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 978 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
 FT DOMAIN 23 521 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 522 544 POTENTIAL.
 FT DOMAIN 545 978 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 590 939 PROTEIN KINASE.
 FT NP_BIND 596 604 ATP (BY SIMILARITY).
 FT BINDING 624 624 ATP (BY SIMILARITY).
 FT ACT_SITE 794 794 BY SIMILARITY.
 FT MOD_RES 825 825 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 464 464 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 487 487 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 978 AA; 109722 MW; CA4D663F98205CA9 CRC64;
 Query Match 23.2%; Score 1222.5; DB i; Length 978;
 Best Local Similarity 34.0%; Pred. No. 2.5e-74;
 Matches 306; Conservative 145; Mismatches 319; Indels 131; Gaps 26;
 QY 134, VTE-----TQAGEYLLHQTQSERANVTYVLTFTVNRDQ-LYVLRPPYFRKMNQALLCI-- 186
 DB 83 ITKAEATNTGNYTC---TNKGSSIIYVFRDPEKFLIDLIDPLYGKEENDTLVRCPLT 139
 QY 187 -----SEGVPPEP-TVEWVLCSSHRESCKEAGPVVRKEEKVLHFGTDIRC-- 232

Db 140 DPEVNTYSLATGCEGKPLPKOLTFV-----ADPKAGITIRNVKREYHRL-----CLH 185
 QY 233 CARNALGRE-CTKLFITDLNQAPOS-----TLQPLFKUQGEPLWIRCKALHVNHGFLGT 285
 Db 186 CSANQKQKSMLSKFTLKRAAIAKAVPVSVSKTSYLLREGEFAVTCLIKDVSSVDSM 245
 QY 286 WELEDKALEEGSVPEMGTSTNRTMIRILLAFVSVGRNDTGYTCSSSHPSQSALVTI 345
 Db 246 WIKENSQSKAQTCKNSWHQDPSYLRQERLTISSARVNDSGVPMYANNITFGSANVTIT 305
 QY 346 LE---KGFINA-TSSQBEYELDPEYKFCFSVRFKAYPR-IRCTWIFSOASPFCEORGLD 400
 Db 306 LEVVDKGFINIFPMNMTTFVNDGENVDLVVEYEAYPEKPHQIYMNRT----- 355
 QY 401 GYSISKCECHK-----NKPGEYIFPAENDDAQFTKMTLINIRKK 439
 Db 356 --STDKWDDYPKSESNIRYVNEHLHLRLKGTGGTYTFHVSNSDVNSVTFNVTNNTK 413
 QY 440 POVLANASA--SQASCSDDGYPLPSWTWKCKSDKSPNCTEPI-PEGVNMKKANRKFVGQW 496
 Db 414 PEILTHDLVNGMLQCVAGPEPTIDWYFCPTQRCSPVPGVDVQVQIONSSVSPFKL 473
 QY 497 VSSSTLAMSBAKGLLYKCCAYNSMGTSCTIFLNSPGPPFPFIQDN----- 542
 Db 474 VVYSTIDDDSTFKHNGTVECRAYNDVGKSSASF-----NPAFKGNKKEQIHAHTLFTPL 527
 QY 543 ISFVATIGLCLPFIWLVILVILCHYKQKQFRYESQLOMI-QVTGPLDNEYFYVDFRDYED 601
 Db 528 IGFVIAAGLMCIFVMIL-----TYKLOKPMYEVQMKVVEEING---NNYVVIDPTQLPYD 580
 QY 602 LKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOAVVMKLEKADSCKEALMS 661
 Db 581 HKWEFPNRLSFGKTLGAGAFGVVEATAYGLIKSDAAMTVAVVMKLEKADSCKEALMS 640
 QY 662 ELKMMTHLGHNDITVNLGACTLSGPVYLIFEYCYCGDLLNLYRSKREKPHRTWTE---- 717
 Db 641 ELKVLSYLGNHNMIVNLGACTIGCTPLVITEYCYCGDLLNLYRSKREKPHRTWTE---- 700
 QY 718 --TPKENFSSYPYFQAHSSNM---PQSRVQLHPPLDQLSGFNGNSIHSEDELEYENQ 772
 Db 701 VALYKNLLHSEKSSCNDSTNEYMDMKFQSVYVPTKADK-----RRSARIGSYIRDTV 755
 QY 773 KRLAEEEDDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICD 832
 Db 756 PAIMEDDELALDL---EDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRITKICD 812
 QY 833 FGLARDILSDSSVYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSIVNPNY 892
 Db 813 FGLARDIKDSDNYVVKGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSIVNPNY 872
 QY 893 FGLPVDANFYKLIQSGFKMEOPPFYATGIIYFMOSCHAFDSKRPSPNLTSLFCCQLAE 952
 Db 873 FGLPVDANFYKLIQSGFKMEOPPFYATGIIYFMOSCHAFDSKRPSPNLTSLFCCQLAE 932
 QY 953 A 953
 Db 933 S 933
 RESULT 7
 KWMS HUMAN STANDARD; PRT; 972 AA.
 AC P07333;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Macrophage colony stimulating factor 1 receptor precursor (CSF-1-R)
 DE (EC 2.7.1.12) (Fms proto-oncogene) (c-fms) (CD115 antigen).
 GN CSF1R OR FMS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89239490; PubMed=2524025;
RA Hampe A., Shamoon B.M., Gobet M., Sherr C.J., Galibert F.;
RT "Nucleotide sequence and structural organization of the human FMS
RL proto-oncogene.";
RN [2]
RP Oncogene Res. 4:9-17(1989).
RX SEQUENCE FROM N.A.
RX MEDLINE=86175013; PubMed=2421165;
RA Cousens L., Van Beveren C., Smith D., Chen E., Mitchell R.L.,
RA Isacke C.M., Verma I.M., Ullrich A.;
RT "Structural alteration of viral homologue of receptor proto-oncogene
RL fms at carboxyl terminus.";
RN [3]
RP Nature 320:277-280(1986).
RX SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=97179223; PubMed=9027509;
RA Andre C., Hampe A., Lachaume P., Martin E., Wang X.P., Manus V.,
RA Hu W.X., Galibert F.;
RT "Sequence analysis of two genomic regions containing the KIT and the
RL FMS receptor tyrosine kinase genes.";
RN [4]
RP Genomics 39:216-226(1997).
RX SEQUENCE OF 1-16 FROM N.A.
RX MEDLINE=89261741; PubMed=2524648;
RA Visvader J., Verma I.M.;
RT "Differential transcription of exon 1 of the human c-fms gene in
RL placental trophoblasts and monocytes.";
RN [5]
RP Mol. Cell. Biol. 9:1336-1341(1989).
RX SEQUENCE OF 1-16 FROM N.A.
RX MEDLINE=86281820; PubMed=3525854;
RA Wheeler E.F., Roussel M.F., Hampe A., Walker M.H., Fried V.A.,
RA Look A.T., Rettemier C.W., Sherr C.J.;
RT "The amino-terminal domain of the v-fms oncogene product includes a
RL functional signal peptide that directs synthesis of a transforming
CC glycoprotein in the absence of feline leukemia virus gag sequences.";
CC [1]. Virol. 59:224-233(1986).
CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:13-21(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1999017666.g.htm".
CC -----
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CC EMBL; U63963; AAB51696.1; -
CC EMBL; M14002; AAA35849.1; -
CC EMBL; X03663; CAA27300.1; -
CC PIR; S08123; TVHUMD.
CC HSSP; P11362; 1PFGK.
CC Genew; HGNC:2433; CSF1R.
CC MIM; 164770; -
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR003600; Ig_Like.
CC InterPro; IPR001824; RTKinaseIII.

DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG_Like; 3.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain; Repeat; Polymorphism.
FT SIGNAL 1 19
FT CHAIN 20 972
FT MACROPHAGE COLONY STIMULATING FACTOR I
FT RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 20 512
FT TRANSMEM 513 537
FT DOMAIN 538 972
FT DOMAIN 24 104
FT DOMAIN 107 197
FT DOMAIN 204 298
FT DOMAIN 299 399
FT DOMAIN 400 505
FT DOMAIN 582 910
FT NP_BIND 588 596
FT BINDING 616 616
FT ACT_SITE 778 778
FT DISULFID 42 84
FT DISULFID 127 177
FT DISULFID 224 278
FT DISULFID 419 485
FT MOD_RES 699 699
FT MOD_RES 708 708
FT MOD_RES 809 809
FT CARBOHYD 45 45
FT CARBOHYD 73 73
FT CARBOHYD 153 153
FT CARBOHYD 240 240
FT CARBOHYD 275 275
FT CARBOHYD 302 302
FT CARBOHYD 335 335
FT CARBOHYD 353 353
FT CARBOHYD 412 412
FT CARBOHYD 428 428
FT CARBOHYD 480 480
FT VARIANT 969 969
FT CONFLICT 54 54
FT SEQUENCE 972 AA; 107983 MW; A8D99BE237573FE8 CRC64;
SQ
Query Match 23.2%; Score 1221.5; DB 1; Length 972;
Best Local Similarity 32.5%; Pred. No. 2.9e-74;
Matches 330; Conservative 152; Mismatches 331; Indels 201; Gaps 33;
QY 76 VYEAAVVEAESGSIITQVQLATPGDLSCLWVFKHSSIGCQPHFDLQNRGVSMAL--- 132
DB 22 VIEPSVPELVVKGAT--VTLRCVGVNGSVEMDGPSPS-----PHWTLYSDG--SSSILSTN 72
QY 133 NVITQAGEVLLHLIQSERANYTVLTVNVRTQTLVLRPY-----FRKMNQDALL-C 185
DB 73 NATFQNTGTYRCTEPGDPGLGSSAAIHLYKDP-----ARPNVLAQEVVVFEDQDALLPC 127
QY 186 ISEGVPEPTVEWVLCSSHRESCKEEGPAVVRKEEK-----VLHE---LF 226
DB 128 L----LTDPLV-----BAGSLVVRGRLMRHTNYSFSPHGTIIRAKIQ 171
QY 227 GTDIRCCARNALGRECTKLTFTIDLNQAPQSTLP-----QLFLKVGEPPLTRCKAI 276

Db 172 SDYQCSALMG-GR---KVMISIRLKVKQVPCPPALTLVPAELVIRGEAAQIVCSAS 227
Qy 277 HYNHGFLTWELDKALEBSYEMSTYSNRTWIRILLAFVSSVGRNDGYTCSS-- 334
Db 228 SVDVNFDFLOHNHTKL---AIPQSDFNHRVQ-KVLTNLNDQDFQAHAGNSCVASNV 283
Qy 335 --KHPQSALVTILEKGFNINATSQB-EYEDPYERKFCFSVRPKAYPRIR-CTWIFSQAS 390
Db 284 QGKH-STSMFRVVSAYNLNLSQNLIOEVTYVGEGLNKLKVMVEAYEGLGFNWTY---- 338
Qy 391 FPCQRLGDEGVISKPCDHKNP-----GEYIFVAEN 423
Db 339 -----LGPFSHQBPPLANATTKOTYRHTFTLSLRLKPSAGRYSLARN 385
Qy 424 DDAQFTMETLNRKPKOV-----LANASQASQSSDGYPLPSWTWKCKSDKSPNCTEE 478
Db 386 PGWRALTFTLURYPPVSVIWFINGSGT-LLCAASGYPPQNVVTWLOCSGHTDRCEA 444
Qy 479 IPEGVNVN---KKNARKVFCQWVSSSTLNNSEAGKLLVKKCCAYNSMGTSCTIFLNSPG 534
Db 445 QVLQVNDPPPEVLSQEPFKVTVQSLLTVETLEHNTQYECRAHNSVSGSGWAFIPISAG 504
Qy 535 PFPPIODNISFYATIGLC---LPIVVLVILCHYKKQFRYSQLOMIQVTPGLDNEYF 591
Db 505 AHTHPDEFLFTPVWACMSIMALLLLLLLYKKQKPKYQVRWKIIE--SYEGNSYT 562
Qy 592 YVDFRYEYDLKWEFFRENLEKGVLSGAGFGVMNATAGISKTGYSIQVAVKMLKEKA 651
Db 563 FIDPTQLPYNEKWEFFRNLIQFGKTLGAGAFGKVEATFGLGKEDAVLVKAVKMLKSTA 622
Qy 652 DSEKALMSLKMVTHLGHNDVNLGACTLGGPVYLVFEVCCYGDLLNLYRSKREKF 711
Db 623 HADEKALMSLKMVTHLGHNDVNLGACTHGGPVLVFEVCCYGDLLNLYRSKREKF 680
Qy 712 HRTWTEIFKEHNFSSYPTFOAHNSNMPGSRVQLHPPLDQSLGFGNSNTHSEDE----- 766
Db 681 -----AMLGP---SLSPQDPEGGVDYKNIHLEKKYVRD 712
Qy 767 -----IEYENQKLAEE---EEDLNLVTFEDLLCFAYQVAKMGFELEFK 808
Db 713 SGFSQGVDTYEMRPVSTSNDSFSDQDLKEDGRPLERLDLHFSQVAQGNFALASK 772
Qy 809 SCVHRDLAARNVLVTHGKVKVVICDGLARDILSDSSVVRGNARLPVKWMAPELSPFGIY 868
Db 773 NCIRHDAARNVLVTHGKVKVVICDGLARDILSDSSVVRGNARLPVKWMAPELSPFGIY 832
Qy 869 TIKSDVMSYGILLWEIPLSGLVNYPPIVDANFYKLIQSGFKMGPQPYATEGIYFVMSQC 928
Db 833 TVQSDVMSYGILLWEIPLSGLVNYPPIVDANFYKLIQSGFKMGPQPYATEGIYFVMSQC 892
Qy 929 WAFDSKRPSPFNLTSLGQLAAEAEACITSHLPKQAPQOQGLRAQSPQ 982
Db 893 WALEPHTRPFTFOQICSLF--OEQAQEDRRERDYNLNPSSS---RSGGSGSSSE 941

RESULT 8
KFMS_MOUSE STANDARD; PRT; 977 AA.
AC P09581; Q90B9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
DE (EC 2.7.1.12) (fms proto-oncogene) (c-fms).
GN CSF1R OR CSFMR OR FMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88217329; PubMed=2966922;
RA Rothwell V.M., Rohrschneider L.R.;

RT "Murine c-fms cDNA: cloning, sequence analysis and retroviral
RL expression.";
RN Oncogene Res. 1:311-324 (1987).
RP REVISIONS.
RA Rothwell V.M.;
RL Submitted (SEP-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RX MEDLINE=93181280; PubMed=8441691;
RA de Parseval N., Bordereaux D., Gisselbrecht S., Sola B.;
RL "Reassessment of the murine c-fms proto-oncogene sequence.";
RN Nucleic Acids Res. 21:750-750 (1993).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fietischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690 (2001).
RP SEQUENCE OF 1-16 FROM N.A.
RX MEDLINE=93268269; PubMed=8497248;
RA Yue X., Favot P., Dunn T.B., Cassady A.I., Hume D.A.;
RL "Expression of mRNA encoding the macrophage colony-stimulating factor
RT receptor (c-fms) is controlled by a constitutive promoter and tissue-
RL specific transcription elongation.";
RN Mol. Cell. Biol. 13:3191-3201 (1993).
RP AUTOPHOSPHORYLATION SITES.
RX MEDLINE=90258890; PubMed=2160591;
RA van der Geer P., Hunter T.;
RL "Identification of tyrosine 706 in the kinase insert as the major
RT colony-stimulating factor 1 (CSF-1)-stimulated autophosphorylation
RL site in the CSF-1 receptor in a murine macrophage cell line.";
CC Mol. Cell. Biol. 10:2991-3002 (1990).
CC -I- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -I- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC -----
CC EMBL; X06368; CAA29666.1; ALT SEQ.
CC EMBL; AK004947; BAB23691.1; -
CC EMBL; S62219; -, NOT_ANNOTATED_CDS.
CC -----
CC DR
CC DR
CC DR

DR PIR,*S01880; TVMSMD.
DR HSP; P11362; IFGK.
DR MGD; MGI.1339758; Csfir.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG like; 3.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TYFG; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 977
FT DOMAIN 20 511
FT TRANSFEM 512 536
FT DOMAIN 537 977
FT DOMAIN 24 104
FT DOMAIN 107 197
FT DOMAIN 204 298
FT DOMAIN 299 397
FT DOMAIN 398 503
FT DOMAIN 580 913
FT NP_BIND 586 594
FT BINDING 614 614
FT ACT_SITE 776 776
FT DISULFID 42 84
FT DISULFID 127 177
FT DISULFID 224 278
FT DISULFID 417 483
FT MOD_RES 697 697
FT MOD_RES 706 706
FT MOD_RES 807 807
FT CARBOHYD 45 45
FT CARBOHYD 73 73
FT CARBOHYD 302 302
FT CARBOHYD 335 335
FT CARBOHYD 389 389
FT CARBOHYD 410 410
FT CARBOHYD 449 449
FT CARBOHYD 478 478
FT CARBOHYD 491 491
FT CONFLICT 446 446
FT CONFLICT 553 553
FT CONFLICT 616 616
FT CONFLICT 744 744
FT CONFLICT 814 814
SQ SEQUENCE 977 AA; 109178 MW; 7EDF8310CCF98906 CRC64;
Query Match 23.2%; Score 1219; DB 1; Length 977;
Best Local Similarity 33.6%; Pred. No. 4.4e-74;
Matches 319; Conservative 148; Mismatches 327; Indels 154; Gaps 31;
QY 78 EAATVEAESGSIITLQVLAATPGDLSCLWFKHSSGLGCPHFQDQNRGIVSMALNTVET 137
Db 36 ETVTLRCVNSGSEWD-----GPISPYWTLDPSPGS-----TLTRNATFK 77
QY 138 QAGBY-LLHIQSERANYTVLFTVNRDTQLYV-----LRRPYFRMENQDALL-CIS 187
Db 78 NTGYTRCTELEDPMAGSTTI-----HLVVKDPAHSWLLAQAEVTVVEQEAFLPCL- 128
QY 188 EGVPEPTVEWLCSSHRESCKEGPAVRK-----EEKVLHFLGTDIRCC 233

Db 129 --ITDPALK-----DSVSLMEGRGQVLKRTVYFSPMRGFIIRKAKVL-----DSNTYVC 177
QY 234 ARNALGRECTKL-FTIDLN-----QAPQSTL-PQLPLKV-GEPLWIRCKAIHVNHGFLTW 286
Db 178 KTMVNGRESTGTGLWLVKVRVHPPEPPQIKLEPSKLRIRGEAAQVCSATNAEVENFVL 237
QY 287 BLEDKALE--EGSYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTC-SSSKHPSQSALV 343
Db 238 KRGDTKLEIPLNSDFQDNYKKVRAL-----SLNAVDFQDAGIYSCVASNDVGRTRATM 291
QY 344 T--ILEKGFINATSSQE--EYIDPYEKFCFSVRKAYPRIR--CTWIFSOASPPCEORGLE 399
Db 292 NFQVVEGAYLNLTSQSLQEVSGVDSLLITVHADAYPSIQHYNNTYLGPPE--DQKLE 350
QY 400 -----DGYSISKFDH--KNKPGEYIFYAENDDAQFTKMTFLNIRKPKQVLANASQ 450
Db 351 FITQRIAYRYTFFKLNRVKASEAGQYFLMAQNKAGMNLTFELTRYPPPEVSVTMPVN 410
QY 451 AS-----CSSDCYPLPSPWTWKCKSDKSPNCTBEIPGVVN-----KKANRKVFCQWSSSTL 502
Db 411 GSDVLFCDVSGYPOPSVTWMECRGHTDRCEAQAQLQVWNDTHPEVLSOKPFDKVIQSQL 470
QY 503 NMSEAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQDNISFYATIGLC---LPIIVVL 559
Db 471 PIGTLKHNMTYFCKTHNSVGNSSQYFRAVSLGQSKQLPDESFTFPVVVACMSVMSLLVLL 530
QY 560 IVLICHYKQFRYESQLQMTQ-VTGPLDNEYFYVDFRDYEDYDLKWEPPRENLEFGKVLG 618
Db 531 LLLLLYKQKPKYQVRWKIIERYEG---NSYTFIDTQLPYNEKWEPPRNQLQFGKTLG 587
QY 619 SGARGVNATAYGISKTGVSIOAVKMKKADSCVCEKALMSLKMTHLGHHDNINVL 678
Db 588 AGAFKVVVEATAFGLGKEDAVLVKAVKMLKSTAHADKEKALMSLKMTHLGHHDNINVL 647
QY 679 LGACTLSPVYLIFEYCCYDOLLNVLRSKRE-----KFRHTWTET 718
Db 648 LGACTHGGPVLVITEYCCYDOLLNVLRSKRE-----KFRHTWTET 707
QY 719 FKEHNFSSYPTFOAHSNMPGSRVQLHPLDQLSGFNGNSIHSEDEIEYENQRLAEE 778
Db 708 RRDGSGFS-----SQGVDTYVEMRPVSTSSDSFFKQD-----L 740
QY 779 BEEDNLVITPFDLLCFAYOVAKGHEFLEKSCVHRDLAARNVLVTHGKVVKICDFGLARD 838
Db 741 DKEASRPLELDLHFFSSQVAGMAFLASKNCIHRDVAARNVLLTSGHVAKIGDFGLARD 800
QY 839 ILSDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIIFSLGVNYPGIPVD 898
Db 801 IMNDSNVVVKGNARLPVKWMAPESLFDCVYTVQSDVWSYGILLWEIIFSLGVNYPGIPVD 860
QY 899 ANFYKLQSGFKMEQPPFYATEGIFYVMQSWAFDSKRPSFNLTSFL 946
Db 861 NKFYKLVDGYQMAQPVFAPKNIIYSIMQSCWDLPTREPTFOQICFLL 908
RESULT 9
KIT_BOVIN
ID_KIT_BOVIN STANDARD; PRT; 977 AA.
AC P43481;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCPR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

(EC 2.7.1.112) (fms proto-oncogene) (c-fms).
 DE CSF1R OR CSFMR OR FMS.
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Wistar; Tissue=Skeletal muscle;
 RX MEDLINE=93001225; PubMed=1389227;
 RA Borycki A.G.; Gullier M.; Leibovitch M.P.; Leibovitch S.A.;
 RT "Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence
 RL analysis and regulation during myogenesis.";
 RL Growth Factors 6:209-218(1992).
 CC -1- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
 CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X61479; CAA43706.1; -
 DR PIR: S16385; S16385.
 DR HSP; P11362; IFGK.
 DR InterPro; IPR000719; Ruk_pkinase.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003598; IG_C2.
 DR InterPro; IPR003600; IG_Like.
 DR InterPro; IPR001824; RKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG_Like; 3.
 DR SMART; SM00408; IGG2; 1.
 DR SMART; SM00219; TyrK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 978
 FT MACROPHAGE COLONY STIMULATING FACTOR I
 FT RECEPTOR.
 FT DOMAIN 20 511
 FT TRANSMEM 512 536
 FT DOMAIN 537 978
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 104
 FT DOMAIN 107 197
 FT DOMAIN 197 204
 FT DOMAIN 204 298
 FT DOMAIN 299 397
 FT DOMAIN 398 503
 FT DOMAIN 580 914
 FT NP BIND 586 594
 FT BINDING 614 614
 FT ACT SITE 776 776
 FT DISULFID 42 84
 FT DISULFID 127 177
 FT DISULFID 224 278
 FT DISULFID 417 483
 FT MOD_RES 697 697
 FT PHOSPHORYLATION (AUTO-) (IN VITRO)

(BY SIMILARITY).
 FT MOD_RES 706 706
 FT PHOSPHORYLATION (AUTO-) (IN VIVO)
 FT (BY SIMILARITY).
 FT MOD_RES 807 807
 FT PHOSPHORYLATION (AUTO-) (IN VITRO)
 FT (BY SIMILARITY).
 FT CARBOHYD 45 45
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 73 73
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 302 302
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 335 335
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 389 389
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 410 410
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 449 449
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 478 478
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 491 491
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 978 AA; 109264 MW; 0A68456EF56BC7E3 CRC64;
 Query Match 23.0%; Score 1210; DB 1; Length 978;
 Best Local Similarity 33.5%; Pred. No. 1.8e-73;
 Matches 318; Conservative 147; Mismatches 329; Indels 154; Gaps 31;
 QY 78 EAATVEVAESGSITLQVQLATPGDLSCLWVFKHSSIGCOPHFDLQNRGIVSMALNVET 137
 DB 36 ETVTLRCVNSGVND-----GPISPYWTLDPSPGS-----TLTRNATFK 77
 QY 138 QAGEY-LLHIQSERANYTLFTVNRDITLYV-----LRRPYPRKMNQDALL-CIS 187
 DB 78 NTGTYRCTELEDPMAGSTI-----HLYVKDPAHWNLLAQEVTVVGGQAVLPCL- 128
 QY 188 EGVPEPTVWVLCSSHRESCKEKGPAVRK-----EKVLHELPGTDIRCC 233
 DB 129 --ITDPALK-----DSVSLMREGGRVLRKTVYFFSAMRGFIIRKAKVL-----DSNTYVC 177
 QY 234 ARNALGRECTKL-FTIDLN-----QAPOSTL-PQLFLKV-GEPLWIRCKAIHVNHGGLTW 286
 DB 178 KTMVNGRESTGTGWLKVRNVHPEPPQIKLEPSKLVIRGEAAQIVCSATNAEVENVIL 237
 QY 287 ELEDKALE--EGSYFEMSTYSTNRMTIRILLAFVSVGRNDTGYYTC-SSSKHPSOSALV 343
 DB 238 KRGDTKLEIPLNSDFQDNYKKVRAL-----SLNAVDFQDAGIYSCVASNDVGTATM 291
 QY 344 T--ILEKGFINATSQE-EYEIDPYEKFCFSVRFKAYPRIR-CTWIFSOASPFCEORGLE 399
 DB 292 NFQVVEASVNLNLTSEQSLQEVSGVDSLTLTVHADAYPSIQHYNVNLYLGPFPPE-DQKLE 350
 QY 400 -----DCYSISKCDH--KNKPGEYIPIYAENDDAQFTKMTFLNIRKKPOVLANSASQ 450
 DB 351 FITQRAIYRYTFLKFLNRYKASEAGQYFLMAQNKAGMNNLTFLTILRYPEVSVTWMPVN 410
 QY 451 AS-----CSSDGYPLPSWTWKCKSDKSPNCTEIPGCVN-----KANRKYFGQWVSSSTL 502
 DB 411 GSDVLCFVSGVGPQPSVTWMECRGHTDRCDQAALQVWNDTHPEVLSQLPDKVITQSOL 470
 QY 503 NMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGFPFPFIQDNISFYATIGLC---LPFIIVL 559
 DB 471 PIGTLKHNMTYFCKTHNSVGNSSQYFRAVSLGSKQLPDESFTPTVVVACMSVNSLLVLL 530
 QY 560 IVLI CHYKKQRYESOLOMIO-VTGPLDNEYVDPRDYEYDLKWEPPRENLEFGKVLG 618
 DB 531 LLLLYLYKKQPKYQVRWKIIRYEG---NSYTFIDPTQLPYNEKWEFFPRNNLPQFKTLG 587
 QY 619 SGAFGRVMNATAVGSKTGVSTOAVKMLKEKADSKCEKALMSELKMTWHLGHHDNIVNL 678
 DB 588 AGAFGRVVEATAFGLGEDAVLKAVVMUKSTAHADEKEALMSELKINSINGHOGHEINVL 647
 QY 679 LGACTLSGEPVLIFFEYCCYGDLLNLYLSKRE-----KPHRTWTEI 718
 DB 648 LGACTHGGFVLVITEYCCYGDLLNLYLSKRE-----KPHRTWTEI 707
 QY 719 FKEHNPSSYPTFOAHNSNMPGSRVQLHPPLDQLSGFNGNSIHSDEIEYENOKLAE 778
 DB 708 RRDSGFS-----SQGVDTVEMRPVSTSSSDSPFKQD-----L 740
 QY 779 EREDNLVLTFFDLCCFAYQVAKMEFLEPKSCVHRDLAARNVLVTHGKVKIKCDFGLARD 838


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Db 741 DKPSRPLELWDLHFSQVQAQWAFASKNCIHRDVAARNVLLTSGHVAKIGEGFLARD 800
QY 839 ILSDSSVYVRNARLPVKWMAPESEFEGYITKSDVMSYGILLWEIFSLGNVPYGPVD 898
Db 801 IMDSNTVYVKNARLPVKWMAPESEFEGYITKSDVMSYGILLWEIFSLGNVPYGPILVN 860
QY 899 ANFKVLTQSGKMEQPPFATGIFVWQSCWAFDSRKEPSPNLTSLF 946
Db 861 NKFYKVLKGYQMAQPVFAPKPNYISIMQSCWDLBETRRPTQQICFL 908

RESULT 11
KIT_CANFA
ID KIT_CANFA STANDARD; PRT; 975 AA.
AC O97799;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN Kit.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99142897; PubMed=9989791;
RA Ma Y., Longley B.J., Wang X., Blount J.L., Langley K., Caudhey G.H.;
RT "Clustering of activating mutations in c-KIT's juxtamembrane coding
RT region in canine mast cell neoplasms.";
RL J. invest. Dermatol. 112:165-170(1999).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC EMBL; AF04249; AAD02327.1; -.
CC HSSP; P11362; IFGK.
CC InterPro; IPR00719; Euk_pkinase.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003600; Ig like.
CC InterPro; IPR001824; RtkKinaseIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00047; Ig; 2.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 2.
CC SMART; SM00409; IG; 2.
CC SMART; SM00410; IG; 1.
CC SMART; SM00219; TyKc; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
CC PROSITE; PS00240; RECEPTOR TYR_KIN_III; 1.
CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;

```

```

KW Immunoglobulin domain.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 975 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT DOMAIN 25 519 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 520 542 POTENTIAL.
FT DOMAIN 543 975 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 588 936 PROTEIN KINASE.
FT NP_BIND 594 602 ATP (BY SIMILARITY).
FT BINDING 622 622 ATP (BY SIMILARITY).
FT ACT_SITE 791 791 BY SIMILARITY.
FT MOD_RES 822 822 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. ) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. ) (POTENTIAL).
SQ SEQUENCE 975 AA; 109335 MW; 8F570BDB9F05B1CB CRC64;

Query Match 22.9%; Score 1207; DB 1; Length 975;
Best Local Similarity 31.9%; Pred. No. 2.8e-73;
Matches 330; Conservative 165; Mismatches 375; Indels 166; Gaps 34;

QY 31 LPVIKCVLISHENNGSSAGKPPSSVYRMVRGSPEDLOCTPRROSEGTVEYEAATVEVAESGSI 90
DB 11 LCVLLLLLLGVRGTSS--QPS-----VSCEPSPSIHPAKSELIVSVDG- 54

QY 91 TLQVQLATPGDLSCLVWPKHSSLGCPHFDLQNRGIVSMALNVTTQAGEYLLHQISER 150
DB 55 ELRLSCTDGFVK--WTPE--TLG-QLNENTHNEWITEKA-----EAGTGTGNTCTNR 102

QY 151 ANYTVLFTVVRD--TOLVLRARPYERKMNQDALLACISGEVPEPTVWVLCSSHRESCKE 209
DB 103 DGLRSIYVVRDPAKFLVDLPYKREGNDTLVR-----PLTDEVTWYSURGC-- 153

QY 210 EGPVAVRKEEVLHFLGTDIR-----C--CARNALGRE-CTKLTFTIDLNAQPS- 256
DB 154 BGKPLKDLTVPADPKAGITIRNVKREYHRLCHCSAQDKGTVLTKKFTLVKRAAIRAV 213

QY 257 -----TLQPLFKVGEPLWIRCKAIHNVHFGLTWELEDKALEEGSYFEMSTYSTNRMT 311
DB 214 PWSVSKTSSLLKEGEAPVMCFIKDVSFVDSMMWIKENSQQTNAQTQSNWHHGDNFPE 273

QY 312 RILLAFVSSVGRNDTGYTCCSSSKHPSQSALVTILE---KGFINA-TSQOEYEIDPYEK 367
DB 274 RQEKLISSARVNSDGVPMCVANNTFGSANVTTTLEVVVDKGFNIFPMWSTTIFVNDGQN 333

QY 368 FCFSVRPKAYPR-IRCTWIFSQASF--PCEQRGLDGYISIKFCDH-----KNKPGSY 417
DB 334 VDLIVEYEAYPKPEHQWIYMNRTFTDKWEDYPKSDNESNRYVSELHLTLRKGNEGTY 393

QY 418 IFYAENDDAQFTKMTFLNIRKKPQVLANASQA--SCSSDGYPLPSPWTKKCSKSPNC 475
DB 394 TFOVSNDSVNSVTFNVYVNTKPEILLTHESLTNGMLQCWVAGPEPAVGWYFCPGAQR 453

QY 476 TEEI-PEGVWKNKANRKYVFGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETFLNSPG 534
DB 454 SVPIGPMVDVQNSLSLSPSGKLKVQSSIDYSAFKNGTVECRAYNVNGRS--SAFNF--- 508

QY 535 PFPTIQDNISFYATIGLCLPFIV-----VLIVLICHVKYKQFRYESOLOMI-QVTGLD 587
DB 509 -FAFKEQIHPHTLFTPLLIIGFVIAAGMMCIIVMLITYKYLQKPMYEVQWVVEEING--- 564

QY 588 NEYFYVDFRDYEDLKWEPFRENLEFGVLGSGAFGRVNNATAYGISKTGVSIOAVKML 647
DB 565 NNYVYIDPTQLPYDHKWEFPNRNLSFGKTLGAGAFGVVEATAYGLIKSDAAMTAVAKML 624

QY 648 KEKADSCKEALMSELKQWTHLGHHDNINVLGACTLSGPVYLIFFEYCCYGLLLNVLRSK 707

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Db 625 KPSAHLTEREALMSELKVLGYLGNHNVLLGACTVGGPTLVITEYCCYGDLLNFLRRK 684
QY 708 REKPHRTWTETFEKHNPSSTYPTQAHNSNMPGSRVQLHPPLDQLSGFNGNSHTSDEI 767
Db 685 RDSFICSKQE---DHG-----EVALYK-----NLHSSKSS 712
QY 768 -----EYENQK-----RLABEEEDLN-----VITFEDLLCFA 795
Db 713 CSDSTNEYMDKFCVSVVFTKADKRSRIGSYIERDVTVPAINMEDDELALDLEDLSFS 772
QY 796 YQAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDILSDSSVYVRGNARLPV 855
Db 773 YQAKGMAFLAKNCNHRDLAARNILLTHGRITKICDFGLARDIKDSDNYVYKGNARLPV 832
QY 856 KWAPESLFGIYTIKSDVMSYGLLWEISLGNVPGIPVDANFYKLQSGFKMQPFP 915
Db 833 KWAPESIFNCVTFESDVMWSYGLFELWELSLGSSPYGMPVDSKFYKMKIEGFRMLSPE 892
QY 916 YATEGIYFVMSQWAFDSRKRSPNLTSLFLGCOLAAEEACIRTSIHLPKQAAPQORGG 975
Db 893 HAPAEWYDINKTWDADPLKRPFPKQIVOLIEKQISDSTN-----HIYSNLAN----- 940
QY 976 LRAQSPQORVKIHRER 991
Db 941 -CSPNPERPVVDHSVR 955

RESULT 12
KIT HUMAN
ID KIT HUMAN STANDARD; PRT; 976 AA.
AC PI0721;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen).
GN KIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Term placenta, and Fetal brain;
RX MEDLINE=88111521; PubMed=2448137;
RA Yarden Y., Kuang W.-J., Yang-Feng T., Coussens L., Munemitsu S.,
RA Dull T.J., Chen E., Schlessinger J., Francke U., Ullrich A.;
RT "Human proto-oncogene c-kit: a new cell surface receptor tyrosine
RT kinase for an unidentified ligand.";
RL EMBO J. 6:3341-3351(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93064697; PubMed=1279499;
RA Giebel L.B., Strunk K.M., Holmes S.A., Spritz R.A.;
RT "Organization and nucleotide sequence of the human KIT (mast/stem
RT cell growth factor receptor) proto-oncogene.";
RL Oncogene 7:2207-2217(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97179223; PubMed=9027509;
RA Andre C., Hampe A., Lachaume P., Martin E., Wang X.P., Manus V.,
RA Hu W.X., Galibert F.;
RT "Sequence analysis of two genomic regions containing the KIT and the
RT FMS receptor tyrosine kinase genes.";
RL Genomics 39:216-226(1997).
RN [4]
RP VARIANT LYS-583.
RX MEDLINE=92291284; PubMed=1376329;
RA Fleischman R.A.;
RT "Human piebald trait resulting from a dominant negative mutant allele
RT of the c-kit membrane receptor gene.";
RL J. Clin. Invest. 89:1713-1717(1992).

RN [5]
RP VARIANT LEU-584.
RX MEDLINE=92133600; PubMed=1370874;
RA Spritz R.A., Giebel L.B., Holmes S.A.;
RT "Dominant negative and loss of function mutations of the c-kit
RT (mast/stem cell growth factor receptor) proto-oncogene in human
RL piebaldism.";
RL Am. J. Hum. Genet. 50:261-269(1992).
RN [6]
RP VARIANT ARG-664.
RX MEDLINE=92020918; PubMed=1717985;
RA Giebel L.B., Spritz R.A.;
RT "Mutation of the KIT (mast/stem cell growth factor receptor)
RT protooncogene in human piebaldism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8696-8699(1991).
RN [7]
RP VARIANT VAL-816.
RX MEDLINE=94013473; PubMed=7691885;
RA Furitsu T., Tsujimura T., Tono T., Ikeda H., Kitayama H.,
RA Koshimizu U., Sugahara H., Butterfield J.H., Ashman L.K.,
RA Kanayama Y., Matsuzawa Y., Kitamura Y., Kanakura Y.;
RT "Identification of mutations in the coding sequence of the proto-
RT oncogene c-kit in a human mast cell leukemia cell line causing
RT ligand-independent activation of c-kit product.";
RL J. Clin. Invest. 92:1736-1744(1993).
RN [8]
RP VARIANTS PIEBALDISM GLY-791 AND VAL-812.
RX MEDLINE=93322624; PubMed=7687267;
RA Spritz R.A., Holmes S.A., Itin P., Kuester W.;
RT "Novel mutations of the KIT (mast/stem cell growth factor receptor)
RT proto-oncogene in human piebaldism.";
RL J. Invest. Dermatol. 101:22-25(1993).
RN [9]
RP VARIANT PIEBALDISM 893-GLU--PRO-896 DEL.
RX MEDLINE=96287384; PubMed=8680409;
RA Riva P., Milani N., Gandolfi P., Larizza L.;
RT "A 12-bp deletion (7818del12) in the c-kit protooncogene in a large
RT Italian kindred with piebaldism.";
RL Hum. Mutat. 6:343-345(1995).
RN [10]
RP VARIANT GIST VAL-559 DEL.
RX MEDLINE=98361155; PubMed=9697690;
RA Nishida T., Hirota S., Taniguchi M., Hashimoto K., Isozaki K.,
RA Nakamura H., Kanakura Y., Tanaka T., Takabayashi A., Matsuda H.,
RA Kitamura Y.;
RT "Familial gastrointestinal stromal tumours with germline mutation of
RT the KIT gene.";
RL Nat. Genet. 19:323-324(1998).
CC -|- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -|- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A DEVELOPMENTAL
CC ABNORMALITY KNOWN AS PIEBALDISM. AN AUTOSOMAL DOMINANT GENETIC
CC DISORDER OF PIGMENTATION CHARACTERIZED BY CONGENITAL PATCHES OF
CC WHITE SKIN AND HAIR THAT LACK MELANOCYTES.
CC -|- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A GASTROINTESTINAL
CC STROMAL TUMOR (GIST).
CC -|- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -|- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD117 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd117.htm"
CC -|- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/KITID127.html".
CC -----
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EMBL	X06182	CAA29548.1	-	
EMBL	X69301	CAA49159.1	JOINED	
EMBL	X69302	CAA49159.1	JOINED	
EMBL	X69303	CAA49159.1	JOINED	
EMBL	X69304	CAA49159.1	JOINED	
EMBL	X69305	CAA49159.1	JOINED	
EMBL	X69306	CAA49159.1	JOINED	
EMBL	X69307	CAA49159.1	JOINED	
EMBL	X69308	CAA49159.1	JOINED	
EMBL	X69309	CAA49159.1	JOINED	
EMBL	X69310	CAA49159.1	JOINED	
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EMBL	X69316	CAA49159.1	JOINED	
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DR	HSSP	P11362	LFKG	
DR	GENE	HGNC:6342	KIT	
DR	MIM	164920	-	
DR	MIM	172800	-	
DR	MIM	606764	-	
DR	InterPro	IPR000719	Euk_pkinase	
DR	InterPro	IPR003006	Ig_MHC	
DR	InterPro	IPR003598	Ig_c2	
DR	InterPro	IPR001824	RTKinaseIII	
DR	InterPro	IPR001245	Tyr_pkinase	
DR	Pfam	PF00047	ig; 1	
DR	Pfam	PF00069	pkinae; 1	
DR	ProDom	PD000001	Euk_pkinase; 2	
DR	SMART	SM00408	IGC2; 1	
DR	SMART	SM00219	TyPKC; 1	
DR	PROSITE	PS00107	PROTEIN KINASE ATP; 1	
DR	PROSITE	PS00109	PROTEIN KINASE TYR; 1	
DR	PROSITE	PS00240	RECEPTOR TYR KIN III; 1	
DR	PROSITE	PS50011	PROTEIN KINASE DOM; 1	
KW	Proto-oncogene	Tyrosine-protein kinase; Receptor; Transmembrane;		
KW	Transferase	Glycoprotein; Phosphorylation; ATP-binding; Signal;		
KW	Immunoglobulin domain; Disease mutation			
FT	SIGNAL	1		
FT	CHAIN	23	976	MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT	DOMAIN	23	520	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	521	543	POTENTIAL.
FT	DOMAIN	544	976	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	589	937	PROTEIN KINASE.
FT	NP_BIND	595	603	ATP (BY SIMILARITY).
FT	BT BINDING	623	623	ATP (BY SIMILARITY).
FT	ACT SITE	792	792	BY SIMILARITY.
FT	MOD_RES	823	823	PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	CARBOHYD	130	130	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	145	145	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	283	283	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	300	300	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	320	320	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	352	352	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	367	367	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	486	486	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARIANT	559	559	MISSING (IN GIST).
FT				/FTId=VAR_007965.
FT	VARIANT	583	583	E -> K (IN PIBALDISM).
FT				/FTId=VAR_004104.
FT	VARIANT	584	584	F -> L (IN PIBALDISM).
FT				/FTId=VAR_004105.
FT	VARIANT	664	664	G -> R (IN PIBALDISM).

[illegible]

Db 779 GMAFLASNCNTHRLAARNILLTHGRITKICDGLARDIKNDNSYVVGKGNARLPVKWMAP 838
 Qy 861 ESLFEGITIKSDVWSYGILLWEIFSLGWNYPGIPVDANVYKLIQSGFKMEQPEYATEG 920
 Db 839 ESIFNCVITFSDVWSYGIFLWEIFSLGSSYPGMPVDKFKYMIKEGFRMLSPHAPAE 898
 Qy 921 IYFVWQSWAFDSRKPSFNLTSFLGQLAEA 953
 Db 899 MYDIMKTCDWADPLKRPFFKQIVOLIEKQISES 931

RESULT 13
 KIT_CHICK
 ID_KIT_CHICK STANDARD; PRT; 960 AA.
 AC Q08156;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Brain;
 RX MEDLINE=9329295; PubMed=7685729;
 RA Sasaki E., Okamura H., Chikamune T., Kanai Y., Watanabe M.,
 RA Naito M., Sakurai M.;
 RT "Cloning and expression of the chicken c-kit proto-oncogene.";
 RL Gene 128:257-261(1993).

-1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGH IN THE BRAIN AND TESTES AND ALSO
 CC PRESENT IN THE BURSA OF FABRICIUS, HEART, KIDNEY, LUNG, SPLEEN
 CC THYMUS AND OVARY.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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CC ENBL; D13225; BAA02506.1; -.
 CC PIR; JN0677; JN0677.
 CC HSSP; P11362; IFGK.
 CC InterPro; IPR00719; Euk_pkinase.
 CC InterPro; IPR003596; IG_c2.
 CC InterPro; IPR01824; RTKinaseIII.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00047; ig; 3.
 CC Pfam; PF00069; pkinase; 1.
 CC ProDom; PD000001; Euk_pkinase; 2.
 CC SMART; SM00408; IGC2; 1.
 CC SMART; SM00219; Tyrc; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 CC PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain.
 FT SIGNAL 1 24
 FT CHAIN 25 960
 FT DOMAIN 25 505
 FT TRANSMEM 506 530
 FT DOMAIN 531 960
 FT DOMAIN 575 913
 FT NP_BIND 581 589
 FT BINDING 609 609
 FT ACT_SITE 777 777
 FT MOD_RES 808 808
 FT CARBOHYD 76 76
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 FT CARBOHYD 149 149
 FT CARBOHYD 269 269
 FT CARBOHYD 286 286
 FT CARBOHYD 306 306
 FT CARBOHYD 318 318
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 FT CARBOHYD 469 469
 SQ SEQUENCE 960 AA; 107311 MW; 0E93850527AB68F6 CRC64;

Query Match 22.4%; Score 1181; DB 1; Length 960;
 Best Local Similarity 31.8%; Pred. No. 1.5e-71;
 Matches 310; Conservative 159; Mismatches 356; Indels 150; Gaps 30;

Qy 45 GSSACKPSYRMVRCSPEDIOCTPRQSEGVYEAATVEVAEGSSITLQVOLATPGDLSC 104
 Db 24 GSPVHESSLVNVNKEELKCN-----EAGPVTFWTFQNSDPSAKR 65
 Qy 105 L-----WYFKHSSLCQPHFDLQNRGIVSMALNVETQAGEYLLHQSERANYTVLFTV 159
 Db 66 ISNEKEWTKNATRIDIGRYECKSG-----SIVN-----SFYV 99
 Qy 160 NVRTQLVLRPYPVKMKNODALLCISEGVPEPTVWVLCSSHRESCKEAGPAVVRKEE 219
 Db 100 FVKDPNVLFVDSLTYGKEDSDILLVCLTPDP-VLNFTLRKCDGKPLPKNTFFIPNPK 158
 Qy 220 ---KVLHELFTDIRCCAR-NALGRECTKLTIDINQAP-OSTLPOL-----FLKVG 266
 Db 159 GIINKVQSFSGYQCLAKNGVEKISEHIF---LNVRPVHKALPVIITLSKSYELLKEG 215
 Qy 267 EPLWIRCKAIHVNHGFLTWELEDKALEEGSYFEMSTYSTNRTMIRILLAFVSSVGRNDT 326
 Db 216 EEFVTCIITDVSVKASWISYKSAIVTSKRNLDGYERK----LTLNRSVGUNDS 271
 Qy 327 GYTCSSSKHP--SOSALVTI--LEKGFNATSOE-EYEDPYEKFCSVRFKAYPRIR 381
 Db 272 GEFTC-QAENPFKGTNAVTLKALAKGFVRLPATWMTTIDINAGONGNLTVEAYPK-- 328
 Qy 382 CTWIFSQSPFCEORGLDEGYSISKFDHKNK-----PGEYIF 419
 Db 329 -----PKEEYVMYMETLQNSSDHYKFKTVGNNSYTSSELHLRLKGTGGIYTF 378
 Qy 420 YAENDDAQFTKMTLNIRKKQVLANASASQ--ASCSDGYPLPSWTKKCDKSPNCTE 477
 Db 379 FVSNDSASSVTFFVYVKTKPEILLTDLMLGNDILOCVATGFFPATIYTWFCPTGTEORCLD 438
 Qy 478 E---IPEGVWNKKANRKY--FGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTIFLNS 532
 Db 439 SPTISPMDVKVSYTNSSVPSFERILVESTVNAS-MFKSTGTTCCEASSNGDK-SSVFFNF 496
 Qy 533 PGPPFFIODNISFYA-----TIGCLPFIIVLVILCHKKYKQFRYESQLOMI-QVTG 584
 Db 497 A-----IKEQIRTHFTLPTLLIAFGVAAAGLCIIIMWILYIYLPKPKYQVQWVEEING 551
 Qy 585 PLDNEYFYVDRDYEDLKWEEFFRENLEFGKVLGSAFGRVNNAATYGISKTVGSIQAV 644

Db 552 ---NNVYIDPTQPYDHKWEFFRNRLSFGTLGAGAFGKVEVETATAGLFSKSDAMTVAV 608
Qy 645 KWLKEKADSCKEALMSKLMTHLGHNDINVLGLACTLSGPPVYLIFECYCGDLLNLYL 704
Db 609 KWLKPSAHLTEREALMSKLYLGNHINIVNLGACTIGGPTLVITEYCYGDLNLF 668
Qy 705 RSKREKP-----HRTWTE--IFKEHNFSSYPTFOA-HSNSNPGSREVQLHPDQLSGFN 757
Db 669 RRRKDSFTCPKHEEAAVYENLLHQAEPTADAVNEMDMKPGSVAVPPKADKKRPVK 728
Qy 758 GNSIHSEDEIEYENOKRLAEEEDLNLVTFEDLLCPAYQVAKGWEFLKPSKVHRLDAA 817
Db 729 SGS-----YTDQVTLMLBEDLALDVEDLLSFSYQVAKGWSFLAKSKCHRLDAA 780
Qy 818 RNVLVTHGVKVICDFGLARDILSDSSVYVRGNARLPVKWMAPELPGIYTIKSDVMSY 877
Db 781 RNIILLTHGRITKICDFGLARDIRNDSNVYVKGARLPVKWMAPELPGIYTIKSDVMSY 840
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Db 841 GILLWELFSLGSSPPGMPVDSKFKYMKIKEYRMFSPSPSPPEMYDINKSCWDADLPQRP 900
Qy 938 SFPNLTSLFGCOLAE 952
Db 901 TFKQIVQLIEQOLSD 915

RESULT 14
KIT_FELCA
ID_KIT_FELCA STANDARD; PRT; 978 AA.
AC Q28889;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase kit) (c-kit).
GN KIT.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RA MEDLINE=95140426; PubMed=7530827;
RX Herbst R., Munemitsu S., Ullrich A.;
RT "Oncogenic activation of v-kit involves deletion of a putative
RT tyrosine-substrate interaction site";
RL Oncogene 10:369-379 (1995).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane receptor.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC
CC EMBL: S76596; AAB33207.1;
CC HSP; P11362; 1FGK.
DR InterPro:IPR000719; Euk_pkinase.

DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR001824; KinaseIII.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; ig; 1.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Ruk_pkinase; 2.
DR SMART: SM00409; IG_2.
DR SMART: SM00410; IG_like; 1.
DR SMART: SM00219; TyfK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 22
FT CHAIN 23 978 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT DOMAIN 23 521 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 522 544 POTENTIAL.
FT DOMAIN 545 978 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 590 938 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 596 604 PROTEIN KINASE.
FT BINDING 624 624 ATP (BY SIMILARITY).
FT ACT_SITE 793 793 ATP (BY SIMILARITY).
FT MOD_RES 824 824 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 978 AA; 109449 MW; 6D45472E07440B6B CRC64;
Query Match 22.4%; Score 1178.5; DB 1; Length 978;
Best Local Similarity 31.6%; Pred. No. 2.3e-71;
Matches 313; Conservative 162; Mismatches 373; Indels 143; Gaps 30;
Qy 36 CVLISHENNGSSAGKPSYRMVRSGLDQTPRQSGTGYEATVEAESGSLQVQ 95
Db 12 CVLLLLRVQTGSSQPSA-----SPGEWSLPSIH-PATSELIVSAGDEIRLL 57
Qy 96 LATPGDLSCLVWFKHSSILGCGPHFDLQNRGIVSMALNVTEQAGEYLLHIOSEANVT 155
Db 58 CTDPGFVK--WTFE--TLG-QSSEITHNEWITEKA-----EATNTGNVTC---TNGGGUSS 105
Qy 156 LFTVNVRD--TOLYLVRRPFRKMNODALLCI-----SEGVPPEP----- 193
Db 106 SIYVVRDPALFLVDLPYKGDHDTLVRCPLTDPVNTYSLRCGCKPLPKDLTFVTD 165
Qy 194 -----TVEWVLCSSHR--ESCKEGPAVVRKEEVKLHFLFGTDIRCCARNALGRBCTKLF 246
Db 166 PRAGITIRNVKREYHRLCLHCSAD-----RKGKSVLSKKFTLKVRAAIR-----AVP 212
Qy 247 TIDLNAQFQSTLPQLFLKVGEPFLWIRCKAIHVNHGFLGTWELEDKALBEGSYFEMSTYST 306
Db 213 VVVSQASH-----LLREGEFFSYMCLIKDVSSVSDSMWIKENSPQTNAAQPSQSNWHQG 266
Qy 307 NRTMIRILLAFVSSVGRNDTGYITCTSSSKHPSQSALVTILE---KGFINA-TSSQBEYBI 362
Db 267 DFNFRQRELTISSARVNDSGVMFYANNTFGSANVTITLEVVAKGFINIFPMANTTIIV 326
Qy 363 DPEYKFCFSVREPKAYPR-IRCTWIFSOASFPCQERGLDGYGISKFDHK----- 411
Db 327 NDGENVDLIVEAYPKPEHQRWVYM-----NRTLTDKWDYPKSDNESNRYVSELH 379

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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:51:00 ; Search time 70.9642 Seconds
(without alignments)
2880.307 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQRDRLLLVLSV.....RGLRAQSPORQVKIHRRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	24.1	976	13 Q9W755	Q9W755 brachydanio
2	1234.5	23.5	974	11 Q63702	Q63702 rattus ratt
3	1232.5	23.4	978	11 Q63116	Q63116 rattus norv
4	1220	23.2	954	13 Q91909	Q91909 xenopus lae
5	1215.5	23.1	974	13 Q98SU3	Q98SU3 danio dangi
6	1215.5	23.1	977	13 Q98SU1	Q98SU1 danio nigro
7	1214	23.1	977	13 Q918N6	Q918N6 brachydanio
8	1209.5	23.0	979	6 Q8WN23	Q8WN23 canis fami
9	1208	22.9	964	6 Q8W744	Q8W744 sus scrofa
10	1207	22.9	964	6 Q8TQ01	Q8TQ01 sus scrofa
11	1207	22.9	964	6 Q8TQ00	Q8TQ00 sus scrofa
12	1205	22.9	978	6 Q9XS93	Q9XS93 canis fami
13	1204.5	22.9	977	13 Q98SU2	Q98SU2 danio kerri
14	1201	22.8	948	6 Q9T8D7	Q9T8D7 trichosurus
15	1198.5	22.8	977	13 Q98SU4	Q98SU4 danio albol
16	1194	22.7	972	4 Q99662	Q99662 homo sapien

17	1188.5	22.6	975	13 P79750	P79750 fugu rubrip
18	1173	22.3	945	6 Q77589	Q77589 equus cabal
19	1170.5	22.2	724	6 Q9MYN0	Q9MYN0 bos taurus
20	1136	21.6	1059	13 Q9D849	Q9D849 brachydanio
21	1126.5	21.4	1087	13 Q9PUF6	Q9PUF6 gallus gall
22	1110	21.1	1097	11 Q8R406	Q8R406 rattus norv
23	1073	20.4	1019	13 Q8UVR8	Q8UVR8 fugu rubrip
24	1060	20.1	1048	13 P79749	P79749 fugu rubrip
25	1013.5	19.3	986	13 Q8UVR9	Q8UVR9 fugu rubrip
26	997.5	18.9	923	6 Q97745	Q97745 sus scrofa
27	980	18.6	1379	13 P79701	P79701 coturnix co
28	974	18.5	1327	13 Q8QHL3	Q8QHL3 gallus gall
29	961	18.3	1363	11 Q91ZT1	Q91ZT1 rattus norv
30	957	18.2	1301	13 Q8UWU9	Q8UWU9 brachydanio
31	946	18.0	1173	13 Q9PTL0	Q9PTL0 brachydanio
32	939	17.8	563	11 Q925F7	Q925F7 rattus norv
33	937.5	17.8	1345	11 Q8VCD0	Q8VCD0 mus musculu
34	901.5	17.1	323	11 Q9EQ22	Q9EQ22 rattus norv
35	877.5	16.7	323	11 Q9EQ24	Q9EQ24 rattus norv
36	833	15.8	345	13 Q9PVU7	Q9PVU7 letheron
37	820.5	15.6	350	13 Q91416	Q91416 xenopus lae
38	798	15.2	796	13 Q91287	Q91287 pleurodeles
39	793	15.1	766	4 Q96KM2	Q96KM2 homo sapien
40	793	15.1	785	4 Q96KM1	Q96KM1 homo sapien
41	793	15.1	819	4 Q96KM0	Q96KM0 homo sapien
42	791	15.0	824	13 Q90749	Q90749 gallus gall
43	790.5	15.0	806	13 Q90200	Q90200 brachydanio
44	790.5	15.0	820	4 Q96KL9	Q96KL9 homo sapien
45	788.5	15.0	922	13 Q90413	Q90413 brachydanio

ALIGNMENTS

RESULT 1

ID	Q9W755	PRELIMINARY;	PRT;	976 AA.
AC	Q9W755;			
DT	01-NOV-1999 (TrEMBLrel. 12, Created)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DB	Kit receptor tyrosine kinase.			
GN	Kit.			
OS	Brachydanio rerio (Zebrafish) (Zebra danio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=93396707; PubMed=10393121;			
RA	Parichy D.M., Rawls J.F., Pratt S.J., Whitfield T.T., Johnson S.L.;			
RT	"Zebrafish sparse corresponds to an orthologue of c-kit and is			
RT	required for the morphogenesis of a subpopulation of melanocytes, but			
RT	is not essential for hematopoiesis or primordial germ cell			
RT	development."			
RL	Development 126:3425-3436(1999).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-			
CC	PROTEIN KINASES.			
DR	EMBL; AF153446; AAD41890.1; -			
DR	HSSP; P11362; 1FGK.			
DR	ZFIN; ZDB-GENE-980526-464; kit.			
DR	InterPro; IPR000719; Euk_pkinase.			
DR	InterPro; IPR003598; Ig_C2.			
DR	InterPro; IPR003600; Ig_Like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR001824; RfKinaseIII.			
DR	InterPro; IPR001245; Tyr_pkinase.			
DR	Pfam; PF00047; Ig_3.			
DR	Pfam; PF00069; pkinase; 1.			
DR	ProDom; PD000001; Euk_pkinase; 2.			
DR	SMART; SM00408; IGC2; 1.			


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DR SMART; SM00410; IG like; 1.
DR SMART; SM00219; TyTKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase
SQ SEQUENCE 976 AA; 109278 MW; A80AA01658C1A2DA CRC64;

Query Match 24.1%; Score 1268; DB 13; Length 976;
Best Local Similarity 36.6%; Pred. No. 1.5e-102;
Matches 318; Conservative 138; Mismatches 302; Indels 110; Gaps 29;

QY 177 MENQDALLCISGVPETVEWLVCSHRESCKEKGPAV--VRKEEKVLHFGTDIRCCA 234
DB 138 MNLNLOKQ--DGQPLEN-----SLRYSASLETGVSQVKRKEGFCVCGTLDAAVT 189
QY 235 RNALGRECTKLTIDLQAQPOSTLP-----QLFLKVGELWIRCKAIHVNHGFLTWE 287
DB 190 KS--GR-----YQTVRLVDPDPPITLGGQQRVLLTGGKLSLSCSTSNVNSDIANKWK 242
QY 288 LE---DKALBEGSYFEMSTYNTMIRILLAFVSSVGRNDTGYTCSSSHPSQSA--- 341
DB 243 APNGVNSVHONSHL-----LTEPITHVTRTALSLSSVTMQDAGNYSCEAINEKGTAKPV 298
QY 342 LVTTLEKGFNATS--SOEEVIDYKPCFSVRKAYPRIC--TWIFSQAQFPCEQRGLE 399
DB 299 WVNIEYKGFNITSDVNSRVRAGESLSLRVNMVNAVPKPTFTFSNYS----- 346
QY 400 DGVYSIKFCOH-----KMKPGYIFVANDDAQFTKMTLNIK 438
DB 347 -GVKLTNTDTHVTSRTHGNSYTSSELKVLRLKVSSEGIYTFSCNLRDATITQTTEVHVS 405
QY 439 KPQVLANASA--SOASCSSDGYPLPSWTW-----KKCSKSPNCTBEIPEGVWNKKAN 489
DB 406 KPQIVSYEGPIDGQVRCVAEGYPTQIKWYICDLPKSHRCSNLL-NATQE-EEDVVTVTMT 463
QY 490 RKVFGQVSSSTLNSMAGKLLVKCCAYNSMGTSCTETIFLNSPGPPP---FIQDNISFY 546
DB 464 NPPFGKAVESRLNITKNNYATLE--CVASANGEIVTYLFSISENTVPHELTPLLIGFV 521
QY 547 ATIGLCPLFIIVLVILVILCHYKKQFRYESQLQIVTQPLNEXFYVDYDREYDYLKWEF 606
DB 522 AAIVI-----LVLLILVILVYKMQPKYQIQWKVIE--GIHGNVYVYIDTQLPYDHOEFP 575
QY 607 PRENLEFGKVLGSGAFGRVMNATAYGKTSQVSVQAVKMLKEKADSCKEKALMSLKM 666
DB 576 PRDKLRFGKTLGSGAFKGVKVENTAYGSKADTVMTVAVKMLKPSAHAKKEALMSLKV 635
QY 667 THLGHNDINVLNLAGCTLSGPVYLIFEVCCYGDLLNLYRSKREKPHRTWTEIFKEHNFS 726
DB 636 SYLGNHINVLNLAGCTVGGPTLVITEYCCFGDILNLFRLRRRVFYFT---TLGEDAYR 692
QY 727 YPTQAHNSNMPGSRREVQLHPP--LDQLSGNGNSIHSEDEIEYENQKELAEEDLN 785
DB 693 NVMQSEPNDRNG--YNTMKPSVLGILSSNRRSLNKGD--SYSDSDAVSEILQEDGLT 748
QY 786 LTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDILSDSY 845
DB 749 LDTEDLLSFSYQVAKGMDFLASKNCIHRDLAARNILLTQGRVAKICDFGLARDITDSNY 808
QY 846 VVRGNARLPVKWMAPELIFEGYITKSDVMSYIGILLWEIFSLGNVPYPGIPVDANFYKLI 905
DB 809 VVKGARLPVKWMPESIFECYFTFSDVMSYIGILLWEIFSLGSSPYFGMPVDSKFKYKI 868
QY 906 QSGFMEQFPFATGCIYFVWQSCWAFDRKRPSPNLTSTFLCCQLAEA-EACITRTSHL 964
DB 865 KEGYRMESPFSPSMYDINHSCWDADVPKRPSPFSKIVEKIEQQISDSTKGIYLNFFSRL 928
QY 965 PKQAPOQGGRLAQSPQROVKIHRERS 992
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Db 929 P--AAP-----GPRESSH---VHRLNS 947

RESULT 2
Q63702 PRELIMINARY; PRT; 974 AA.
AC Q63702;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-kit receptor tyrosine kinase isoform.
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN/FWAI;
RA Tsujimura T., Tono T., Yamazaki M., Nomura S., Kitamura Y.;
RT "Two isoforms of rat c-kit receptor tyrosine kinase.";
RL Nucleic Acids Res. 0:0-0(0).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; X62491; CAA44354.1; -.
DR HSSP; P11362; IFGK.
DR InterPro; IPR00719; Euk_pkinase.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 3.
DR SMART; SM00219; TyTKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 974 AA; 108955 MW; B9FAD9BA0DA190D CRC64;

Query Match 23.5%; Score 1234.5; DB 11; Length 974;
Best Local Similarity 32.3%; Pred. No. 1.3e-99;
Matches 323; Conservative 176; Mismatches 340; Indels 161; Gaps 37;

QY 36 CVLISHENNGSSAKPSSYRMVRGSPEDLOCTPRQSGTVYEAATVEAEGSITLQVQ 95
DB 12 CVLLVLRGQTGTQPSA-----SPGSPSPSIQPAQSELIVEAGD-TIRLT 57
QY 96 LATPGDLSCLVFXHSSILGCGPHDQNGIVSMALNV-TETQAGEVLLHITQSERANVT 154
DB 58 CTDPAFKV-KWTFE-----ILDVRIENKQSEWIR--EKAEATH 92
QY 155 VLFT-----VNVRD--TQVYLRPPYFRKMENQDALLCISEGVPEPTV-EWVLC 200
DB 93 GKYTCVSGSLRSSIYFVRDPAVLFLVGLPLFGKENDALVRC---PLTDPQVSNYSLI 149
QY 201 SSHRESC-----KEGPVAVRKEEKVLHFGTDIRCCARNALGRECTKLTIDLNQ 252
DB 150 ECDGKSLPTDLKFVNPKNAGITIKNVRAYHRLC---IRCAAQREGKWRSDKFTLKVRA 206
QY 253 A----POSTLPQL--FLKVGELWIRCKAIHVNHGFLTW-----ELEDKALEE 295
DB 207 AIKAIPVVSVPETSHLLKEGDTFTVICTKDVSTSVDSMWIKLNPOPOSKAQQVKNRSHQ 266
QY 296 GSYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTCSSSHPSQSA---ILEKGFIN 352
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Db 267 GDF-----NYERQETLT-----ISSARVNDSGVFMFCYANNTFGSANVTTLTKVVEKGFIN 316
Qy 353 --ATSSQEEYEDPYEKFCSVRFKAYPR-IRCTWIFSOAQFPCQORGLE-----DGYGIS 405
Db 317 IPVKNVTTFVTDG-ENVDLVVEFAYPKPHQOIYNNRT--PTNRGEDIYKSDNQNI 373
Qy 406 KFCDH-----KNKPGYEYIFAENDDAQFTKMTFLNIRKQPQLA--NASASQASCSDD 456
Db 374 RYVNELRLTRLKGTEGGTYTFLVNSDVSAVTFDVTYNTKPEILTYDRLMNGRLQCVAA 433
Qy 457 GYPLPSWTWKCKSDKSPNCTEIPB-GVWNKANKRVQGVWSSSTLWNSAGKGLLVKC 515
Db 434 GFPEPTIDWYFCTGAERQCTVEVPVVDVQIQNASVSPFGKLVVQSSIDSVFRHNGTVEC 493
Qy 516 CAYNSMGTSCTIFLNSPGPPF-----IQDN-----ISFYATIGLCLPFIWLVILCH 565
Db 494 KASNAVGKS--SAFFN-----FAFKGNSKEIQPHLTFTPLLLIGFVVVYTAGL----MGIIWVLA 543
Qy 566 KYKQKQFYESQLOMI-OVTGPLDNEYFYVDPRDYEDYDLKWFPPRENLEFGKVLGSGAFGR 624
Db 544 KYLQKPMYEVQWKVVEEING--NNYVYIDPTQLPYDHHKWFPPRNRLSFGKTLGAGAFGK 600
Qy 625 VMAATAYGISKTGVSIOQAVKMLKEKADSCKEALMSELKMWTHLGHHDNIWNLGACTIL 684
Db 601 VWEATAYGLIKSDAAMTAVAVKMLKPSAHLTEREALMSELKVLVYLGNHNIWNLGACTV 660
Qy 685 SGPVYLIFCYCCGDLNLYLASKREKHFRTWTEIFKEHNFSSYPTFQAHSSNSMPGSRV 744
Db 661 GGPTLVITEYCCYGDLNLFLLRRKDSF--IFSKEOEQADAALYKNLLSHKSSCDSSNEY 718
Qy 745 QLHPPLDQLSGFN-----GNSIHSEDEIYENQRLAEEDENLVLTFFDLCLCA 795
Db 719 -----MDMKPGVSVVPTKDKRSARIDSYIERDVTPEIMDEDELALDL----EDLLSFS 770
Qy 796 YQVAKGMEFLBKFCSVRHDLAARNVLTGHVKVKICDFGLARDILSDSSVYVVRGNARLPV 855
Db 771 YQVAKGMAFLASKNCIHRDLAARNILTHGRITKICDFGLARDIRNDSNVYVYVKGARLPV 830
Qy 856 KWAPEISIFEGYITKSDVWSYGILLWEIFSLGVNYPYGPVDFANFYKLIOSGFKWEOFP 915
Db 831 KWAPEISIFNCYVTFESDVWSYGILWELFSLGSGSPYGPMPVDSKPYKMKIEGRFMLSPE 890
Qy 916 YATEGYFVWMOCSWAFDSRKFSPNLTSLFLGCLQALAEAE 955
Db 891 HAPAAVEMVMTCDWDADLPKPTFKQVVLIEKQISDSSK 930

RESULT 3
Q63116 PRELIMINARY; PRT; 978 AA.
AC Q63116
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-kit receptor tyrosine kinase.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA MEDLINE=32003944; PubMed=1912577;
RA Teujimura T., Hirota S., Nomura S., Niwa Y., Yamazaki M., Tono T.,
RA Morii E., Kim H., Kondo K., Nishimune Y., Kitamura Y.;
RT "Characterization of a mutant allele of rats: A 12-base deletion in
RT tyrosine kinase domain of c-kit gene.";
RL Blood 78:1942-1946(1991).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; D12524; BAA02094.1; -.
DR HSSP; P11362; 1FGK.

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DR InterPro; IPR000719; Ruk_pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; TykinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG-like; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 978 AA; 109341 MW; 0958C33F19889051 CRC64;

Query Match 23.4%; Score 1232.5; DB 11; Length 978;
Best Local Similarity 32.2%; Pred. No. 2e-99;
Matches 323; Conservative 176; Mismatches 340; Indels 165; Gaps 37;

Qy 36 CVLISHENNGSAGKPPSSYVRVGRGSPEDLQCTPRQSEGTVYEAATVEVAESGSIQLQV 95
Db 12 CVLLVLLRGQTGTSQPSA-----SPGFSPSPSIQPAQSELIVEAGD-TIRLT 57
Qy 96 LATPGDLSCLVWFHSSIGCQPHDLQNRGIVSMALNV-TETQAGEYLLHIOSEYANYT 154
Db 58 CTDPAFVK--WTFE-----ILDVRIENKQSEWIR--EKAETHT 92
Qy 155 VLFT-----VNVRD-TQLYVLRPYPRFMENODALLCISEGVEPTV-EWVLC 200
Db 93 GKTYCTVSGSLRSSIYFVRDPVAVLFLVGLPLFGKEDNDALVRC---PLTDQVSNYSLI 149
Qy 201 SSHRESC-----KEGPAVVRKEEVLHFGTDIRCCARNALGRECTKLTFTIDLNQ 252
Db 150 ECDGKSLFTDLKFVNPVKGATIKVVKAYHRLC---IRCAAQREGKWRSDKFTLKVRA 206
Qy 253 A-----POSTLPQL--FLKVGPLWIRCKAIHNVHGLTW-----ELEDKALBE 295
Db 207 AIKAIPVVSVPETSHLLKEGDTFTVICTIKDVTSTVDSVMWIKLNPQPOSKAQVKRNSWHQ 266
Qy 296 GSYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVT---ILEKGFIN 352
Db 267 GDF-----NYERQETLT-----ISSARVNDSGVFMFCYANNTFGSANVTTLTKVVEKGFIN 316
Qy 353 --ATSSQEEYEDPYEKFCSVRFKAYPR-IRCTWIFSOAQFPCQORGLE-----DGYGIS 405
Db 317 IPVKNVTTFVTDG-ENVDLVVEFAYPKPHQOIYNNRT--PTNRGEDIYKSDNQNI 373
Qy 406 KFCDH-----KNKPGYEYIFAENDDAQFTKMTFLNIRKQPQLA--NASASQASCSDD 456
Db 374 RYVNELRLTRLKGTEGGTYTFLVNSDVSAVTFDVTYNTKPEILTYDRLMNGRLQCVAA 433
Qy 457 GYPLPSWTWKCKSDKSPNCTEIPB-GVWNKANKRVQGVWSSSTLWNSAGKGLLVKC 515
Db 434 GFPEPTIDWYFCTGAERQCTVEVPVVDVQIQNASVSPFGKLVVQSSIDSVFRHNGTVEC 493
Qy 516 CAYNSMGTSCTIFLNSPGPPF-----IQDN-----ISFYATIGLCLPFIWLVILCH 561
Db 494 KASNAVGKS--SAFFN-----FAFKGNSKEIQPHLTFTPLLLIGFVVVYTAGL----MGIIWVLA 543
Qy 566 KYKQKQFYESQLOMI-OVTGPLDNEYFYVDPRDYEDYDLKWFPPRENLEFGKVLGSG 620
Db 544 VLYAYLQKPMYEVQWKVVEEING--NNYVYIDPTQLPYDHHKWFPPRNRLSFGKTLGAG 600
Qy 621 AFRVMMATAYGISKTGVSIOQAVKMLKEKADSCKEALMSELKMWTHLGHHDNIWNLG 680
Db 601 AFGKVVEATAYGLIKSDAAMTAVAVKMLKPSAHLTEREALMSELKVLVYLGNHNIWNLG 660

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Qy 681 ACTLSGPVYLIFECYCCGDLNLYRSKREKTHRTWTETFEKHNFSSTPTQAHNSNMPG 740
Db 661 ACTVGGPLVITECCYCGDLNLYRSKREKTHRTWTETFEKHNFSSTPTQAHNSNMPG 718
Qy 741 SREVLQHPPLDQSGFN-----GNSIHSDEIEYENQKRLABEEEDNLVLTPEDL 791
Db 719 SNEY-----NDMKFGSVVYPTKTKRSARIDSVIERDVTTPAIMEDELALDL---EDL 770
Qy 792 LCPAYQVAKGMEFLFKSCVHRDLAARNLVTHGKVKICDFGLARDILSDSSVVRGNA 851
Db 771 LSFYQVAKGMAFLASKNCIHRDLAARNILTHGRITKICDFGLARDIRNDSNYYVRGNA 830
Qy 852 RLPVKWAPESLFGIGYTIKSDVMSYGILLWEIFSLGWNVPYGPVDFANFYKLIQSGFKM 911
Db 831 RLPVKWAPESIFNCVITYFSDVMSYGILLWEIFSLGSSPYGPMVDKFKYMKIEGFRM 890
Qy 912 EQPPYATGTYFVMSQWAFDSRKRSPFNLTSLFGQLAEAE 955
Db 891 LSPEHAPAMYEVMKTCWDADPLKRPPTKQVQLIEKQISDSK 934

RESULT 4
Q91909 PRELIMINARY; PRT; 954 AA.
AC Q91909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-kit-related kinase 1 (Xkrki) precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP MEDLINE=9534496; PubMed=7619732;
RA Baker C.V., Sharpe C.R., Torpey N.P., Heasman J., Wylie C.C.;
RT "A Xenopus c-kit-related receptor tyrosine kinase expressed in
RT migrating stem cells of the lateral line system.";
RL Mech. Dev. 50:217-228(1995).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; Z48770; CAA88688.1; -.
DR HSPSP; P11362; IFCG.
DR InterPro; IPR007119; Euk_pkinase.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG like; 2.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Signal; transferase; transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1
SQ SEQUENCE 954 AA; 106859 MW; 9749845CBE0B537D CRC64;
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Query Match 23.2%; Score 1220; DB 13; Length 954;
Best Local Similarity 32.0%; Pred. No. 2.4e-98;
Matches 315; Conservative 160; Mismatches 321; Indels 188; Gaps 35;
Qy 77 YEAAVEVAESSITLQVQLATPGDLSC-----LWVFKHSSLGCPHFDLQNRGIVSMA 130
Db 15 YTGDAVPKINGEDRVTWVGDKVSLCERDAHLVTLAFQKSLMKKPR-DLKSRLP----- 68
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Qy 131 ILAVTET-----QAGEYLLHIQSERANYTVLFTVNVVDTQLYLRRPYRQME 178
Db 69 -LNNSETDQPFVIIKADLRHIGRYICNTTETQENTSV--SLFVNDPAPFIDIFDVT 125
Qy 179 NQDAL-LCISEGVPPTVVEWVLCSSHRESCKEBGPAVVRKEEKLHFLFGTDIRC----- 232
Db 126 GADIVGMCFP---TDPMDIAI-----EKC--DGSPLPE-----NFTFTTIEAGITIK 169
Qy 233 -----CARNALGR-ECTKLFTIDLNAQPOSTLPQLFL-----KVGPLMIR 273
Db 170 TVQLAFDSCYVCSGKSGTGVKSTFSIHVKPVPKK-VPTVFLSKSRQLVKTGSPFEVTC 228
Qy 274 KAIHNVHGFGLTW-ELEDKALEBGSYFEMSTYSTRNMTIRILLAFVSSVGRNDTGYTCS 332
Db 229 AVLDFSTVKAQWLDVKEGVTKQANFRSSNVFSNLTLS-----DCVPYSESRFTTCQ 282
Qy 333 SSKHPSQ---SALVTILEKGFINATSOE-EYEDPVEKFCFSVRFKAYPR-IRCTWIFS 387
Db 283 AENAIGQVNATFTLDVIDVGVNLTVENTTISYNAGDNLVLYIDAYPHDDGWTYF 342
Qy 388 QASFPQORGLDGYISKFCDHKN-----KPGYIFVAENDDAQTKMF 432
Db 343 NETL---LNTSDHYVATK--DEGNRRYVSELHLIRLKGTEGVYFTYTTNSDDDDASVSF 396
Qy 433 TLNTRKXPOVLANASQAS--CSSDGYPLPSWTWKKCSKSPNCTEIPGVNKK--A 488
Db 397 NIQVTRPEILIAERTSEGTLQCVATGPPVPAIOMYFCPGEQRCQTDYPLSPVNEKFI 456
Qy 489 NRKVGOWSSSTLNMSEAGKGLLVCCAYNSMGTS-----CETIFLNSPGP 535
Db 457 ENSSLGRIVESTIDVDNLKNGTVQCVASNEVSAYSVFSAIKEKLRTHLFT----- 511
Qy 536 PFIQDNISFYATIGLCPLPFIWLVILVILCHYKKQFYESQLOMI-QVTGLDNEIFYVD 594
Db 512 -PLL---IGFTAAAGL---MCIAVAVLMYKLOPKVEIQWKVVEING---NNYVVID 560
Qy 595 PRDYEYDLKWEFPRENLEFGVILSGAGRVNATAYGISKTGSIQVAVKMLKEADSC 654
Db 561 PTQLPYDNKWEFPDRDLRCFCGKILGAGAPGVVEATAYGLLKEDSRLTAVAVKMLKPSAHT 620
Qy 655 EKEALMSELKMTHLGHNDINVLNLLGACTLSPGVVLYPEYCYCGDLLNLYRSKREKPHRT 714
Db 621 EREALMSELKVLVSLGHKHNIVNLLGACTVGPPLVITEYCYCGDLLNLYRSKREKPSF 677
Qy 715 WTEIFKEHNFSSYPTFOAHNSNMPGSRVOLHPPLDOLSGFNGNSIHSDEIEYENOK- 773
Db 678 -----ICPKFEDNS-----EALYKXNL-----LNRDMGCEGMSEYIDMKP 713
Qy 774 -----RLAEEEEEDLNVLTPEDLNLYRSKREKPHRT 810
Db 714 AVSYVVPKTKDKRRSGSFGDQSVSVIPEEDL-ALDTEDLINFSYQAQGNFLASKNC 772
Qy 811 VHRDLAARNLVTHGKVKICDFGLARDILSDSSVVRGNAARLPVKWMAPELSPGIVTI 870
Db 773 IHRDLAARNILTHGRITKICDFGLARDIRNDSNVVKGARLPVKWMAPELSPGIVTI 832
Qy 871 KSDVMSYGILLWEIFSLGWNVPYGPVDFANFYKLIQSGFKMEQPEYATEGTYFVMSQWA 930
Db 833 ESDVMSYGILLWEIFSLGSSPYPRIPVDSKFKYMKIKDGYRMSPECAPLEMYEIMRSCWN 892
Qy 931 FDSRKRPSFPNLTSLFGQLAEAE 954
Db 893 SDPLKRPTFKQIVQWVEQQLSDSK 916

RESULT 5
Q98SU3 PRELIMINARY; PRT; 974 AA.
AC Q98SU3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001824; RTKinaseIII.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00047; Ig_4.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 2.
DR SMART: SM00409; IG_4.
DR SMART: SM00408; IGc2; 1.
DR SMART: SM00410; IG_like; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferrase; Transmembrane.
FT VARIANT 60 V -> L.
FT VARIANT 103 A -> S.
FT VARIANT 742 P -> S.
FT VARIANT 899 E -> D.
SQ SEQUENCE 977 AA; 109881 MW; CF54E129FAB10E3E CRC64;

Query Match 23.1%; Score 1215.5; DB 13; Length 977;
Best Local Similarity 33.5%; Pred. No. 6.3e-98;
Matches 334; Conservative 160; Mismatches 356; Indels 147; Gaps 35;

QY 54 YRMVGRSPEDLQCTPR-RQSEGTVEATVEABSGSITLQVLAATPDLSCLM---VFK 109
DB 13 FGQVQGWSE-----PRRLNSGAL--AGTDVILDSGS---PLQLVCEGDPVTFPPRAK 62

QY 110 HSLGCGPHDLQNRGIVSMALNVTTQAGEY-LLHQSERANYTLFTVNRDQ-LY 167
DB 63 H-----KRYISKEYGKIRSFVEKATVDFTGYKCVYINGSDSLASSVHVFRDRLVF 117

QY 168 V-----LRRPVRKQENQDALLCISEGVPETVWLVCSHRECKBGPVAVRKEEKVL 222
DB 118 VSPSSSLR--YVRK-EGEDLLPCLLTPDAT-DFTFRMNGSAAPYGMNATFPRKQVL 173

QY 223 ----HELFGTDIRCCARNALGRECTKLTIDINQAPSTLPQLFLK-----VGEPLWI 271
DB 174 IRNVHPGFNADYICARIGGAEKVKISINVIOQLRPP-PYVYLKRYEVKLVGERLQI 232

QY 272 RKAIVNHGFGLTWELEDKALEGSEFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTC 331
DB 233 SCTNNFNFYNVVTWTHSSKRLPKE--EKSTMEGDLRAIESILT-ISSVQLSDTGNITC 289

QY 332 SSSKHPQSALVT---ILEKGFINAT---SSOEY-----BIDPVKFCFSVRFKAYPRI 380
DB 290 TQNEAGANSSTQLLVVDEPYIRLSPKLSKLTGRLSIEVSEGEDVDLGLVLEAYPPL 349

QY 381 RC-TW---IFSQAFPCQR--GLEGGYSISKFCDHKN--KPGEYIFYAENDDAQFTKMF 432
DB 350 TSWETPTSHNASLP-ENRFVNHNDRYEALLFLKRLNFEIGQYTLNVKNSMKSASITP 408

QY 433 TLNIRKPKQVLAN-ASASQACSSDGYPLPSWTWKKCKSDKSPNCTHEI-----PGVWNKK 487
DB 409 DIKMYTKPVARVKVENVTTLSRSGYPAPSLWYQCTGIRTCPTENTDLPQIQTOTVE 468

QY 488 ANRKFVGVWSSSTLNMSSEAGKLLVKCCAYNSMCTSCETIFLNSPGFPFPIQDNISFYA 547
DB 469 FQKESFGAVGVESLTVG-PNRRMTVVCVAFNLVQGGSDTFSMD-----VSQOIFTS 520

QY 548 TIGLCLPFIV--VLIVLICHYKQKQFYESQLQIVTQGLDNEFYVYDFRDYEDLKE 605
DB 521 MCGSTVAMVVLGLLIFMIYKVKQKPRYERWKIEATN--GNVYTFIDPTQLPYNKEWE 578

QY 606 PPRENLBEKVLGSGAFGRVNNATAYGSKTGVSIQAVKMLKEKASCEKALMSSELKM 665
DB 579 PPRDKLKLGTGLGAFGKVKVVEATYGLGKEDNITRVAVKMLKASAHDPDEREALMSSELKI 638

QY 666 MTHL6HHDNIVNLLGACTLISGVPVLIIFYCCYCGDLLNLYRSKREK----- 711

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QY 459 PLPSWTWKCKSDKSPNCTEEL-PEGVNNKANKRVFGQWVSSSTLNMSEAGKGLLVKCCA 517
Db 437 PEPADVYFCEGAEQRCVPIGPMVQWQNSLSPSGKLIVQSSIDYSAFPHNGTVEGRA 496
QY 518 YNSMGTSCTETIFLNSPGFFPIQON-----ISFYATIGLCULPFIIVLVLVI 563
Db 497 YNNVGRS--SAFFN-----FAFKGNSKEQIHPTHTLFTPLLIGFVIAAGM---MCIIWML 546
QY 564 CHYKKQFRYESQLOMI-QVTGPLDNEFYVDFRDEYDLKWEFPRENLERKGLGSGAF 622
Db 547 TYKQLQPMYEVQWQVVEEING---NNYVIDPTQLPYDQHKWEPNRLSFGKTLGAGAF 603
QY 623 GRVNNATAYGISTKGVSTQAVAKMLKKADEKALMSLKMTHLGHHDNIIVNLLGAC 682
Db 604 GKVEATAYGLIKSDAAMTAVAKMLKPSAHLTEREALMSLKVSLGNWNIIVNLLGAC 663
QY 683 TSLGPFVYLIFCYCCYGBLLNLYRSKRKFHRTWTTEIFKEHNFSSYPTFOAHNSMFGSR 742
Db 664 TVGGFTLVITEYCCYGBLLNLFRRKRDSFICKQE---DHG----- 701
QY 743 EVQLHPPLDQLSGNGNSIHSEDI-----EYENQK-----RLAEE 779
Db 702 EVALYK-----NLLHSKSSCDSTNEYMDKPGVSVVPTKADKRRSARIOSYI 751
QY 780 BEDLN-----VLTFEDLLCFAYOVAKGMEFLPKSCVHRDLAARNVLVTHGKVVKI 830
Db 752 ERDVTPEIMDEDLADLEDDLSFSYQVAKGMAFKNCICHRDLAARNILLTHGRITKI 811
QY 831 CDFGLARDILSDSYVYVGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVN 890
Db 812 CDFGLARDIKDINSYVYVGNARLPVKWMAPESIENCYVTFESDVMSYGIPLWELFSLGSS 871
QY 891 PYGPIVDANFYKLIQSGFQMEQFPYATEGIYFVQSCWAFDSKRPSPNLTSLFCQL 950
Db 872 PYGMPVDSKEYFKMKEGFRLSPHEPAENYDINKTCWDADPLKRPFTKQIVOLIEKQI 931
QY 951 AEAEAEACIRTSIHLPKQAPQOGRGLRAQSPQORQVKKIHR 991
Db 932 SDSTN-----HIYSNLN-----CSPNPERPVVDHSVR 959

RESULT 9
O97744 PRELIMINARY; PRT; 964 AA.
ID O97744
AC O97744
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Mast/stem cell growth factor receptor (Fragment).
GN KIT1*0101.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HAMPSHIRE BREED; TISSUE=LEUKOCYTE;
RX MEDLINE=98391767; PubMed=9724328;
RA Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT pig.";
RL Genome Res. 8:826-833(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HAMPSHIRE BREED; TISSUE=LEUKOCYTE;
RA Marklund S.;
RL Thesis (1997), Department of Animal Breeding and Genetics,
RL Swedish University of Agricultural Sciences, Uppsala, SWEDEN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES
CC EMBL; AJ243228; CAAL1196.1; -.
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DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003593; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00219; TyTKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON_TER 964 964
SQ SEQUENCE 964 AA; 108287 MW; 90E72EDFABI35887 CRC64;

Query Match 22.9%; Score 1208; DB 6; Length 964;
Best Local Similarity 32.6%; Pred. No. 2.8e-97;
Matches 319; Conservative 168; Mismatches 362; Indels 130; Gaps 32;

QY 38 LISHENNGSAGKPSRYMVRGSPEDLOCTPRROSEGTVEYAAATVEVAESSITIQVOLA 97
Db 16 LLLRVQTGSS--QPSV-----SPEEL-----SPPSIHPAKSELIVSAGD-EIRLFT 59
QY 98 TPGDLSCLWFKHSSLCQCPHFDLQNRGIVSMALLNVTTQAGEYLLHIQSERA----- 151
Db 60 DPG--SVKWTPE--TLG-----QUSENTHAEWIV-----EKAEAMNTG 93
QY 152 NYTVL-----FTVNVRTQ--LYVLRPPYFRKMNODAL-----LCISE 188
Db 94 NYTCNEGGLSSSIYVVRDPDEKLFVDPPLYGK-EDNDALVRCPDTPVNTSYLTGCE 152
QY 189 GVPEP-TVEWVLCSSHRESCKEKGPAVVKKEKVLHELFGTDIRC--CARNALGRE-CTK 244
Db 153 GKPLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLHCSANQGGKSVLSK 198
QY 245 LFTIDLNAQPOS-----TLPQLFKVCEPLWIRCKAIHNVHFGLTWELEDKALEESY 298
Db 199 KFTLKVRAAIRKAVPVAVSVKASYLLRGEGBFAVMCLIKDVSSSVSDSMW-IRENSOTKAQV 257
QY 299 FEMSTYSTNRTMIRILLAFVSSVGRNDTGYTCSSSHPSQSALVTILE---KGFINA-T 354
Db 258 KNSWHQGDFFNLQERLTISSARVNDSGVFMVCYANNFTGSAVNTTILEVVDKGFINTFP 317
QY 355 SSQBEYEIDPYEKFCSFVRKAYPR-IRCTWIFSQ--ASFPEQRGLBEGVYSISKPDHK 411
Db 318 MMNTTVFVNDGEDVDLIVEYEAYPEHQRWIYMRATATDKWEDYPKSENEINRYVSEL 377
QY 412 N-----KPEGEYFYAENDDAQFTKMTINIRKKPQVLAN--ASASQASCSDDGYPLPS 462
Db 378 HLTLKLGTEGTYTFLVSNADVNSVTVNVYNTKPELTTHDRLMNGMLQCVAAGFPPEPT 437
QY 463 WTWKCSKSKSPNCTEEL-PEGVNNKANKRVFGQWVSSSTLNMSEAGKGLLVKCCAYNSM 521
Db 438 IDWTFPCGTEORCSPVPGVDVQVQNSSVSPFGKLVLIHSSIDYSFAFKNGTVECRAYNDV 497
QY 522 GTSCTETFLNSPGFFPIQDNISFYATIGLCULPFTV-----VLIVLICHYKKQFRYES 575
Db 498 GKS--SAFFN-----FAPKEQIHAHTLFTPLLIGFVIAAGMCIIVMLTYKYLQKPMYEV 551
QY 576 QLQMI-QVTGPDNEYFYVDFRDEYDLKWEFPRENLERKGLGSGAFGRVNNATAYGIS 634
Db 552 QWKVVEEING---NNYVIDPTQLPYDQHKWEPNRLSFGKTLGAGAFGVVVEATAYGLI 608
QY 635 KTGVSIQVAVKMLKEKADSCKEALMSLKMTHLGHHDNIIVNLLGACTLSGPVVLIEY 694
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609 KSDAAMTAVKMLKPSAHLTEREALMSKLVLSYLGHNHNVNLLGACTIGGPTLVITEY 668
QY 695 CCYGDLLNLRKREKPHRTWTETFEKHNPSSTYTFQAHNSNMPGSRVOLHPPDLQLS 754
Db 669 CCYGDLLNLRKRDSPFCISKQDHEAALYKNLLHSKSSCSDSTNEYMDKPGVSYV 728
QY 755 GFNGNSHSEDEIEYENQKELABEEEDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRD 814
Db 729 PTKADKRSARIGSYTERDVTTPAIMEDELALDLELLSFSYQVAKGMFLASKNCIHRD 788
QY 815 LAARNVLVTHGKVKVCKDFGLARDILSDSYVVRGNARLPVKWMAPELSLEGITKSDV 874
Db 789 LAARNILLTHGRITKICDFGLARDIKNDSYVVKGNARLPVKWMAPEISFNCVTFESDV 848
QY 875 WSGYILLWEIFSLGVNPPGIPVDANFYKLIQSGFKMEQPFYATEGYFVMQSCWAFDSR 934
Db 849 WSGYIFLWELFSLGSSPYGMPVDSFYKMIKEGFRMLSPHAPAEYDINKTCWDADPL 908
QY 935 KRPSFNLTSFLGCQALAE 953
Db 909 KRPTFKQIVOLIEKQISES 927
RESULT 10
Q9TQO1
ID Q9TQO1 PRELIMINARY; PRT; 964 AA.
AC Q9TQO1
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Mast/stem cell growth factor receptor (Fragment).
GN KITI*0201.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RA Marklund S.;
RL Thesis (1997), Department of Animal Breeding and Genetics,
RL Swedish University of Agricultural Sciences, Uppsala, SWEDEN.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RX MEDLINE=98391767; PubMed=9724328;
RA Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT pig.";
RL Genome Res. 8:826-833(1998).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AJ223229; CAAL1197.1; -.
DR HSSP; P11362; 1FGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG_1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
FT Transmembrane; Tyrosine-protein kinase.
KW NON_TER 964 964
SQ SEQUENCE 964 AA; 108315 MW; 996C3C46201358A8 CRC64;
Query Match 22.9%; Score 1207; DB 6; Length 964;
Best Local Similarity 32.6%; Pred. No. 3.5e-97;
Matches 319; Conservative 168; Mismatches 362; Indels 130; Gaps 32;
QY 38 LISHENNNGSSAGKPSYRMVGRGSPEDLQCTPRROSECTVYEAATVEAESGSILOVQLA 97
Db 16 LLRLVOTGSG--QPSV-----SPEL-----SPSIHPAKSELIVSAGD--BIRLFT 59
QY 98 TPGDLSCLMWFKHSSLCQCPHFLQNRGIVSMALNVTTETQAGEYLLHIQSER----- 151
Db 60 DPG--SVKWTFE--TLG-----QISENTHAEWIV-----EKAEMNTG 93
QY 152 NYTVL-----FTVNRVDTQ--LYVLRPRFRKMNODAL-----LCISE 188
Db 94 NYTCTNEGGLSSIIYVVRDPEKFLVLDPLYGK--EDNALVRCPLTDPEVTNYSLTGCE 152
QY 189 GVPEP--TVEWVLCSSHRESCKEKGPAVVRKEEVHLHFLGTDIRC--CARNALGRE--CTK 244
Db 153 GKPLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLHCSANQGGKSVLSK 198
QY 245 LFTIDLNOAPOS-----TLPOLFLKVGEPILWIRCKAIHVNHGFLTWELDKALEGSY 298
Db 199 KFTLVRAAIRAVPVAVKASVLLREGEBAFVAVCLIKDVSSSVDSMW--IRENSQTKAQV 257
QY 299 FEMSTYSTNTRMIRILLAFVSSVRGNDTYTTCSSSKHPQSALVTILE---KGFINA--T 354
Db 258 KRNSWHQGDNFRLRQERLTJISSRVNDSGVFMVCYANNVTFGSANVTTLLEVVDKGFNI 317
QY 355 SSQEEVHIDYKFCFSVRKAYPR--IRCTWIFSQ--ASFPCEORGLEDGYSISKFCDHK 411
Db 318 MMNTTVFVNDGEDVDLIVEYEAYPKPHRQWYMNRTATDKWEDYPKSENSNRYVSEL 377
QY 412 N-----KPEGYIFYAENDDAOFTKMTLNIRKPOVLAN--ASASQASCSDDGYPUPS 462
Db 378 HLTRLKTEGEGTTFVLVSADNVSSVTFNVVNTKPEILTHDRLMNGMLQCVAGFPPEPT 437
QY 463 WTKKCSKSPNCTEET--PEGVNKKANRVFGOWSSSTLNMSSEAGKGLLVKCCAYNSM 521
Db 438 IDWYFCPTGTEQRCSPVPGVDVQIQNSSVSPFGKLVHSSIDYSFAKHNGVTECRAYNDV 497
QY 522 GTCETIFLNSPGPPPIQDNISFYATIGLCPLPIV-----VLIVLICHYKKQFRYES 575
Db 498 GKS--SAFFN-----FAPKEQIHATHTLFTPLLIGFVIAAGMMCIIVMILTYKLOKPMYEV 551
QY 576 QLOMI--QVTGPLDNEYVDPRDYEDLKWEFFPRENLEFFKVLGSGAGFGRVNNATAYGIS 634
Db 552 QMKVBEING--NNVYIIDPTQLPYDKHWEFFPRNRLSFGTKLGAGAPGKVEATEAYGLI 608
QY 635 KTVGSIQVAVKMLKEKADSKCEKALMSKMTLHGHHDNIVNLLGACTLSGPVYVLIPEY 694
Db 609 KSDAAMTAVKMLKPSAHLTEREALMSKLVLSYLGHNHNVNLLGACTIGGPTLVITEY 668
QY 695 CCYGDLLNLRKREKPHRTWTETFEKHNPSSTYTFQAHNSNMPGSRVOLHPPDLQLS 754
Db 669 CCYGDLLNLRKRDSPFCISKQDHEAALYKNLLHSKSSCSDSTNEYMDKPGVSYV 728
QY 755 GFNGNSHSEDEIEYENQKELABEEEDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRD 814
Db 729 PTKADKRSARIGSYTERDVTTPAIMEDELALDLELLSFSYQVAKGMFLASKNCIHRD 788
QY 815 LAARNVLVTHGKVKVCKDFGLARDILSDSYVVRGNARLPVKWMAPELSLEGITKSDV 874
Db 789 LAARNILLTHGRITKICDFGLARDIKNDSYVVKGNARLPVKWMAPEISFNCVTFESDV 848
QY 875 WSGYILLWEIFSLGVNPPGIPVDANFYKLIQSGFKMEQPFYATEGYFVMQSCWAFDSR 934
Db 849 WSGYIFLWELFSLGSSPYGMPVDSFYKMIKEGFRMLSPHAPAEYDINKTCWDADPL 908


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QY 935 KRPSFNNLTSLGCOLAEA 953
DB 909 KRPTFKQIVOLIEKOISES 927

RESULT 11
Q9TQ00 PRELIMINARY; PRT; 964 AA.
AC Q9TQ00
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Mast/stem cell growth factor receptor (Fragment).
GN KIT1*0202.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RA Marklund S.;
RL Thesis (1997), Department of Animal Breeding and Genetics,
RL Swedish University of Agricultural Sciences, Uppsala, SWEDEN.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RX MEDLINE=98391767; PubMed=9724328;
RA Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT pig.";
RL Genome Res. 8:826-833(1998).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AJ223230; CAAL1198.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG_1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; TyRKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON TER 964
SQ SEQUENCE 964 AA; 108287 MW; 1B21292A962E9191 CRC64;

Query Match 22.9%; Score 1207; DB 6; Length 964;
Best Local Similarity 32.6%; Pred. No. 3.5e-97;
Matches 319; Conservative 168; Mismatches 362; Indels 130; Gaps 32;

QY 38 LISHENNGSSAGKPSRYMRGSPEDLQCTPRRSEGTVEAATVEAEGSITLQVOLA 97
DB 16 LLLRVQTGSS--QPSV-----SPEEL-----SPSIHPAKSELIVSAGD-EIRLFT 59

QY 98 TPGDLSCLVFKHSLGCGQPHFDLQNRGIVSMALNVTETQAGEYLLHIOSERA----- 151
DB 60 DPG--SVKWTTE--TLG-----QLSENTHAEWIV-----EKAEMNTG 93

QY 152 NYTVL-----FTVYVDTQ-LYVLRPPYFRKMNQDAL-----LCISE 188

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DB 94 NYTCTNEGGLSSSIYVVRDPEKFLVDPPLYGK-EDNDALVRCPLTDPVTVNVLGCE 152
QY 189 GVPEP-TVEWLVSSHRESCKEGPAVVRKEEKVLHFLFTDIRC--CARNALGRE-CTK 244
DB 153 GKPLPKDLTEV-----ADPRAGITIRNVKREYHRL-----CLHCSANQGKSVLSK 198
QY 245 LFTIDLNOAPQS-----TLPQLFLKVGEPLEWIRCKAIHVNHGFGLTWELEDKALEGSGY 298
DB 199 KFTLKVRRAALRAVPVAVKASVLLREGEFAVNCILKDVSSSVDSNM--IRENSQTQAOV 257
QY 299 FEMSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSHPSQSALVTILE---KGFINA-T 354
DB 258 KRNSWHQGDENFLRQEKLTISSRVNDSGVFMCYANNTFGSANVTTLTLEVVDKGFNIFF 317
QY 355 SSQEEYIDPYEKFCSVRFAKPR-IRCTWIFSQ--ASFPCEORGLEDGYSISKFDCHK 411
DB 318 MMNTTTFVNDGEDVDLIVEYEAYPKPEHQRQIYMNRTATDKWEDYPKSENESIRIYVSEL 377
QY 412 N-----KPEYIFYAENDDAQFTKMFTLNIRKPOVLAN--ASASQASCSGDPYPLPS 462
DB 378 HLTRLKTEGGTYTFLVSNADVNSSVTFNVTNTPKPEILTHDRLMNGMLQCVAAAGFPEPT 437
QY 463 WTWKCKSDKSPNCTEEI-PEGVWVKKANRVFGOWVSSSTLNMSSEAGKGLLVKCCAYNSM 521
DB 438 IDWYFCPTQRCSPVPGVDVOIQNSSVSPFGKLVHSSIDYSAPFKHNGTVECRAYNDV 497
QY 522 GTCETIFLNSPGPFPIQDNISFYATIGLCPPIV-----VLIVLCHKYKQFYRES 575
DB 498 GKS--SAFFN-----FAFKEQIHATLFTPLLLIGFVIAAGMMCIIVMLITVYKLPWYEV 551
QY 576 OLQMI-QVTGPLDNEYEVDFROVEYDLKWEPFRENLEFGKVLGSGAFGRVMNATAYGIS 634
DB 552 QWKVEEING---NNYVIIDPTQLPYDHKWEFPFNRRLSFGKTLGAGAFKVEATEAYGLI 608
QY 635 KTGVSIQVAVKMLKEKADSCKEALMSSELKXMTHLGHHDNIVNLLGACTLSGPPVYLIFEY 694
DB 609 KSDAAMTVAVKMLKPSAHLTEREALMSSELKVLVSLGNHMIIVNLLGACTIGGPTLVITEY 668
QY 695 CCYGDLNLYLRKREKPHRTWTEIFKEHNFSSTYPTFOAHNSNMPGSGREVOLHPLDOLS 754
DB 669 CCYGDLNLYLRKREKPHRTWTEIFKEHNFSSTYPTFOAHNSNMPGSGREVOLHPLDOLS 728
QY 755 GFNGNSIHSDEIEYENOKRLABEEEDNLVLTPEDLICFAYOVAKGMEFLFESCVHRD 814
DB 729 PTKADKRRSARIGSYIERDVTPTAIMEDEDLALDLELLSFSYQVAKGNAPLASNCIHRD 788
QY 815 LAARNVLVTHGKVVKICDFGLARDILSDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDV 874
DB 789 LAARNILLTHGRITKICDFGLARDIKDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDV 848
QY 875 WSYGILLWEIPLSLGVNYPGIPVDANFYKIQSGFKMEQPPYATEGIYFVNMOSWAFDSR 934
DB 849 WSYGILLWEIPLSLGVNYPGIPVDANFYKIQSGFKMEQPPYATEGIYFVNMOSWAFDSR 908
QY 935 KRPSFNNLTSLGCOLAEA 953
DB 909 KRPTFKQIVOLIEKOISES 927

RESULT 12
Q9XS93 PRELIMINARY; PRT; 978 AA.
AC Q9XS93
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIT.
GN C-KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

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[1]
RN SEQUENCE FROM N.A.
RP TISSUE=CEREBELLUM;
RA London C.A., Galli S.J., Yuuki T., Hu Z.-Q., Helfand S.C.,
RA "Spontaneous canine mast cell tumors express tandem duplications in
RT the proto-oncogene c-kit.";
RL Exp. Hematol. 0:0-0(1999).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSP-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF099030; AAD28369.1; -.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR0003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 978 AA; 109651 MW; 5AC31E5AC4E9910F CRC64;

Query Match 22.9%; Score 1205; DB 6; Length 978;
Best Local Similarity 31.5%; Pred. No. 5.4e-97;
Matches 329; Conservative 167; Mismatches 387; Indels 160; Gaps 33;

QY 14 LIAVLVSMILETTNQDLPVVKVLISHENNGSSAGKPSYRVVRGSPEDLQCTPRQSE 73
DB 11 LCVILLLLLLGVGTGSSQPSV-----SPGEPFL----- 38

QY 74 GTVYEATVEVABSGSITLQVLATPGDLSCLWVFHSSIGCPHFLQNRGIVSMALN 133
DB 39 PSIHAKSELIVSGD-ELRLSCTDPGVK--WTFE--TLG-QLNENTHNEWITEKA--- 89

QY 134 VTQAGEYLLHQSERANTVLTFTVNRD-TOLVLRURYFRKMNQDALLCISGVPE 192
DB 90 ---EAGHTGNYTCTNRDGLSRISYVFRDPAKLFLVDLPYKGEKNDTLVRC----- 138

QY 193 PTVEWVLCSSHRESCKEAGPAVVRKEKVLHELFGTDIR-----C--CARNALGRE 241
DB 139 PLTDPEVTNYSLRG--EGKPLPKDLTFVADPKAGITIRNVKREYHRLCLHCSADQKRT 196

QY 242 -CTKLFITDLNQAPOS-----TLPQLFKVGEPLWIRCKAIHVHNGFGLTWLEDKALE 294
DB 197 VLSKKTLKVRAIRAVPVVSVKTSLLKEGAFSWCFCIKDVSSFVDSNW-----IK 250

QY 295 EGSYFEMSTYST-----NRTMIRILLAFVSGVNRDGTGYTCSSKHPQSALVTILE-- 347
DB 251 ENSQTNAQTQSNWGHGDFNPERQEKLIISARVNDGVFMCYANNTFGSANVTITLEV 310

QY 348 -KGFINA-TSSQEYEDDPYKFCFSVRFKAYPR-IRCTWIFSOASF--PCBQRGLDEGY 402
DB 311 DKGFIFIPMMSTTIFVNDGENVDLIYVEYAYPKPEHQOQIYMNRTFTDWDWEDPKSDNE 370

QY 403 SIGKFCDH-----KNKPEYIFVAENDDAQFTKMTLIRKKPQVLANASAOA--SC 453
DB 371 SNRYVSELHLRLKNGEGTYTFQVNSDVNSVTNVVNTKPELITHTSLTNGMLQC 430

QY 454 SSDGYPLPSTWTKKCDKSPNCTEEI-PEGVWKNKARKVFGQWVSSSTLNMSEAGRL 512
DB 431 VVAGFPPEAVDWYFCPGAQRCSVPVIGPMDVQMGNSSLSFGKLVQSSIDYSAFKNGT 490
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QY 513 VKCAVNSMGTSCETIFLNSPGPPFPIQDN-----ISFYATIGLCPLPFIW 558
DB 491 VECRAYNNVGRS--SAFFN---FAPKGSKEQIHPHTLFTPLLIGFVIAAG---MCI 540

QY 559 LIVLICHYKKQFRYESOLOMI-QVTGPLDNEYFYVDFRDYEDLKWFEFFRENLEFGKVL 617
DB 541 IVMLITYKYLKPMYEVQWKVBEING---NNVYVIDPTQLPYDHKWEFFPNRLSFGKTL 597

QY 618 GSAGFRVMNATAVGTSKTVSQVAVKMLKEKADSCKEALMSELKMTHTLGHNDITVN 677
DB 598 GAGAFGKVBEATAYGLIKSDAAMTAVAMLKPSAHLTERALMSELKVLVSLGNHMINVN 657

QY 678 LLGACTLSGGEVYLIFEYCCYCDLLNLRSKREKPHRTWTIFKEHNFSSYPTFOAHNS 737
DB 658 LLGACTVGGPTLVITEYCCYCDLLNLRKRKDSFICSKQEDHGEVALYKNLLHSKSSCS 717

QY 738 MPGSREVQLHPPDLQJSGFNNGSIHSEDEITEYENQKRLAEEEDLN-----VLT 788
DB 718 DSTNEYMDMKP-----GDSYVVPVKADRRSRIGSYIERDVTTPAIMEDELALDL 768

QY 789 EDLLCFAYQVAKGMELEFKSCVHRDLAARNVLVTHGVKVKICDFGLARDILSSSVYVR 848
DB 769 EDLLSFSYQVAKGMAFLASKNCHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVK 828

QY 849 GNARLPVKWMAPESLPFGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYKLIOS 908
DB 829 GNARLPVKWMAPESFNCVYTFESDWSYGIFLWELFSLGSSPYGMPVDSKFKYKMEG 888

QY 909 FKMEQPYATEGIYFVMSQWAFDSRKRPSFNLTSLFGCOLAEAEACITSIHLPKQA 968
DB 889 FRMLSPEHAPAEWYDIMKTCDWADPLKRPSTKQIVOLIEKQISDSTN-----HI 941

QY 969 APOQRGLRAQSPORQVYKIHRR 991
DB 942 AN-----CSPNPERPVVDHSVR 958

RESULT 13
Q98SU2 PRELIMINARY; PRT; 977 AA.
AC Q98SU2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase Fms.
OS Danio rerio (Karr's danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=38750;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359118; PubMed=11466528;
RA Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
RT diversification in Danio.";
RL Dev. Genes Evol. 211:319-328(2001).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSP-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF324480; AAK15302.1; -.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
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DR SMART; SM00408; IGC2; 1.
DR SMART; SM00220; S.TK; 1.
DR SMART; SM00219; TyK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane.
FT VARIANT 31 P -> L.
FT VARIANT 148 L -> F.
FT VARIANT 218 R -> K.
FT VARIANT 263 I -> M.
FT VARIANT 490 R -> K.
FT VARIANT 594 E -> A.
FT VARIANT 614 G -> R.
FT VARIANT 926 N -> T.
FT VARIANT 934 A -> T.
FT VARIANT 938 A -> V.
SQ SEQUENCE 977 AA; 110294 MW; AAB2FF2A20D66090 CRC64;
Query Match 22.9%; Score 1204.5; DB 13; Length 977;
Best Local Similarity 32.2%; Pred. No. 5.9e-97;
Matches 334; Conservative 166; Mismatches 363; Indels 173; Gaps 36;
QY 12 LLLVLSVLETVNQLPVKVLISHENNGSSAGKPSRYMRVSGSPEDLQCTPRRQ 71
DB 5 LLLIGI--LFGQVQWSEPOIRL-----NSGAPAG--TDVILDSGSPQLVLC----- 48
QY 72 SEGVTEAATVEVAESGSIITLQVOLATFGDLSCLVFKHSLGQCPHFDLQNRGIVSMAI 131
DB 49 -EG-----DGPVTFPLRLA-----KH-----KRYISKEVGKIRSFV 79
QY 132 LNVETQAGY-LLHIOSEANRYVLTAVNRDQ-LYV---LRPFYRKMENODALL-C 185
DB 80 EKATVDPTGTYKCVIYNENDSNLSSVHVFRDRLVFSVPSITLRYVRK-EGEDLLLP 138
QY 186 ISEGVPEPTVEVWLCSHRSCKEEG-PAVVRKEEVL---HELFGDIRCCARNALGR 240
DB 139 L---LTPDNDATDMFRMDNGSAAYPGNATFDPRKGLIRNVHFGFNADYICARIGAE 195
QY 241 ECKLFTIDLNAQOSTLPOLFLK-----VGEPLMIRKAIHVNHGFLGTWELEDKAL 293
DB 196 KVSIFINSIQLRFP-PYVLLRNEVVKLVGERLQISCTNNPNFYVNVVTHSSRL 254
QY 294 EBSYFEMSYNTNRMIRILLAFVSSVGRNDTGYTCSSSKHPSQALVT---ILSKGP 350
DB 255 PKAE--EKSTIEGRDLAIESILT-IPSVQSDNGNITCTQNEAGANSSTTQLLVVDEPY 311
QY 351 INAT---SSQBEY-----EIDPYKFCFSVRFKAYPRIC---TWIFSOASFPCEOR-- 396
DB 312 IRLSPKUSSKLTNRGLSIEVSEGDVGLVLIAYPLTSHKWTPTSHNASLP-ENRFY 370
QY 397 GLEDGYISKFCOHKN--KPGXEYFYAENDDAOPTKMTLIRKKPOVLAN-ASASQASC 453
DB 371 NHNDRYEALLFLKELNEEIGQYTLNVKNSMKSASITFDIKMYTKPVARKVWENVTLSC 430
QY 454 SSDGYPLPSTWTKCSKSNCTEEI---PEGVWNKANRVKPGQWSSSTLNMSAGK 509
DB 431 RSYGYPAPSLWYQCTGIRTCPTENTDLOPIQTQVFEFOKESFGAVGVESVLTVG-PNR 489
QY 510 GLLVKCCAYNSMGTSCRTIFLNSGPPFPFDNLISFVATIGLCIPFIV--VLIVLICHY 567
DB 490 RMTVVCVAFNLVGGSDTFSMD-----VSDQLFTSAMCGSTVAMVVLGLLLIFMIYKY 542
QY 568 KQOPRYESQLQMIQVTPGLDNEYFYVDFRDYEDLKWFEFFRENLEFGKVLGSGAFGRVMN 627
DB 543 KQPRYIRKWIIEATN--GNVYTFIDPTQLPYNEKEFEFPDRDLKLGKTLGAGEFGKVE 600
QY 628 ATAYGISKTGVSIOVAVKMLKEKADSCKEALMSLKMTHLGHHDNI-VNLLGACTLSGP 687
DB 601 ATAYGLGKEDNITGVAVKMLKASAHDPDEREALMSLKLHLGQHKNI-VNLLGACTHGGP 660

QY 688 VYLIFECYCGDLNLNLYRSKREF-----HRTW-----TEI 718
DB 661 VLVITEYCCCHGDLNLFIRSKAEFLNFVMTIPNPEPMTDYKNVSTERMFVRSDSGISST 720
QY 719 FKXHNFSYPTFOAHNSNMPGSRVQLHPLDQLSGNFSIHSEIEIYENOKRLAE 778
DB 721 CSHYLDMPRPVTSRPTNSTLDSSECQ----- 747
QY 779 EEDLNVLTPEDLLCFAYOVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVLCDPGLARD 838
DB 748 --EDSWFLDMDDLLRFSSQAQGLDFLAANKNCIHRDMAARNVLLTNSRKAICDFGLARD 805
QY 839 ILSDSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEISLGVNPPGIPVD 898
DB 806 IMDNSVYVKGNAELPVKMAPESEIFECVTVQSDVMSYGIMLWEISLGSKSPFNILVD 865
QY 899 ANFYKLITQSGFKMEQPPFYATEGIIYVQMSQWAFDRKRPSPFNITSLFGCOLAE-AEAC 957
DB 866 SKFYKMIKCGYQMSRPDPAPPMTYIMKMCWNLDAERPTFSKISQIMQLGETSEQD 925
QY 958 IRTSIHLPKQAAPQOR 973
DB 926 NQYKNIPAEAEAEQQ 941
RESULT 14
Q9TTD7
ID Q9TTD7 PRELIMINARY; PRT; 948 AA.
AC Q9TTD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Stem cell factor receptor (Fragment).
GN C-KIT.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawrence S.B., Greenwood P., Tisdall D.J., McNatty K.P., Fidler A.E.;
RT "Partial cDNA sequence of the c-kit homologue of brushtail possum
RT (Trichosurus vulpecula).";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE131209; AAF22141.1;
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00089; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
KW Immunoglobulin domain; Receptor; Tyrosine-protein kinase.
FT NON TER 948
SQ SEQUENCE 948 AA; 106323 MW; 708E0258FFC4D07D CRC64;
Query Match 22.8%; Score 1201; DB 6; Length 948;
Best Local Similarity 33.0%; Pred. No. 1.2e-96;
Matches 314; Conservative 148; Mismatches 356; Indels 134; Gaps 29;
QY 77 YEATVEVAESGSIITLQVOLATPGDLSCL-----WFKHSLGQCPHFDLQNRGIVSMA 130
DB 33 YSSPSITPARS---QLTVNFGSEIKLSCDLHFVNWTFFENAAAL---HLE-SSRTTETWL 84
QY 131 ILNVETQAGYLLHIOSEANRYVLTAVNRDQ-LYV---LRPFYRKMENODALL----- 183

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Db 85' TTNAQAQDGRYTC---TNKMGSLSSIIYVFKDPKILFLDLLLYGNEGSDALVNCVPVD 141
Qy 184 -----LCISGVDEP-----TVEWLCSHRESCKEEGPAVVRKEKVLH 223
Db 142 PEVNTFTLRUCGKPLKDLTLIPDIQGIITKNVK-RSHNKC-----184
Qy 224 ELFGTDIRCCARNALGRECTKLTFTDLNQAPOSTLPOL-----FLKVGEPWLIRCKAI 276
Db 185 -----PQCSAQDQCLKSLDRMTLKVRAPOS-VPEVSLLOQTNYLLRGETFOATCMIK 237
Qy 277 HNHGFGTLWELEDKALEBGSVFENSTSTNTMIRILLAFVSSVGRNDTGYTTCSSSK- 335
Db 238 DVASSVSWNIKNNRI---STHTQSRHSGDYAYERQDILTISPRVNDGVFTCFANNT 294
Qy 336 --HPSQSALVTILEKGFNA-TSSQBEYEIDPYEKFCSVRKAVPR-IRCTWIFSQAQSF 391
Db 295 FGPANVTATKVRKEGFNIFPQMTTIFINDGENIDLVEYEAAPKPHLOMIYNGTV 354
Qy 392 PCEQRGLDGYG-----ISKFCOHKNK-----PGEYIFYAENDDAQFTKMTLNI 436
Db 355 TDKW---DDYTKPGSESTIRYISEL--HLNRLKGTGGPGYTFVSNSDVSTSVTFKVIV 408
Qy 437 RKKPQVILANASQA--SCSSGYPPLPSWTWKCKSDKSPNC-TBEIPEGVWKNKANRVF 493
Db 409 KTKPBILTSDRMLNGLLQCAAGFPEPTIDWYFCPGTEQRCSTSVLPMDVKTNSMLPPF 468
Qy 494 GOWSSSTLNSEACKGLLVKVCAYNSMGTSCTETPLNSPGPFPFTQDNISFVATIGLCI 553
Db 469 GKIVVESTIDSAFRYNGTVECKANDVGKS--SAFN-----FAIKEQITSHLFTPLLI 522
Qy 554 PFIV-----VLIVLICHYKKQFYVESLOMI-QVTGPLDNEFYFVDRDYEDLKWEP 606
Db 523 GFVVAAGLMCVIIVILTYKYFOKPMYEVQWKVEEING---NNYVVIDTQPLPDHKNWF 579
Qy 607 PRENLFGKVLGSGAFGRVMNATAYGISTGVSIOVAVKMLKEKADSCKEALMSLQWM 666
Db 590 PRNRLSFGKTLGAGAFGKVEATEAGLFLKSDAAMTVAVKMLKPSAHLTREALMSLKV 639
Qy 667 THLGHHDINVLGACTLSGPPVLYFEVCCYGDLLNLSREKKEHRTWTETFKH----722
Db 640 SYLGNHMIANLGLACTIGGPTLVITEYCCYGDLLNFLRRKDSF-----ICSRHEDIA 693
Qy 723 NFSSYPTFOAHNSNMPGSR--VOLHPPDLQSLGFGNGSIHSEDETEYENQKRLABEESE 781
Db 694 EAALYNILQKSESCDGANEMDMKPGVYVVPYTKAEKERSARVGSYIERDVTYAIMED 753
Qy 782 DLNVLTFEDLLCFAYQVAKGMFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDILS 841
Db 754 DELALDIEDLLSFSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARHKN 813
Qy 842 DSSYVVRGNARLPVKWMAPESLFEGIYITIKSDVWSGILLWIFSLGVNPNYPGIPVDANF 901
Db 814 DSNYVVGNGARLPVKWMAPESLFNCVYTFESDVWSYGIFLWELFSLGSSPYFGMPYDSKF 873
Qy 902 YKLIQSGFMKEOPFYATEGIIYFVWOSCAFDSDRKRPSFNLTSFLGCOLAE 953
Db 874 YKMIKEGFRMLSPECAPPENYIMKSCWNEDPLQRTFKLIVQLIEQQLLDS 925

RESULT 15
Q98SU4
ID Q98SU4 PRELIMINARY; PRT; 977 AA.
AC Q98SU4
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase Fms.
OS Danio albolineatus (pearl danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=27699;
RN [1]
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RP SEQUENCE FROM N.A.
RA MEDLINE=21359118; PubMed=11466528;
RX Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
RT diversification in danio.";
RL Dev. Genes Evol. 211:319-328 (2001).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF324478; AAK15300.1; -.
DR HSPG; P11362; IFCK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig_4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transmembrane.
FT VARIANT 57 57 L -> V.
FT VARIANT 164 164 A -> V.
FT VARIANT 325 325 R -> P.
FT VARIANT 326 326 G -> C.
FT VARIANT 327 327 L -> P.
FT VARIANT 328 328 S -> A.
FT VARIANT 328 328 S -> F.
FT VARIANT 366 366 E -> D.
FT VARIANT 398 398 Q -> K.
FT VARIANT 419 419 K -> R.
FT VARIANT 431 431 P -> R.
FT VARIANT 431 431 T -> S.
FT VARIANT 611 611 N -> I.
FT VARIANT 706 706 I -> T.
FT VARIANT 926 926 S -> T.
FT VARIANT 952 952 E -> D.
SQ SEQUENCE 977 AA; 109802 MW; 109802 MW; FBFA4AE73BDF463B CRC64;

Query Match 22.8%; Score 1198.5; DB 13; Length 977;
Best Local Similarity 33.3%; Pred. No. 2e-96;
Matches 325; Conservative 162; Mismatches 365; Indels 123; Gaps 33;

Qy 84 VAESGSITLQVOLATPGLDLSCLWVPKHSGLGCPHFDLQNGIV-----SMAILNVT 136
Db 37 IYDSGS---PQLQVCEGDAPVTFL-----PRLAKHKRYISKVGKTRSPHVEKATV 84

Qy 137 TQAGEY-LIHQISERANYTVLFTVNVDRDQ-LYV-----LRRPYPRKMNQDALLCISEG 189
Db 85 DFTGYTKCVYINENDSNMSSVHVFDVRSRVLFVSPTSLSR--YVRK-EGEDLLPCLLT 141

Qy 190 VPEPTVEWVLCSSHRESCKEEGPAVVRKEEVL-----HELFGTDIRCCARNALGRECTKL 245
Db 142 DPDAI-DFTFRMDNGSAAPYGNMNAFTDPRKGLVLRNVHPGFNADYICISARIGGAEKVSKT 200

Qy 246 FIDLNQAQOSTLPQLFLK-----VGEPLWIRCAIHVNHGFGTLWELEDKALEEGSY 298
Db 201 FGINIQLRFP-PYVYLKRNRYVVLGKGLQISCTTNNPNFSYNTVTHSSRLPKAE- 258

Qy 299 FEMSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVT---ILEKGFINAT- 354
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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:38:17 ; Search time 55.9718 Seconds
(without alignments)
2361.629 Million cell updates/sec

Title: us-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQRSDRLLLVLSV.....RGGLRAQSPQVQKIHRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5264	100.0	992	14 AAR37502	Murine flk-2. Mus
2	5264	100.0	992	16 AAR67815	Flk2 receptor prot
3	5264	100.0	992	16 AAR67535	Mouse flk-2. Mus
4	5264	100.0	992	17 AAR97418	Human foetal liver
5	5264	100.0	992	18 AAW19874	Murine flk-2 recep
6	5264	100.0	992	20 AAY08616	Murine flk-2 prote
7	5256	99.8	992	14 AAR44994	Murine flk-2 recep
8	5256	99.8	992	14 AAR31375	Murine flk-2. Mus
9	5239	99.5	992	13 AAR28038	Murine flk-2. Mus
10	5102	96.9	1000	16 AAR81868	Flk2/flt3 tyrosine

11	4436.5	84.3	993	16 AAR75961	Human STK-1. Homo
12	4429.5	84.1	993	16 AAR67816	Flk2 receptor prot
13	4429.5	84.1	993	16 AAR67536	Human flk-2. Homo
14	4429.5	84.1	993	17 AAR97419	Murine foetal live
15	4429.5	84.1	993	18 AAW19873	Human flk-2 recep
16	4429.5	84.1	993	20 AAY08617	Human flk-2 protei
17	4426.5	84.1	993	14 AAR37503	Human flk-2. Homo
18	4421.5	84.0	993	14 AAR44995	Human flk-2 recep
19	4420.5	84.0	993	16 AAR81869	Human flk2/flt3 ty
20	4417.5	83.9	1167	14 AAR31376	Human flk-2. Homo
21	4409.5	83.8	983	19 AAW63588	Human receptor typ
22	4408	83.7	986	19 AAW63587	Human receptor typ
23	4408	83.7	986	19 AAW63589	Human receptor typ
24	4404	83.7	994	19 AAW63586	Human receptor typ
25	2806.5	53.3	665	19 AAW63585	Human receptor typ
26	2373.5	45.1	749	19 AAW78002	Protein pMON32390.
27	2226.5	42.3	481	15 AAR47579	Soluble Flk-2. Mu
28	1223.5	23.2	972	23 AAU11935	Colony stimulating
29	1223	23.2	975	22 AAE07144	Murine Kit/stem ce
30	1223	23.2	975	22 AAE07148	Mutant murine Kit/
31	1221.5	23.2	972	23 AAU79039	Human macrophage c
32	1221.5	23.2	972	23 AAU11936	Colony stimulating
33	1221.5	23.2	972	23 AAU11941	Colony stimulating
34	1221.5	23.2	972	23 AAU73585	Colony stimulating
35	1221.5	23.2	1055	22 ABG15479	Novel human diagno
36	1220.5	23.2	972	23 AAU11934	Colony stimulating
37	1220.5	23.2	972	23 AAU11937	Colony stimulating
38	1219.5	23.2	972	23 AAU11940	Colony stimulating
39	1216.5	23.1	972	23 AAU11938	Colony stimulating
40	1215	23.1	977	21 AAY51322	Bovine c-kit bK-1
41	1212.5	23.0	972	23 AAU11939	Colony stimulating
42	1197.5	22.7	2129	22 ABG15478	Novel human diagno
43	1197.5	22.7	2129	22 ABG20749	Novel human diagno
44	1196	22.7	976	22 AAE07145	Human Kit/stem cel
45	1196	22.7	976	22 AAU00375	Human stem cell gr

ALIGNMENTS

RESULT 1
AAR37502
ID AAR37502 standard; Protein; 992 AA.
XX AAR37502;
AC AAR37502;
XX
DT 19-OCT-1993 (first entry)
XX
DE Murine flk-2.
XX
KW Murine; receptor; protein; tyrosine kinase; pTK; flk-2; primitive;
KW hematopoietic cell; mature; family; conserved; region;
KW catalytic domain; c-kit; fetal liver kinase; flk; fetal; spleen;
KW thymus; adult; brain; bone marrow; multipotential; CPU-Blast colony;
KW hierarchy; transduction; T-lymphoid; lineage.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /note= "Hydrophobic leader sequence"
FT Protein 28..992
FT /note= "Mature murine flk-2"
FT Domain 28..544
FT /note= "Extracellular receptor domain"
FT Region 545..564
FT /note= "Transmembrane region"
FT Domain 565..992
FT /note= "Intracellular catalytic domain"
FT Domain 618..623
FT /note= "Catalytic sub-domain"
FT Domain 811..819
FT /note= "Catalytic sub-domain"

FT Domain 832..834
 FT /note= "Catalytic sub-domain"
 FT Domain 857..862
 FT /note= "Catalytic sub-domain"
 FT Domain 872..878
 FT /note= "Catalytic sub-domain"
 FT Region 736..812
 FT /note= "flk-2 signature sequence"
 XX
 PN WO9310136-A.
 XX
 PD 27-MAY-1993.
 XX
 XX 16-NOV-1992; 92WO-US09893.
 XX
 PR 15-NOV-1991; 91US-0793065.
 XX
 XX (UYPR-) UNIV PRINCETON.
 XX
 XX Lemischka IR;
 XX
 XX WPI; 1993-182479/22.
 DR N-PSDB; AAQ40914.
 XX
 XX Totipotent haematopoietic stem cell receptors, their ligands and
 PT DNA sequences - for treating anaemia(s) and bone marrow damage
 PT due to e.g. cancer chemotherapy or radiotherapy
 XX
 PS Claim 37; Fig 1a; 127pp; English.
 XX
 XX This sequence represents the murine receptor protein tyrosine kinase
 CC (pTK), flk-2. The nucleic acid encoding this receptor is expressed
 CC in primitive hematopoietic cells and not in mature hematopoietic
 CC cells. Members of this family of pTK's can be recognised by the
 CC conserved amino acid regions in the catalytic domain. This family
 CC of pTK's also contains c-kit. These new receptors are termed fetal
 CC liver kinases (flk's) after the tissue in which they were discovered.
 CC flk-2 is also expressed in fetal spleen, fetal thymus, adult brain
 CC and adult bone marrow. flk-2 is expressed in individual multipotential
 CC CFU-Blast colonies capable of generating numerous multilineage colonies
 CC upon replating. It is likely therefore, that flk-2 is expressed in
 CC the entire primitive portion of the hematopoietic hierarchy. This is
 CC consistent with flk-2 being important in transducing putative self-
 CC renewal signals from the environment. flk-2 is the first receptor
 CC pTK known to be expressed in the T-lymphoid lineage.
 XX
 SQ Sequence 992 AA;

Query Match 100.0%; Score 5264; DB 14; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MRALAQRSDRRLLLVLSVMILEFTVTTNODLPVVKCVLISHENNGSSAGKPSYRMVRGS 60
 Qy 61 PEDLOCTPRROSEGVYEAATVAEASGSIITLOVLATPGDLSCLVWPKHSLGQCPHFD 120
 Db 61 PEDLOCTPRROSEGVYEAATVAEASGSIITLOVLATPGDLSCLVWPKHSLGQCPHFD 120
 Qy 121 LQNRGIVSMALINVTETQAGEVLLHQSERANYTVLFTVNVDRDTOLYVLRPRPKRMENQ 180
 Db 121 LQNRGIVSMALINVTETQAGEVLLHQSERANYTVLFTVNVDRDTOLYVLRPRPKRMENQ 180
 Qy 181 DALLCISGEVPEPTVEVWLCSSHRESCKEKGPAVVRKEEKLHFGTDIRCCARNALGR 240
 Db 181 DALLCISGEVPEPTVEVWLCSSHRESCKEKGPAVVRKEEKLHFGTDIRCCARNALGR 240
 Qy 241 ECTKLTIDLNOAQPOSTLPQLFKVGBELWIRCKAIHNVHGFGLTWELEDKALEGSGYFE 300
 Db 241 ECTKLTIDLNOAQPOSTLPQLFKVGBELWIRCKAIHNVHGFGLTWELEDKALEGSGYFE 300
 Qy 301 MSTYTNTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPQSALVTILEKGFINATSSQEEY 360

Db 301 MSTYTNTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPQSALVTILEKGFINATSSQEEY 360
 Qy 361 EIDPYEYKFCFSVRKAYPRIRCTWIFSOASFPCEORGLEDGYSISKCDHKNKGEYIFY 420
 Db 361 EIDPYEYKFCFSVRKAYPRIRCTWIFSOASFPCEORGLEDGYSISKCDHKNKGEYIFY 420
 Qy 421 AENDDAOFTKMTNIRKPPVLANASASQSSDGYPLPSMTWTKKSDKSPNCTEIP 480
 Db 421 AENDDAOFTKMTNIRKPPVLANASASQSSDGYPLPSMTWTKKSDKSPNCTEIP 480
 Qy 481 EGVNKKANRKFVCGWVSSSTLNMSKGLLVKCCAYNSMGTSCTIFLNSPGPPFIQ 540
 Db 481 EGVNKKANRKFVCGWVSSSTLNMSKGLLVKCCAYNSMGTSCTIFLNSPGPPFIQ 540
 Qy 541 DNISFYATIGLCLPFIIVLIVLICHKYKKQPRYESOLOMIQVTPGLDNEYFYVDFRDEY 600
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 Qy 601 DLKWEFPRENLEFGKVLGSGAFGRVMNATAYIGSKTGVSIQVAVKMLKEKADSCKEALM 660
 Db 601 DLKWEFPRENLEFGKVLGSGAFGRVMNATAYIGSKTGVSIQVAVKMLKEKADSCKEALM 660
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 Db 661 SELKXMTHLGHHDNIIVNLGACTLGGPVYLIFFYCCYGGDLLNLYLSRKREKPHRTWTEIFK 720
 Qy 721 EHNFSYPTFOAHNSNMPGSRREVQLHPPLDQSGFNNGSIHSEDEIYEYENQKRLAESEE 780
 Db 721 EHNFSYPTFOAHNSNMPGSRREVQLHPPLDQSGFNNGSIHSEDEIYEYENQKRLAESEE 780
 Qy 781 EDLNVLFEDLCLFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 Db 781 EDLNVLFEDLCLFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 Qy 841 SDSSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPYGPVPDAN 900
 Db 841 SDSSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPYGPVPDAN 900
 Qy 901 FYKLIQSGFKMEQFPYATEGYIFVWQSCWAFDSRKRPSFPNLTSLFGQLAEABACIRT 960
 Db 901 FYKLIQSGFKMEQFPYATEGYIFVWQSCWAFDSRKRPSFPNLTSLFGQLAEABACIRT 960
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 Db 961 SIHLPKQAAPQORGLRAQSPQORVKIHRERS 992

RESULT 2
 AAR67815
 ID AAR67815 standard; Protein; 992 AA.
 XX
 AC AAR67815;
 XX
 DT 16-AUG-1995 (first entry)
 XX
 DE Flk2 receptor protein-tyrosine-kinase.
 XX
 KW Mouse Flk2; receptor protein-tyrosine-kinase; primitive
 KW hematopoietic cell; fetal liver kinase; diagnostic ligand
 KW isolation; bone marrow disease therapy.
 OS Mus musculus.
 XX
 Key Location/Qualifiers
 FH Peptide 1..27
 FT /note= "signal peptide"
 FT Protein 28..992
 FT /note= "mature protein"
 FT Domain 28..544
 FT /note= "extracellular receptor domain"
 FT Domain 545..564
 FT /note= "transmembrane region"

FT Domain 565..992
FT /note= "intracellular catalytic domain"
FT Domain 618..623
FT /note= "catalytic sub-domain"
FT Domain 811..819
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FT Domain 832..834
FT /note= "catalytic sub-domain"
FT Domain 857..862
FT /note= "catalytic sub-domain"
FT Domain 872..878
FT /note= "catalytic sub-domain"
FT Region 709..785
FT /note= "signature sequence typical of Flk2"
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PN WO9500554-A.
XX
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XX 05-JAN-1995.
XX
XX 17-JUN-1994; 94WO-US06944.
XX
XX
XX 18-JUN-1993; 93US-0080244.
XX 21-JUN-1993; 93US-0081508.
XX 23-NOV-1993; 93US-0157490.
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI; 1995-052014/07.
XX N-PSDB; AAQ81012.
XX
XX Ligand for receptor protein tyrosine kinase - useful for the
XX stimulation of primitive haematopoietic stem cells causing
XX proliferation and/or differentiation
XX
XX Disclosure; Fig 1a; 131pp; English.
XX
XX The sequence corresponds to a mouse Flk2 (fetal liver kinase)
XX receptor protein-tyrosine-kinase, which is expressed in primitive
XX hematopoietic cells but not in mature hematopoietic cells. The
XX protein is useful in isolation of receptor ligands, which have
XX applications in diagnosis of bone marrow disorders and in
XX stimulating proliferation and/or differentiation of primitive
XX hematopoietic stem cells.
SQ Sequence 992 AA;

Query Match 100.0%; Score 5264; DB 16; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 PEDLQCTPRROSEGTVEAAVTEVAESGSILOVQLATPGDLSCLVWFKHSLGCQPHD 120
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DB 121 LQNRGIVSMALNTVETQAGELYLHIQSERANYTVLFTVNVVRDQLVYLRPPYFRKMENQ 180
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DB 181 DALLCISGEVPEPTVWVLCSSHRESCKEGPAVVRKEEYVLFPGTDIRCCARNALGR 240
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DB 241 ECTKLFTIDLNAQOSTLPQLFLVKGPELWIRCKAIHVNHGFGLTWELEDKALEGSYFE 300
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Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
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Db 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOASPCPCORGLDGYISKFCDHKNKPGEYIFY 420
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Db 421 AENDDAQFTKMTNIRKPPQVLANASQASCSDDGYPLPSWTWKKCSKSPNCTEIP 480
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Db 481 EGVNKKANRKFQGVSSSTLNMSKAGLLVKCCAYNSMGTSCTETIFLNSPGPFPIQ 540
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Db 541 DNISFYATIGLCLPFIIVLIVLICHYKKOPRYESQLOMIQVGTPLDNEYFVVDPRDYEY 600
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Db 601 DLKWEFFPRENLEFGKVLGSGAGFGRVMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
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Db 661 SELKQWTHLGHHDNIIVNLLGACTLGGPVYLIFECYCGDILLNLYLSKREKPHRTWTEIFK 720
QY 721 EHNFSYPTFOAHNSNSMPGSRREVQLHPPLDQSGFNGNSIHSEDEIYEYENQKRLAEDEE 780
Db 721 EHNFSYPTFOAHNSNSMPGSRREVQLHPPLDQSGFNGNSIHSEDEIYEYENQKRLAEDEE 780
QY 781 EDNLVLTFFEDLLCFAYQVAKGMEFLEPKSCVHRDLAARNVLTHTGKVVKICDFGLARDIL 840
Db 781 EDNLVLTFFEDLLCFAYQVAKGMEFLEPKSCVHRDLAARNVLTHTGKVVKICDFGLARDIL 840
QY 841 SDSSYVVRGNARLPVKWMAPESLFEGITTKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 841 SDSSYVVRGNARLPVKWMAPESLFEGITTKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
QY 901 FYKLIQSGFKMEOPFYATEGIYFVWQSCWAFDSRKRPSFPNLTSLFGCOLAEAEACIRT 960
Db 901 FYKLIQSGFKMEOPFYATEGIYFVWQSCWAFDSRKRPSFPNLTSLFGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPQORGLRAQSPQORQVKIHRERS 992
Db 961 SIHLPKQAAPQORGLRAQSPQORQVKIHRERS 992

RESULT 3
AAR67535
ID AAR67535 standard; Protein; 992 AA.
XX
AC AAR67535;
XX
DT 04-JUL-1995 (first entry)
XX
DE Mouse flk-2.
XX
KW Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
KW hematopoiesis; stem cell.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= sig_peptide
FT Domain 28..544
FT /label= Extracellular_receptor_domain
FT Region 545..564
FT /label= Transmembrane_region
FT Domain 565..992
FT /label= Intracellular_catalytic_domain
XX

PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 26-JUN-1992; 92US-0906397.
 PR 12-NOV-1992; 92US-0975049.
 PR 30-APR-1993; 93US-0055269.
 PR 31-OCT-1994; 94US-0252517.
 XX (UYPR-) UNIV PRINCETON.
 PA Lemischka IR;
 XX
 PI
 XX
 DR WPI; 1996-392678/39.
 DR N-PSDB; AAT38733.
 XX
 PT Anti-fœtal liver kinase 2 (flk-2) antibodies - useful in assays,
 PT for isolating haematopoietic stem cells expressing receptor and for
 PT obtaining ligands
 XX
 PS Claim 1; Columns 27-34; 50pp; English.
 XX
 CC The present sequence is human foetal liver kinase 2 (flk-2), a
 CC protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
 CC raised against the extracellular portion of flk-2 can be used to
 CC assay for flk receptors on the surface of primitive haematopoietic
 CC stem cells, and to isolate positive cells. The antibodies can also
 CC be used as, or to obtain ligands, which stimulate the proliferation
 CC and/or differentiation of stem cells. The ligands can be used, e.g.
 CC for treating anaemia, or bone marrow damage resulting from cancer
 CC chemotherapy, or radiation.
 XX
 SQ Sequence 992 AA;

Query Match 100.0%; Score 5264; DB 17; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALQSRDRRLLLVLSVMILETVTNQDLPVVKVLI SHENNGSSAGKPSRYVRVGS 60
 DB 1 MRALQSRDRRLLLVLSVMILETVTNQDLPVVKVLI SHENNGSSAGKPSRYVRVGS 60
 QY 61 PEDLQTPRQSGTVEAATVEAASGSITLQVLAATPGDLSCLMVFKHSSIGCQPHFD 120
 DB 61 PEDLQTPRQSGTVEAATVEAASGSITLQVLAATPGDLSCLMVFKHSSIGCQPHFD 120
 QY 121 LQNRGIVSMALLNVTQAGEYLLHIOSEKANYTVLFTVNVRTOLYVLRPFRKWNQ 180
 DB 121 LQNRGIVSMALLNVTQAGEYLLHIOSEKANYTVLFTVNVRTOLYVLRPFRKWNQ 180
 QY 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
 QY 241 ECTKLTIDLNOAQSTLPQLFLKVGEPILWIRCKAIHVNHGFLTWELEDKALEGSYPE 300
 DB 241 ECTKLTIDLNOAQSTLPQLFLKVGEPILWIRCKAIHVNHGFLTWELEDKALEGSYPE 300
 QY 301 MSTYSTNRTMIRILLAFVSSVGNNDGYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 DB 301 MSTYSTNRTMIRILLAFVSSVGNNDGYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKFCFVSVPKAYPRICRTWIFSQASFPCQKGLDGYISIKFCDHKNKPGYIFY 420
 DB 361 EIDPYEKFCFVSVPKAYPRICRTWIFSQASFPCQKGLDGYISIKFCDHKNKPGYIFY 420
 QY 421 AENDDAQFTKMTLNIRKXQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
 DB 421 AENDDAQFTKMTLNIRKXQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
 QY 481 EGVWNNKANRKYVQGVSSSTLNNAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540
 DB 481 EGVWNNKANRKYVQGVSSSTLNNAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540

QY 541 DNISFYATIGLCPLPFIWLVILVICHYKQFRYESQLOMIQVTPGLDNEYFYVDFRDY 600
 DB 541 DNISFYATIGLCPLPFIWLVILVICHYKQFRYESQLOMIQVTPGLDNEYFYVDFRDY 600
 QY 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIOVAVKMLKEKADSC 660
 DB 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIOVAVKMLKEKADSC 660
 QY 661 SELKMMTHLGHNDINVLGACTLSGVPYLI FEYCCYGDLLNLYRSKREKPHRTWT 720
 DB 661 SELKMMTHLGHNDINVLGACTLSGVPYLI FEYCCYGDLLNLYRSKREKPHRTWT 720
 QY 721 EHNFSYPTFOAHSNNSMPGSRVQLHPPLDQLSGFNGNSIHSEDEIEYENQKEL 780
 DB 721 EHNFSYPTFOAHSNNSMPGSRVQLHPPLDQLSGFNGNSIHSEDEIEYENQKEL 780
 QY 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVVKIC 840
 DB 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVVKIC 840
 QY 841 SDSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPY 900
 DB 841 SDSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPY 900
 QY 901 FYKLIQSGFKMEQPFYATEGIYFVMQSCWAFDSRKRPFPNLTSLFLGCQLAE 960
 DB 901 FYKLIQSGFKMEQPFYATEGIYFVMQSCWAFDSRKRPFPNLTSLFLGCQLAE 960
 QY 961 SIHLPKQAAPQQRGGLRAQSPQKVHRERS 992
 DB 961 SIHLPKQAAPQQRGGLRAQSPQKVHRERS 992

RESULT 5
 AAW19874
 ID AAW19874 standard; Protein; 992 AA.
 XX
 AC AAW19874;
 DT 19-AUG-1997 (first entry)
 XX
 DE Murine flk-2 receptor.
 XX
 KW Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
 KW pTK; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
 KW haematopoietic hierarchy; extracellular domain; soluble form; ligand;
 KW proliferation; differentiation; mammalian; haematopoietic stem cell;
 KW macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse.
 XX
 OS Mus musculus.
 XX
 FH Key
 FT Peptide
 FT /note= "Signal peptide"
 FT Domain
 FT /note= "Extracellular receptor domain"
 FT Region
 FT /note= "transmembrane region"
 FT Domain
 FT /note= "Intracellular catalytic domain"
 FT Active-site
 FT /note= "Catalytic sub-domain"
 FT Active-site
 FT /note= "Catalytic sub-domain"
 FT Active-site
 FT /note= "Catalytic sub-domain"
 FT Active-site
 FT /note= "Catalytic sub-domain"
 FT Peptide
 FT /note= "Signature sequence characteristic of flk-2"
 XX

PN US5621090-A.
 XX 15-APR-1997.
 XX 02-APR-1991; 91US-0679666.
 XX 26-JUN-1992; 92US-0906397.
 PR 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 XX 24-DEC-1991; 91US-0813593.
 PA (UYPR-) UNIV PRINCETON.
 XX Lemischka IR;
 XX WPI; 1997-235228/21.
 DR N-PSDB; AAT72118.
 XX Protein containing the extracellular domain of human flk-2 - used
 PT for identification of primitive haematopoietic cell proliferation
 XX and differentiation stimulatory ligands, e.g. for treating anaemia
 PS Disclosure; Fig 1A; 55pp; English.
 XX This sequence represents murine fetal liver kinase 2 (flk2). flk-2 is
 CC a receptor protein tyrosine kinase (PTK) and is important in transducing
 CC putative self-renewal signals from the environment. flk-2 is expressed
 CC in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
 CC and it is thought that flk-2 is expressed in the entire primitive portion
 CC of the haematopoietic hierarchy. The invention concerns a recombinant
 CC nucleic acid, preferably mRNA, which encodes a protein containing only
 CC the extracellular domain of human flk-2 and lacking the flk-2 intra-
 CC cellular catalytic domain. The resultant protein represents a soluble
 CC form of flk-2 which is used to isolate specific ligands for flk-2. These
 CC ligands can be used to stimulate proliferation and/or differentiation of
 CC mammalian haematopoietic stem cells, in vivo or in vitro, e.g. for
 CC treatment of macrocytic or aplastic anaemia or bone marrow damage caused
 CC by cancer treatment or radiation.
 XX Sequence 992 AA;
 SQ

Query Match 100.0%; Score 5264; DB 18; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQSDRRLLLVLSVMILETVTNQDLPVVKCVLISHENNGSSAGKPSRYMRVGS 60
 DB 1 MRALAQSDRRLLLVLSVMILETVTNQDLPVVKCVLISHENNGSSAGKPSRYMRVGS 60
 QY 61 PEDLOCTPRQSEGTYEATVEAVERSGSITLQVQLATPGDLSCLVWFKHSSILGCOPHPD 120
 DB 61 PEDLOCTPRQSEGTYEATVEAVERSGSITLQVQLATPGDLSCLVWFKHSSILGCOPHPD 120
 QY 121 LQNRGTVSMALNVETQAGEYLHLLHQSERANVTVLFTVNRDVTQYVLRPRFRKWNQ 180
 DB 121 LQNRGTVSMALNVETQAGEYLHLLHQSERANVTVLFTVNRDVTQYVLRPRFRKWNQ 180
 QY 181 DALLCISEGVPEPTVEWLVLCSSHRESCKEAGPAVRKEKVLHELFGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVEWLVLCSSHRESCKEAGPAVRKEKVLHELFGTDIRCCARNALGR 240
 QY 241 ECTKLTIDLNQAPQSTLPOLFLKVEPLWIRCKAIVHNGFGLTWELEDKALEEGSYFE 300
 DB 241 ECTKLTIDLNQAPQSTLPOLFLKVEPLWIRCKAIVHNGFGLTWELEDKALEEGSYFE 300
 QY 301 MSTYSTNRTMIRILLAFVSSVGRNDGYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 DB 301 MSTYSTNRTMIRILLAFVSSVGRNDGYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKFCFVSFRKAYPRIRCTWIFSQASFCEQRLGDEGYSISKFDHKNKPGYIFY 420
 DB 361 EIDPYEKFCFVSFRKAYPRIRCTWIFSQASFCEQRLGDEGYSISKFDHKNKPGYIFY 420

QY 421 AENDDAQFTOMFTLNIRKKPOVLANASASQSSDGYPLPSWTWKCKSDKSPNCTEIP 480
 DB 421 AENDDAQFTOMFTLNIRKKPOVLANASASQSSDGYPLPSWTWKCKSDKSPNCTEIP 480
 QY 481 EGVNKKANRKFVGQWSSSTLNMSSEAGLLVKKCAYNMGTSCTETIFLNSPGPPFIQ 540
 DB 481 EGVNKKANRKFVGQWSSSTLNMSSEAGLLVKKCAYNMGTSCTETIFLNSPGPPFIQ 540
 QY 541 DNISFYATIGLCLPIVVLVLI CHYKKQPRYESQLOMIQVTGPDNEFYFVDFRDIY 600
 DB 541 DNISFYATIGLCLPIVVLVLI CHYKKQPRYESQLOMIQVTGPDNEFYFVDFRDIY 600
 QY 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISTKTVSIOVAVKMLKEKADSCKEALM 660
 DB 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISTKTVSIOVAVKMLKEKADSCKEALM 660
 QY 661 SELKWMTHLGHHDNIVNLGACTLSGPVYLI FEYCCYGDLLNLYRSKRKFHRTWTEIFK 720
 DB 661 SELKWMTHLGHHDNIVNLGACTLSGPVYLI FEYCCYGDLLNLYRSKRKFHRTWTEIFK 720
 QY 721 EHNFSYPTFOAHNSMPSGSEVOLHPPLDOLSGFNGNSIHSEDEIEYENOKRLAESEE 780
 DB 721 EHNFSYPTFOAHNSMPSGSEVOLHPPLDOLSGFNGNSIHSEDEIEYENOKRLAESEE 780
 QY 781 EDLNVLTPEDLICFAVOVAKGMELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 DB 781 EDLNVLTPEDLICFAVOVAKGMELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 QY 841 SDSSYVVRGNARLPVKWMAPELSLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 DB 841 SDSSYVVRGNARLPVKWMAPELSLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 QY 901 FYKLIQSGFKMOPFYATEGIYFVMSQSWAFDSRKPSFPNLTSLFGCOLAABEACIRT 960
 DB 901 FYKLIQSGFKMOPFYATEGIYFVMSQSWAFDSRKPSFPNLTSLFGCOLAABEACIRT 960
 QY 961 SIHLPRQAPQORGGIRAOQPORQVVKIHRERS 992
 DB 961 SIHLPRQAPQORGGIRAOQPORQVVKIHRERS 992

RESULT 6
 AAY08616
 ID AAY08616 standard; Protein; 992 AA.
 XX
 AC AAY08616;
 DT 05-AUG-1999 (first entry)
 XX
 DE Murine flk-2 protein.
 XX
 KW Murine; flk-2; flk-1; cell isolation; fetal liver kinase; receptor;
 monoclinal; polyclonal; antibody; tyrosine kinase.
 XX
 OS Mus sp.
 XX
 PN US5912133-A.
 PD 15-JUN-1999.
 XX
 PF 10-FEB-1998; 98US-0021324.
 XX
 PR 19-NOV-1992; 92US-0977451.
 PR 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 26-JUN-1992; 92US-0906397.
 PR 12-NOV-1992; 92US-0975049.
 PR 30-APR-1993; 93US-0055269.
 PR 31-OCT-1994; 94US-0252498.
 PR 15-FEB-1996; 96US-0601891.

(UYPR-) UNIV PRINCETON.

Lemischka IR:

WPI; 1999-357194/30.
N-PSDB: AAX77514.

N-PSDB: AAX77514.

Isolating hematopoietic cells expressing fetal liver kinase 1 receptors

Disclosure: Fig 1a: 59pp; English.

This invention describes a novel method of isolating cells expressing fetal liver kinase 1 (flk-1) receptors on their surface and comprises binding the cells to a polyclonal or monoclonal antibody specific to the FLK-1 receptor and isolating the cells that have bound to the antibody. The method can be used to isolate hematopoietic stem cells in any mammal but preferably a rat, mouse, rabbit or human. The proteins of the invention belong to the receptor protein family. This sequence represents the murine flk-2 protein which is used in the method of the invention.

Sequence 992 AA:

Very Match	100.0%;	Score 5264;	DB 20;	Length 992;
1st Local Similarity	100.0%;	Pred. No. 0;		
Matches 992;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

1 MRALAORSDDRRLLLLVLSVMILETVTNODLPVIKCVLISHENNNGSSAGKPSSYRMVRS 60

1 MRALAORSRRRLLLVLSVMILET'VTNODLPVICKVLI SHENNGSSAGKPPSSYRMVRGS 60

61 PEDLOCTPRROSEGTVYEAAATVEVAESGSITLQVQLATPGDLSCLWVFKHSSLGCQPHFD 120

61 PEDLOCTPRROSEGTVYEAAATVEVAESGSITLOVQLATPGDLSCLWVFKHSSSLGCQPHFD 120

121 LQNRGIVSMAILNVTTETQAGEYLLHIQSERANYTVLFTVNVRDTQLYVLRPPYFRKMENQ 180

121 LQNRGIVSMAILNVETETQAGEYLLHIQSERANYTVLFTVNVRDTQLVLRPPYFRKMENQ 180

181 DALLCISEGVPEPTVEWVLCSSHRESCKEEGPAVVRKEEKVLHELFGTDIRCCARNALGR 240

181 DALLCISEGVPEPTVEWVLCSSHRESCKEEGPAVVRKEEKVLHELFGTDIRCCARNALGR 240

241 ECTKLFTIDLNOAPOSTLPOLFLKVGEPLWIRCKAIHVNHGFLTWELEDKALEEGSYFE 300

241 ECTKLFTIDLNQAPQSTLPQFLKVGEPLWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300

301 MSTYSTNR TMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360

301 MSTYSTNRTMIRILLAEVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSSQEEY 360

361 EIDPYEKFCFSVRFKAYPRIRCTWIFSQASFCEQRGLEDGYSISKFCDHKNKPGEYIFY 420

361 EIDPYEKFCFSVRFKAYPRIRCTWIFSOASFCEQRGLEDGYSISKFCDHKNKPGEYIFY 420

421 AENDDAOFTKMFTLNIRKKPOVLANASASQASCSDDGYPLPSWTWKKCSDKSPNCTEIP 480

421 AENDDAQFTKMFTLNIRKKPQVLANASASQASCSSDGYPLPSWTWKKCSDKSPNCTEEIP 480

481 EGVWNKKANRKVFGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCETIFLNSPGPPFIQ 540

481 EGVWNKKANRKVFGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCETIFLNSPGPPFIO 540

541 DNISFYATIGLCPLFFIVVLIVLICHKYKKQFRYESOLOMIQVTGPLDNEYFYVDFRDY 600

541 DNISFYATIGLCLEPIVVLVLICHKYKKOFRYESOLOMIOVTGELPDNEFYVDFRDYEX 600

601 DLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIQAVKMLKEKADSCKEALM 660

601 DLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660

Qy	661	SELQWQTHLGHHDINVLNLLGACTLSGDPVYLI	FEYCCYGGDLLNLYRSKBEKFKHTWTEIFK	720
Db	661	SELQWQTHLGHHDINVLNLLGACTLSGDPVYLI	FEYCCYGGDLLNLYRSKBEKFKHTWTEIFK	720
Qy	721	EHNFSYPTTQAHNSNMPGSRVQLHPPLDQLSGFN	SGNHSIHSEDEIYEYENQKRLAESEE	780
Db	721	EHNFSYPTTQAHNSNMPGSRVQLHPPLDQLSGFN	SGNHSIHSEDEIYEYENQKRLAESEE	780
Qy	781	EDLNVLTFEDLLCPAYQVAKGMFELEPKSV	CHVRDLAARNVLVTHGKVVKLCDGLARDIL	840
Db	781	EDLNVLTFEDLLCPAYQVAKGMFELEPKSV	CHVRDLAARNVLVTHGKVVKLCDGLARDIL	840
Qy	841	SDSSYVVRGNARLPVKWMAPESLFEGITYIKSD	VWMSYGILLWEIFSLGNVPYFGIPVDAN	900
Db	841	SDSSYVVRGNARLPVKWMAPESLFEGITYIKSD	VWMSYGILLWEIFSLGNVPYFGIPVDAN	900
Qy	901	FYKLIQSGFKWEQPFYATEGIYFMQSCWAFDS	RKRPSPFNLTSPFGCOLAEAEACIPT	960
Db	901	FYKLIQSGFKWEQPFYATEGIYFMQSCWAFDS	RKRPSPFNLTSPFGCOLAEAEACIRT	960
Qy	961	SIHLPKQAAQPGGLRAQSPQRQVKIHRERS	992	
Db	961	SIHLPKQAAQPGGLRAQSPQRQVKIHRERS	992	

RESULT 7
AAR44994

AA44994
ID AAR44994 standard; Protein; 992 AA.

AC AAR44994:

27-JUN-1994 (first entry)

DE Murine flk-2 receptor protein tyrosine kinase.

Receptor protein tyrosine kinase; pTK family; foetal liver kinase;
KW primitive; totipotent; haematopoietic cell; stem cell; proliferation;
KW mflk; stromal cell.

XX Mus musculus.

Key	Location/Qualifiers
Peptide	1..27
FT	/label= signal_peptide
FT	/note= "hydrophobic leader"
FT	28..992
Protein	/label= flk-2
FT	/note= "mature protein"
FT	28..544
Domain	/label= extracellular_domain
FT	545..564
Region	/label= transmembrane_region
FT	565..992
Domain	/label= intracellular_catalytic_domain
FT	618..623
Domain	/note= "catalytic subdomain"
FT	811..819
Domain	/note= "catalytic subdomain"
FT	832..834
Domain	/note= "catalytic subdomain"
FT	857..862
Domain	/note= "catalytic subdomain"
FT	872..878
Domain	/note= "catalytic subdomain"
FT	

PN US5270458-A.

14-DEC-1993.

02-APR-1991:

02-APR-1991;

XX 26-JUN-1992; 92WO-US05401.
 PF
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 02-APR-1992; 92WO-US02750.
 XX (UYPR-) UNIV PRINCETON.
 PA
 XX Lemischka IR;
 XX
 XX WPI; 1993-036323/04.
 DR N-PSDB; AAQ45247.
 XX
 PT Nucleic acid encoding receptor protein tyrosine kinase - allows
 PT development of ligands to stimulate proliferation and/or
 PT differentiation of mammalian haematopoietic stem cells
 XX
 XX Claim 5; Fig 1a; 78pp; English.
 XX
 CC This sequence represents a murine receptor protein tyrosine kinase
 CC which belongs to a new functional class of protein tyrosine kinases
 CC (ptks). ptks in this class are expressed in primitive mammalian
 CC hematopoietic (pHC) cells but not in mature hematopoietic cells (mHC).
 CC This protein is an example of a receptor ptk and is called fetal liver
 CC kinase 2 (flk-2). flk-2 is expressed in fetal liver, spleen and
 CC thymus, and adult brain and marrow. Expression of flk-2 mRNA occurs
 CC in the most primitive thymocyte subset, which is believed to be
 CC uncommitted. Therefore, thymocytes expressing flk-2 may be multi-
 CC potential. flk-2 is the first receptor tyrosine kinase known to be
 CC expressed in the T-lymphoid lineage.
 XX
 SQ Sequence 992 AA;

Query Match 99.8%; Score 5256; DB 14; Length 992;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEALQSRDRRLLLVLLSVMLLETVTNQLPVKCVLISHENNGSSAGKPSRYMVRGS 60
 DB 1 MEALQSRDRRLLLVLLSVMLLETVTNQLPVKCVLISHENNGSSAGKPSRYMVRGS 60
 QY 61 PEDLOCTPRQSEGTVEATVEAEGSITLQVQLATPGDLSCLVWFKHSSLGCOHPED 120
 DB 61 PEDLOCTPRQSEGTVEATVEAEGSITLQVQLATPGDLSCLVWFKHSSLGCOHPED 120
 QY 121 LQNRGIVSMALLNVTTQAGEYLLHTIQSRANYTVLFTVNVRTDQLYVLRPPYFRKMENQ 180
 DB 121 LQNRGIVSMALLNVTTQAGEYLLHTIQSRANYTVLFTVNVRTDQLYVLRPPYFRKMENQ 180
 QY 181 DALLCISEGVPEPTVEWVLCSSHRECKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVEWVLCSSHRECKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
 QY 241 ECTKLFITDLNOAQPTLQFLKVGEPWIRCKALHVNHGFLTWELDKALEEGSYFE 300
 DB 241 ECTKLFITDLNOAQPTLQFLKVGEPWIRCKALHVNHGFLTWELDKALEEGSYFE 300
 QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYKPCFVSFRKAYPRICRTWIFSQAFFCEQRLGDEGYSISKFDHKNKPGYIFY 420
 DB 361 EIDPYKPCFVSFRKAYPRICRTWIFSQAFFCEQRLGDEGYSISKFDHKNKPGYIFY 420
 QY 421 AENDDAQFTKMTLNIRKKPQVLANASQASCSGYPPLPSMTWKCKSDKSPNCTEIP 480
 DB 421 AENDDAQFTKMTLNIRKKPQVLANASQASCSGYPPLPSMTWKCKSDKSPNCTEIP 480
 QY 481 EGVWNNKANRKFVGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540

DB 481 EGVWNNKANRKFVGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540
 QY 541 DNISFYATIGLCPLFTIVLIVLICHYKQFRYESQLOMIQVTPGLDNEYFYVDFRDYEF 600
 DB 541 DNISFYATIGLCPLFTIVLIVLICHYKQFRYESQLOMIQVTPGLDNEYFYVDFRDYEF 600
 QY 601 DLKWEFPRENLEBFGKVLGSGAFGRVNNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
 DB 601 DLKWEFPRENLEBFGKVLGSGAFGRVNNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
 QY 661 SELKWMTHLGHHDNIVNLGACTLSCGPVYLIFEYCCYGDLLNLYLRKREKHFHTWTEIFK 720
 DB 661 SELKWMTHLGHHDNIVNLGACTLSCGPVYLIFEYCCYGDLLNLYLRKREKHFHTWTEIFK 720
 QY 721 ENHFSYPTFOAHSNMPGSRREVQLHPPLDQLSGFNGNSIHSEDEIEYENQKRLAEEEE 780
 DB 721 ENHFSYPTFOAHSNMPGSRREVQLHPPLDQLSGFNGNSIHSEDEIEYENQKRLAEEEE 780
 QY 781 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 DB 781 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 QY 841 SDSSYYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVPDAN 900
 DB 841 SDSSYYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVPDAN 900
 QY 901 FYKLIQSGFKMQPPFYATGSIYFVMQSCWAFDSRKPSRPNLTSELCQLAEEAEACIRT 960
 DB 901 FYKLIQSGFKMQPPFYATGSIYFVMQSCWAFDSRKPSRPNLTSELCQLAEEAEACIRT 960
 QY 961 SIHLPKQAAPQORGLRAQSPQVQVVIHRRS 992
 DB 961 SIHLPKQAAPQORGLRAQSPQVQVVIHRRS 992

RESULT 9
 AAR28038
 ID AAR28038 standard; Protein; 992 AA.
 XX AC AAR28038;
 XX DT 15-MAR-1993 (first entry)
 XX DE Murine flk-2.
 XX KW Thymidine kinase; TK; haematopoietic; stem cells; proliferation;
 XX OS Mus musculus.
 XX FH Key
 XX FT Peptide
 XX FT Domain
 XX FT Region
 XX FT Domain
 XX FT Region
 XX PN WO9217486-A.
 XX PD 15-OCT-1992.
 XX PF 02-APR-1992; 92WO-US02750.
 XX PR 02-APR-1991; 91US-0679666.
 XX PR 28-JUN-1991; 91US-0728913.
 XX PR 15-NOV-1991; 91US-0793065.
 XX PR 24-DEC-1991; 91US-0813593.

Location/Qualifiers
 1..27 /note= "hydrophobic leader"
 28..544 /note= "extracellular receptor domain"
 545..564 /note= "transmembrane region"
 565..992 /note= "intracellular catalytic domain"
 709..785 /note= "signature sequence of flk-2"

(UYPR-) UNIV PRINCETON.

Lemischka IR;

WPI; 1992-366185/44.

DR N-PSDB; AAQ29954.

Stimulating proliferation and/or differentiation of primitive mammalian haematopoietic stem cells - using ligand that binds thymidine kinase and flk-1 and flk-2

Claim 37; Fig 1a; 94pp; English.

The murine foetal liver kinase (flk) -2 sequence was deduced from that of the flk-2 clone obtd. by standard PCR techniques from stem-cell receptor-contg. tissue cDNA libraries. Suitable tissues include foetal liver, spleen or thymus cells or adult marrow or brain cells. The PCR primers used are based on known sections of the flk-2 gene. The murine flk-2 clone may be used in a vector to transform haematopoietic cells. The thymidine kinase encoded by flk-2 is expressed in primitive but not mature haematopoietic cells. Ligand binding to the TK may be pred. which can stimulate proliferation and/or differentiation of primitive haematopoietic cells in vivo. The ligands can stimulate the proliferation of additional primitive stem cells, differentiation into more mature progenitor cells, or both.

See also AAR28039-41.

Sequence 992 AA;

Query Match 99.5%; Score 5239; DB 13; Length 992;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 989; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRALAQSDRRLLLVLSWILEVTVDLPVVKCVLISHENNGSSACKPSSYRMVRS 60
 DB 1 MRALAQSDRRLLLVLSWILEVTVDLPVVKCVLISHENNGSSACKPSSYRMVRS 60
 QY 61 PEDLOCTPRQSGTGYEAATVEAESSITLQVOLATPGDLSCLWVFKHSLGCGQPHD 120
 DB 61 PEDLOCTPRQSGTGYEAATVEAESSITLQVOLATPGDLSCLWVFKHSLGCGQPHD 120
 QY 121 LQNRGIVSMALNVTTQAGEYLLHQSERANYTLFTVNVVDTQLYVLRPFYRKMEQ 180
 DB 121 LQNRGIVSMALNVTTQAGEYLLHQSERANYTLFTVNVVDTQLYVLRPFYRKMEQ 180
 QY 181 DALLCISGVPEPTVWVLCSSHRESCKEKGPAVYRKEEVLHFGTDIRCCARNALGR 240
 DB 181 DALLCISGVPEPTVWVLCSSHRESCKEKGPAVYRKEEVLHFGTDIRCCARNALGR 240
 QY 241 ECTKLFTDLNOAPOSTLPOLFKYGEPLWIRCKAIHVNHGFLTWLEDKALEEGSYFE 300
 DB 241 ECTKLFTDLNOAPOSTLPOLFKYGEPLWIRCKAIHVNHGFLTWLEDKALEEGSYFE 300
 QY 301 MSTYCTNRTMIRILLAFVSSVGRNDTGYTSCSSKHPSQSALVTILEKGFINATSSQEEY 360
 DB 301 MSTYCTNRTMIRILLAFVSSVGRNDTGYTSCSSKHPSQSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKFCFSVRKAYPRIRCTWIFPSQASFPCEORGLDGYISKFCDHKNKPGYEYIF 420
 DB 361 EIDPYEKFCFSVRKAYPRIRCTWIFPSQASFPCEORGLDGYISKFCDHKNKPGYEYIF 420
 QY 421 AENDDAQFTMTNIRKKPQVLNANASQASCSGDPVLPSTWTKCKSDKSPNCTEIP 480
 DB 421 AENDDAQFTMTNIRKKPQVLNANASQASCSGDPVLPSTWTKCKSDKSPNCTEIP 480
 QY 481 EGVWNNKANRKFVGQWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETFLNSPGFPFIQ 540
 DB 481 EGVWNNKANRKFVGQWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETFLNSPGFPFIQ 540
 QY 541 DNISFYATIGLCPLFTVILVILCHYKQFQRYESQLOMIQVTGPDNBYFVDFRDVEY 600
 DB 541 DNISFYATIGLCPLFTVILVILCHYKQFQRYESQLOMIQVTGPDNBYFVDFRDVEY 600

QY 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOVAVQMLKEKADSCKEALM 660
 DB 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOVAVQMLKEKADSCKEALM 660
 QY 661 SELKQWTHLGHHDNIIVNLLGACTLSGPPVYLIFEYCCYGDLLNLSKREKPHRTWTEIFK 720
 DB 661 SELKQWTHLGHHDNIIVNLLGACTLSGPPVYLIFEYCCYGDLLNLSKREKPHRTWTEIFK 720
 QY 721 EHNFSSTPTFOAHNSNSMPGSRREVQLHPDLQLSGFNGNSIHSEDEIEYENQKRLAESEE 780
 DB 721 EHNFSSTPTFOAHNSNSMPGSRREVQLHPDLQLSGFNGNSIHSEDEIEYENQKRLAESEE 780
 QY 781 EDLNLVTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 DB 781 EDLNLVTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 QY 841 SDSSVYVVGARLPLVKWMAPESLFEGIYTIKSDVWSYGILLWEIISLGVNPPYGPVVDAN 900
 DB 841 SDSSVYVVGARLPLVKWMAPESLFEGIYTIKSDVWSYGILLWEIISLGVNPPYGPVVDAN 900
 QY 901 FYKLIOSGFKMEOPPYATEGYIFVMQSWAPDSRKRPSFPNLTSLPGCOLAEAEACIRT 960
 DB 901 FYKLIOSGFKMEOPPYATEGYIFVMQSWAPDSRKRPSFPNLTSLPGCOLAEAEACIRT 960
 QY 961 SIHLPKQAAPQORGGLRAQSPQKVHRS 992
 DB 961 SIHLPKQAAPQORGGLRAQSPQKVHRS 992

RESULT 10
 AAR81868
 ID AAR81868 standard; Protein; 1000 AA.
 XX
 AC AAR81868;
 XX
 DT 29-FEB-1996 (first entry)
 XX
 DE Flk2/flt3 tyrosine kinase receptor.
 XX
 KW Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;
 XX haematopoiesis; hypoplasia; anaemia; thrombocytopenia; stem cell.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..542
 FI /label= Extracellular_domain
 XX
 FN W09527062-A1.
 XX
 PD 12-OCT-1995.
 XX
 PF 23-MAR-1995; 95WO-US03719.
 XX
 PR 04-APR-1994; 94US-0222299.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bennett BD, Broz SD, Matthews W, Zeigler FC;
 XX
 DR WPI; 1995-358636/46.
 XX N-PSDB; AAT00801.
 DR
 XX
 PT Agonist antibody which binds to flk2-flt3 tyrosine kinase receptor
 PT - enhances proliferation of haematopoietic stem cells, in the
 XX treatment of hypoplasia, anaemia, etc.
 PS Example 1; Page 38-40; 59pp; English.
 XX
 CC Murine stem cell tyrosine kinase receptor flk2 (also called flt3)
 CC (AAR81868) is encoded DNA (AAT00801) obtd. by RT-PCR amplification of
 CC RNA isolated from mid-gestation mouse foetal livers. An flk2/flt3
 CC extracellular domain-IgG1 Fc fusion protein was used to raise

CC agonist antibodies able to bind to, and activate, flk2/flt3.
CC Such antibodies can enhance repopulation of mature blood cell
CC lineages following chemotherapy, radiotherapy, or bone marrow
CC transplantation.
XX
SQ Sequence 1000 AA;

Query Match 96.9%; Score 5102; DB 16; Length 1000;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;

QY 1 MRALAQRSDRLLLVLSWILETVNQLDLPVTKVLI SHENNGSAGRPSSYRMVRGS 60
DB 1 MRALAQRSDRLLLVLSWILETVNQLDLPVTKVLI SHENNGSAGRPSSYRMVRGS 60
QY 61 PEDLOCTPRQSEGTVEAATVEAEGSITLQVQLATPGDLSCLVKFKHSSLCQPHED 120
DB 61 PEDLOCTPRQSEGTVEAATVEAEGSITLQVQLATPGDLSCLVKFKHSSLCQPHED 120
QY 121 LQNRGIVSMALNVTTQAGEYLLHIOSEANVTYVLTNNVVRDTQLVYLRPPYRKMENQ 180
DB 121 LQNRGIVSMALNVTTQAGEYLLHIOSEANVTYVLTNNVVRDTQLVYLRPPYRKMENQ 180
QY 181 DALLCISEGVPEPTVVEWVLCSSHRESCKEKGPAVVRKEEVKVLHFLGTDIRCCARNALGR 240
DB 181 DALLCISEGVPEPTVVEWVLCSSHRESCKEKGPAVVRKEEVKVLHFLGTDIRCCARNALGR 240
QY 241 ECTKLFITDINOAPSTLPOLFLKVGPLMIRCKAIHVNHGFGLTWELEKALEGSEYFE 300
DB 241 ESTKLFITDINOAPSTLPOLFLKVGPLMIRCKAIHVNHGFGLTWELEKALEGSEYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFNATSSOEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFNATSSOEY 360
QY 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAQPCEQRLGEGYSISKPCDHKNKPGYIFY 420
DB 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAQPCEQRLGEGYSISKPCDHKNKPGYIFY 420
QY 421 AENDDAQFTKMTINIRKKQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
DB 421 AENDDAQFTKMTINIRKKQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
QY 481 EGVNWKANRKFVQWTVSSTLNMSAGKLLVKCCAYNSMGTSCTIFLNSPGFPFFPIQ 540
DB 481 EGVNWKANRKFVQWTVSSTLNMSAGKLLVKCCAYNSMGTSCTIFLNSPGFPFFPIQ 540
QY 541 DNISFYATIGLCLPFIIVLVLI CHYKKQPRYESQLQMIQVGTGLDNEYFYVDFRDY 600
DB 541 DNISFYATIGLCLPFIIVLVLI CHYKKQPRYESQLQMIQVGTGLDNEYFYVDFRDY 600
QY 601 DLKWEFPRENLEFGKVLGSGAFGRWMNATAGISKTGVSIQVAVMKLEKADSCKEALM 660
DB 601 DLKWEFPRENLEFGKVLGSGAFGRWMNATAGISKTGVSIQVAVMKLEKADSCKEALM 660
QY 661 SELKQWTHLGHNDINVLGACTLSGPVYLIFCYCCYGDLLNLYRSKREKPHRTWTFIK 720
DB 661 SELKQWTHLGHNDINVLGACTLSGPVYLIFCYCCYGDLLNLYRSKREKPHRTWTFIK 720
QY 721 EHNFSYPTTQAHNSMPSGSRVOLHPPDLQSLGFGNNGSIHSEDEIEYENQKRLAESEE 780
DB 721 EHNFSYPTTQAHNSMPSGSRVOLHPPDLQSLGFGNNGSIHSEDEIEYENQKRLAESEE 780
QY 781 EDLNLVTFEDLLCPAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
DB 781 EDLNLVTFEDLLCPAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 841 SDSSYVVRGNARLPKVMAPESLFEGLTYITKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
DB 841 SDSSYVVRGNARLPKVMAPESLFEGLTYITKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
QY 901 FYKLIOGFKMEQPFYATGEGYFVMQSCWAFDSRKRPSFNLTSFLGCQLAAEAEACIRT 960
DB 901 FYKLIOGFKMEQPFYATGEGYFVMQSCWAFDSRKRPSFNLTSFLGCQLAAEAEACIRT 960

Db 901 FYKLIOGFKMEQPFYATGEGYFVMQSCWAFDSRKRPSFNLTSFLGCQLAAEAEAMYNQ 960
QY 961 -----SIHLPKQAAPQORGLRAQSPORQVKIHRERS 992
DB 961 MGGNVPEHPSIYQNRPLSREAGS-EPPSPQAQVKIHRERS 1000

RESULT 11

AAR75961
ID AAR75961 standard; Protein; 993 AA.
XX AAR75961;
AC AAR75961;
XX 29-DEC-1995 (first entry)
DT Human STK-1.
DE STK-1; receptor PTK; protein tyrosine kinase.
KW Homo sapiens.
OS
PH Key
FT Peptide
FT Location/Qualifiers
FT 1..23
FT /label= signal
FT /note= "unique PTK receptor sequence"
FT Cleavage-site 25..26
FT Domain 35..524
FT /note= "Part of extracellular domain contg. 22 Cys residues marked on Fig. 1"
FT Modified-site 43..45
FT /label= potential N-linked glycosylation site
FT Modified-site 100..102
FT /label= see above
FT Modified-site 151..153
FT /label= see above
FT Modified-site 250..252
FT /label= see above
FT Modified-site 306..308
FT /label= see above
FT Modified-site 323..325
FT /label= see above
FT Modified-site 351..353
FT /label= see above
FT Modified-site 354..356
FT /label= see above
FT Modified-site 473..475
FT /label= see above
FT Modified-site 502..504
FT /label= see above
FT Region 542..562
FT /label= transmembrane spanning region
FT Region 708..782
FT /label= kinase insert region
FT Domain 617..622
FT /label= ATP binding domain
FT Domain 835..840
FT /label= WWAPES motifs
FT /note= "cytoplasmic domain"
FT Peptide 808..813
FT /note= "used to design PCR oligos"
FT Peptide 870..875
FT /note= "used to design PCR oligos"
XX W09519175-A.
PN
XX 20-JUL-1995.
PD
XX 06-JAN-1995; 95WO-US00176.
PE
XX 14-JAN-1994; 94US-0183211.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
PA (UYPE-) UNIV PENNSYLVANIA.

XX Civin CI, Gewirtz AM, Small D;
 XX WPI; 1995-263709/34.
 DR N-PSDB; AAQ91356.
 XX Artificial STK-1 gene and gene-specific anti-sense oligo: nucleotide
 PT used to treat neoplastic diseases and as bone marrow purging agents for
 PT treating leukemia and neoplasia
 XX Disclosure; Fig 1; 66pp; English.
 XX The STK-1 gene encodes a receptor PTK which is expressed in
 CC proliferating hematopoietic stem cells but not in quiescent stem
 CC cells. The STK-1 gene is also expressed in certain malignant cells
 CC of non-hematopoietic origin. An antisense oligo specific for STK-1
 CC is an oligo having a sequence (i) capable of forming a stable
 CC triplex with a portion of the STK-1 gene, or (ii) capable of forming
 CC a stable duplex with a portion of an mRNA transcript of the STK-1
 CC gene. Antisense oligos capable of forming a stable duplex with a
 CC portion of a STK-1 mRNA transcript are given in AAQ91536 FT and in
 CC AAQ91537 and AAQ91538. The antisense oligos of the invention are useful
 CC in the treatment of hematologic malignancies characterized by
 CC STK-1 expression. Several of the conserved domains of PTKs
 CC including the ATP binding domain and the WMAPES motifs are
 CC found in the STK-1 protein (see AAR75961 FT).
 XX Sequence 993 AA;
 SQ

Query Match 84.3%; Score 4436.5; DB 16; Length 993;
 Best Local Similarity 84.2%; Pred. No. 0;
 Matches 837; Conservative 57; Mismatches 89; Indels 11; Gaps 4;

QY 1 MRALQRSRRRLLLVLSWILETTNQLPVIKVLSHENNGSSAGKPPSYRWGRS 60
 DB 1 MPALA-RDAGTVPLLVFSAIFGTITNQLPVIKVLSHENNGSSAGKPPSYRWGRS 59

QY 61 PEDLOCTPQSGTGYEATVAVSSTTLOVATPCGLDCLWVFKHSSIGCOPHFD 120
 DB 60 PEDLGCALRPQSGTGYEAAVEVDVSATITLQVLDAPGNISCLWVFRHSSLNCOPHFD 119

QY 121 LQNRGVSMALNVTTQAGEYLLHQTQSERANTYVLTNNVTRDTQLVLRPFRKXENQ 180
 DB 120 LQNRGVSMVILKMTQAGEYLLFIOSEATNTYLTFTVIRNTLLYLRPFRKXENQ 179

QY 181 DALLCISEGVPEPTVEVLVLCSSHRESCKEGRPAVVRKEKVLHFLGTDIRCCARNALGR 240
 DB 180 DALVLCISEGVPEPTVEVLVLCSSHRESCKEGRPAVVRKEKVLHFLGTDIRCCARNALGR 239

QY 241 ECTKLEFTIDNQAPOSTLPOLFLKVGEPWIRCKAIVHNGFGITWLEDKALEEGSYFE 300
 DB 240 ECTRLFTIDNQAPOSTLPOLFLKVGEPWIRCKAIVHNGFGITWLEDKALEEGSYFE 299

QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILEKGFINATSSOEY 360
 DB 300 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILEKGFINATSSOEY 359

QY 361 EIDPYEKFCSVRPKAVPRICRTWIPQASFPCEQGLEDCYSISKFCDHKNKPGYIFV 420
 DB 360 EIDQYEEFCFSVRPKAVPRICRTWIPQASFPCEQGLEDCYSISKFCDHKNKPGYIFV 419

QY 421 AENDDAQFTKMTNIRKPKQVLNANASQSCSDCYPLPSPWTKKCSKSPNCTEIP 480
 DB 420 AENDDAQFTKMTNIRKPKQVLNANASQSCSDCYPLPSPWTKKCSKSPNCTEIP 479

QY 481 EGVNKKANRKFQWQSSSTLNNSAGKLLVKKCAVNSMTGTSCTIFLNSPGPPFFIQ 540
 DB 480 EGVNKKANRKFQWQSSSTLNNSAGKLLVKKCAVNSMTGTSCTIFLNSPGPPFFIQ 539

QY 541 DNISFYATIGCLPFIIVVLVILCHYKKQFRYESQLQMIQVGTGPLDNEYFYVDFRDEY 600
 DB 540 DNISFYATIGCLPFIIVVLVILCHYKKQFRYESQLQMIQVGTGPLDNEYFYVDFRDEY 599

QY 601 DLKWEFFPRENLEFGKVLGSGAFGRVNMATAYGISKTGVSIVAVKMLKEKADSCKEALM 660
 DB 600 DLKWEFFPRENLEFGKVLGSGAFGRVNMATAYGISKTGVSIVAVKMLKEKADSCSEREALM 659

QY 661 SELKMTLGHHDNIVNLLGACTLSGPVYLIPEYCCYGDLNLYLRSKRKFKHRTWTEIFK 720
 DB 660 SELKMTLGHHDNIVNLLGACTLSGPVYLIPEYCCYGDLNLYLRSKRKFKHRTWTEIFK 719

QY 721 EHNFSYPTFOAHSNMPGSRREVQLHPPLDOLSGPFGNSIHSEDEIEYENOKRLAESEE 780
 DB 720 EHNFSYPTFOAHSNMPGSRREVQLHPPLDOLSGPFGNSIHSEDEIEYENOKRLAESEE 777

QY 781 EDLNVLTFFEDLLCFAYQVAKGMEFFLEKSCVHRDLAARNVLTGHGVKVICDFGLARDIL 840
 DB 778 EDLNVLTFFEDLLCFAYQVAKGMEFFLEKSCVHRDLAARNVLTGHGVKVICDFGLARDIM 837

QY 841 SSSSYVVRGNARLPVKWMAPESEFEGIYTIKSDVWSYGLLWEIFSLGVNYPGIPVDAN 900
 DB 838 SSSSYVVRGNARLPVKWMAPESEFEGIYTIKSDVWSYGLLWEIFSLGVNYPGIPVDAN 897

QY 901 FYKLIQSGFMKEOPFYATEGIVPMOSWAFDSRKPSPFNLTSLFLGCCOLAEAEAC--- 957
 DB 898 FYKLIQSGFMKEOPFYATEGIVPMOSWAFDSRKPSPFNLTSLFLGCCOLAEAEAEYQN 957

QY 958 ----IRTSIHLPKQAAPOQRG-GLRAQSPQRYK 986
 DB 958 VDGRVSECPHYQNRPRPFSREMDLGLLSPOAQVE 991

RESULT 12
 AAR67816
 ID AAR67816 standard; Protein; 993 AA.
 XX AAR67816;
 DT 18-AUG-1995 (first entry)
 XX Flk2 receptor protein-tyrosine-kinase.
 XX Human Flk2; receptor protein-tyrosine-kinase; primitive
 KW hematopoietic cell; fetal liver kinase; diagnostic ligand
 KW isolation; bone marrow disease therapy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..27 /note= "signal peptide"
 FT Protein 28..993 /note= "mature protein"
 FT Domain 28..543 /note= "extracellular receptor domain"
 FT Domain 544..563 /note= "transmembrane region"
 FT Domain 564..993 /note= "intracellular catalytic domain"
 XX WO9500554-A.
 XX 05-JAN-1995.
 XX 17-JUN-1994; 94WO-US06944.
 XX 18-JUN-1993; 93US-0080244.
 PR 21-JUN-1993; 93US-0081508.
 PR 23-NOV-1993; 93US-0157490.
 XX (UYPR-) UNIV PRINCETON.
 XX Lemischka IR;
 XX WPI; 1995-052014/07.
 DR N-PSDB; AAQ81013.

XX

PT Ligand for receptor protein tyrosine kinase - useful for the
 PT stimulation of primitive haematopoietic stem cells causing
 PT proliferation and/or differentiation

XX

PS Disclosure; Fig 1b; 131pp; English.

XX

CC The sequence corresponds to a human Flk2 (fetal liver kinase)
 CC receptor protein-tyrosine-kinase, which is expressed in primitive
 CC hematopoietic cells but not in mature hematopoietic cells. The
 CC protein is useful in isolation of receptor ligands, which have
 CC applications in diagnosis of bone marrow disorders and in
 CC stimulating proliferation and/or differentiation of primitive
 CC hematopoietic stem cells.

XX

SQ Sequence 993 AA;

Query Match 84.1%; Score 4429.5; DB 16; Length 993;
 Best Local Similarity 84.1%; Pred. No. 0;
 Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MRALAQRSDRLRLLLVLSVMILETVTNQDLVPVKVLCVLIHENNGSSAGKPSYRMVRGS 60
 DB 1 MPALA-RDAGTVPLLVFSAMFGTITNQDLVPVKVLCVLIHKNNDSSVGKSSYPWSES 59
 QY 61 PEDLOCTPRQSEGTVEAATVEVAESGITLQVOLATPGDLSCLWVFKHSLGCPHF 120
 DB 60 PEDLGICALRQSSGTVEAAAVEVDVSASITLQVLDPAGNISCLWVFKHSLGCPHF 119
 QY 121 LONRGIVSMALNTVTCAGYILHIQSERANYTVLTVNVRDQLYVLRPYFRKMQ 180
 DB 120 LONRGVSMVILKMTVTCAGSYLLFIQSEATNYTILFTVSRNTLLYLRPYFRKMQ 179
 QY 181 DALLCISEGVPEPTVEVLCSSHRESCKECPAVVRKEKVLHFGTDIRCCARNALGR 240
 DB 180 DALVCISEGVPEPTVEVLCSSHRESCKECPAVVRKEKVLHFGTDIRCCARNALGR 239
 QY 241 ECTKLFTIDLNAQPOSTLPQLFKVGBPLWIRCKAIHVNHGFGLTWELEKALEEGSYFE 300
 DB 240 ECTRLFTIDLNTQPTTLPLQLFKVGBPLWIRCKAVHVNHGFGLTWELEKALEEGSYFE 299
 QY 301 MSTYSTNRTMIRILAFVSSVGRNDTGYYTSSSKHPSQSALVTILEKGFNATSSQBEY 360
 DB 300 MSTYSTNRTMIRILAFVSSVGRNDTGYYTSSSKHPSQSALVTIVGKGFNATSSBDY 359
 QY 361 EIDPYEFCFSVRKAYPRICRTWIFESQSPCORGLEDGYSISKCDHKNKPGCEYIF 420
 DB 360 EIDQYEEFCFSVRKAYPRICRTWIFGRKSPCQKGLDNGYSISKCNHRKHQGEYIF 419
 QY 421 AENDDAQFTKMTLIRKPKQVLANASQASCSGSDGYPLPSWTWKCSKSPNCTEIP 480
 DB 420 AENDDAQFTKMTLIRKPKQVLAEASQASCFSDGYPLPSWTWKCSKSPNCTEIT 479
 QY 481 EGVNWKANRVKFGQWSSSTLNMSERAGLLLVKCCAYNSMGTSCTETIFLNSPGFPPIQ 540
 DB 480 EGVNWKANRVKFGQWSSSTLNMSERAIKGLVKKCCAYNSLGTSCETILLNSPGFPPIQ 539
 QY 541 DNISFYATIGLCPLFPVILVILCHYKKQPRYESOLOMIQVGTPLDNEYFYVDFRDEY 600
 DB 540 DNISFYATIGVCLLFIVLTLILCHYKKQPRYESQLQMVQVGTSSDNEYFYVDFRDEY 599
 QY 601 DLKWEFPRENLEFGKVLGSAFGVMNATAYIGSKTGVSIQVAVKMLKEKADSCKEKALM 660
 DB 600 DLKWEFPRENLEFGKVLGSAFGVMNATAYIGSKTGVSIQVAVKMLKEKADSSERKALM 659
 QY 661 SELKQMTLGHHDHNVNLLGACTLSGPVYLIFECYCYGDLNLYRSKREKPHRTWTIFK 720
 DB 660 SELKQMTLQGSHEINVLNLLGACTLSGPVYLIFECYCYGDLNLYRSKREKPHRTWTIFK 719
 QY 721 EHNFSYPTTQAHNSNSMPGSRREVQLHPPLDLSGFGNNSHSEDEIYENQKLABEEE 780
 DB 720 EHNFSYPTTQSHNSNSMPGSRREVQIHPDSDQISGLHGNFSHSEDEIYENQKLABEEE 777

QY 761 EDLNVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
 DB 778 EDLNVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIM 837
 QY 841 SDSSVVVRGNARLPVKWMAPELSEFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 DB 838 SDSNVVVRGNARLPVKWMAPELSEFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
 QY 901 FYKLQSGFKMEQPFYATGIEYFVMSQSWAFDSRKRPSFPNLTSLFGCOLAAEEAC--- 957
 DB 898 FYKLQNGFKMDQPFYATGIEYIIMQSWAFDSRKRPSFPNLTSLFGCOLAADEEAMYQN 957
 QY 958 ----IRTSIHLPKQAPQORG-GLRAQSPQROVK 986
 DB 958 VDRVSECPHTYQNRPRFSEMDLGLLSQAQVE 991

RESULT 13

AAR67536

ID AAR67536 standard; Protein; 993 AA.

XX AAR67536;

DT 04-JUL-1995 (first entry)

XX Human flk-2.

DE Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
 KW hematopoiesis; stem cell.
 XX Homo sapiens.

XX Key

XX Peptide

XX Domain

XX Region

XX Domain

XX Location/Qualifiers

XX /label= Sig_peptide

XX /label= Extracellular_receptor_domain

XX /label= Transmembrane_region

XX /label= Intracellular_catalytic_domain

XX US5367057-A.

XX 22-NOV-1994.

XX 02-APR-1991;

XX 91US-0679666.

XX 02-APR-1991;

XX 91US-0679666.

XX 28-JUN-1991;

XX 91US-0728913.

XX 15-NOV-1991;

XX 91US-073065.

XX 24-DEC-1991;

XX 91US-0813593.

XX 26-JUN-1992;

XX 92US-0906397.

XX 12-NOV-1992;

XX 92US-0975049.

XX 19-NOV-1992;

XX 92US-0977451.

XX 30-APR-1993;

XX 93US-0055269.

XX (UYPR-) UNIV PRINCETON.

XX Lemischka IR;

XX WPI; 1995-005894/01.

XX N-PSDB; AAQ79069.

XX Murine flk-2 receptor protein tyrosine kinase - used to stimulate

XX proliferation and/or stimulation of primitive mammalian

XX haematopoietic stem cells in vitro or in vivo.

XX Disclosure; Fig. 2A-1F; 69pp; English.

XX cDNAs encoding receptor protein tyrosine-kinases, mouse fetal liver

XX kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAQ79068-70,

XX respectively, and the deduced amino acid sequences in AAR67535-37,

CC respectively.

XX Sequence 993 AA;

Query Match 84.1%; Score 4429.5; DB 16; Length 993;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MRALQSRDRLLLVLSVILETTNODLPVKVLISHENNGSSAGKPPSYRVRGS 60
DB 1 MPALA-RDAGTVPLLVLFVSGAMFTITNODLPVKVLINHKNDSSVGKSSYPWVSES 59

QY 61 PEDLOCTPRQSGTYEATVEABSGSITLQVQLATPCDLSCLWVFKHSSLCQPHFD 120
DB 60 PEDLGALPQSGTYEAAVEVDVSAITLQVLDVAFGNISCLWVFKHSSLCQPHFD 119

QY 121 LQNRGIVSMAILLNVTTQAGEYLLHIOSEBANYTVLFTVNRDQYLVLRPFRKMEQ 180
DB 120 LQNRGVVSMVILKMTQAGEYLLFTQSEATNYTILFTVSIINTLLYLRPFRKMEQ 179

QY 181 DALLCISEGVPEPTVEMVLCSSHRECKEKGPAVVRKEKVLHFLGTDIRCCARNALGR 240
DB 180 DALVCISESVPEPIVEVWLCDSQGESCKESPAVVRKEKVLHFLGTDIRCCARNELGR 239

QY 241 ECTKLFTIDLNOAQSTLPQLFLKVGEPWIRCKAIHVNHGFLGTWELEDKALEEGSYFE 300
DB 240 ECTRLFTIDLNTPTTLQFLKVGEPWIRCKAVVNHGFLGTWELENKALEEGSYFE 299

QY 301 MSTYSTNRTMIRILLAFVSSVGNDRGTCTSSSKHPSQSALVILEKGFINATSSQEEY 360
DB 300 MSTYSTNRTMIRILLAFVSSVARNDRGTCTSSSKHPSQSALVTIVGKGFINATSSSEY 359

QY 361 EIDPEKFCFVSFRKAYPRCTRWISQASFPCEQGLGDEYGISKFCOHKPKGVIFY 420
DB 360 EIDQYEFCEFSFRKAYPQIRCTWTSFPCQEGKGLNGYISKFCNHHKPGGYIFH 419

QY 421 AENDDAQFTKMTNIRKPKQVLANASASQSCSDGYPLPSWTWKCKSDKSPNCTEEIP 480
DB 420 AENDDAQFTKMTNIRKPKQVLANASASQSCSDGYPLPSWTWKCKSDKSPNCTEEIT 479

QY 481 EGVNKKANKRVFGQWSSSTLNNBAGKLLVKCCAYNSMGTSCTIFLNSPGPPPIQ 540
DB 480 EGVNKKANKRVFGQWSSSTLNNBAGKLLVKCCAYNSMGTSCTIFLNSPGPPPIQ 539

QY 541 DNISFYATIGLCPFFVWLIVLCHKYKQFVRESQLOMLOVTPGLDNEYFYVDFRDY 600
DB 540 DNISFYATIGVCLLFIWLTLLCHKYKQFVRESQLOMLOVTPGLDNEYFYVDFREY 599

QY 601 DLKWEPPRENLEFGKVLGSAFGKRVNATAYGSKTGVSIQVAVKMLKERADSCKEALM 660
DB 600 DLKWEPPRENLEFGKVLGSAFGKRVNATAYGSKTGVSIQVAVKMLKERADSSREALM 659

QY 661 SELKMMTHLGHNDINVLGACTLSGPVYLIPYCCYGDLLNLYLSRKREKPHRTWTIFK 720
DB 660 SELKMMTHLGHNDINVLGACTLSGPVYLIPYCCYGDLLNLYLSRKREKPHRTWTIFK 719

QY 721 EHNFSYPTFOAHNSMPCSRVQLHPDLSGFGNHSIHSEDETEYENOKELAESEE 780
DB 720 EHNFSYPTFOAHNSMPCSRVQLHPDLSGFGNHSIHSEDETEYENOKELAESEE 777

QY 781 EDNLVLTFFEDLLCFAYQVAKGMFLEFKSVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
DB 778 EDNLVLTFFEDLLCFAYQVAKGMFLEFKSVHRDLAARNVLVTHGKVVKICDFGLARDIM 837

QY 841 SDSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWIFSLGVNYPGIPVDAN 900
DB 838 SDSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWIFSLGVNYPGIPVDAN 897

QY 901 FYKLIQSGFQWQPFYATEGIYFMQSCWAFDSKRSFNLTSFLGCQLAABEAC--- 957
DB 898 FYKLIQSGFQWQPFYATEGIYFMQSCWAFDSKRSFNLTSFLGCQLAABEANYQN 957

QY 958 ----IRTSIHLPKQAAFPQQR-GLRAQSPQORVK 986

DB 958 VDRVSECPHTYQNRPPFPFSREMDLGLLSPQAQVE 991

RESULT 14

AAR97419

ID AAR97419 standard; Protein; 993 AA.

XX AAR97419;

XX 11-DEC-1996 (first entry)

XX Murine foetal liver kinase 2.

XX Murine; foetal liver kinase 2; flk-2; protein tyrosine kinase;

XX monoclonal; antibody; extracellular domain; receptor assay;

XX haematopoietic stem cell; ligand; stimulation; proliferation;

XX differentiation; treatment; anaemia; bone marrow damage;

XX cancer chemotherapy; radiation.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1..27

XX Peptide /label= sig_peptide

XX Peptide 28..993

XX Domain /label= mat_peptide

XX Domain 28..544

XX Domain /label= extracellular_domain

XX Domain 545..564

XX Domain /label= transmembrane_domain

XX Domain 565..993

XX Domain /label= intracellular_domain

XX US5548065-A.

XX 20-AUG-1996.

XX 02-APR-1991; 91US-0679666.

XX 19-NOV-1992; 92US-0977451.

XX 02-APR-1991; 91US-0679666.

XX 28-JUN-1991; 91US-0728913.

XX 15-NOV-1991; 91US-0793065.

XX 24-DEC-1991; 91US-0813593.

XX 26-JUN-1992; 92US-0906397.

XX 12-NOV-1992; 92US-0975049.

XX 30-APR-1993; 93US-0055269.

XX 31-OCT-1994; 94US-0252517.

XX (UYPR-) UNIV PRINCETON.

XX Lemischka IR;

XX WPI; 1996-392678/39.

XX N-PSDB; AAT38734.

XX Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,

XX for isolating haematopoietic stem cells expressing receptor and for

XX obtaining ligands

XX Claim 1; Columns 39-48; 50pp; English.

XX The present sequence is murine foetal liver kinase 2 (flk-2),

XX a protein tyrosine kinase. Isolated antibodies, pref. monoclonal,

XX raised against the extracellular portion of flk-2 can be used to

XX assay for flk receptors on the surface of primitive haematopoietic

XX stem cells, and to isolate positive cells. The antibodies can also

XX be used as, or to obtain ligands, which stimulate the proliferation

XX and/or differentiation of stem cells. The ligands can be used, e.g.

XX for treating anaemia, or bone marrow damage resulting from cancer

XX chemotherapy, or radiation.

SQ Sequence 993 AA;		Query Match Best Local Similarity 84.1%; Score 4429.5; DB 17; Length 993; Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;
QY 1 MRALAQSRDRRLLLLVLSVMILETVNQDLPVTKVLSHENNGSSAGKPSRYRMVGRS 60		XX AAW19873 standard; Protein; 993 AA.
DB 1 MPALA-RDAGTVPLLVVFSAMIFGTTNQDLPVTKVLIHNKNDSSVGKSSYPVMVSES 59		XX AAW19873;
QY 61 PEDLOCTPROSECTVYEAATVEVAESGSTITLOVLATPGDLSCLWVFKUSSLCQPHFD 120		XX AC AAW19873;
DB 60 PEDLGALRPSQSGTYEAAVEVDVSATITLQVLDPAGNISCLMWFKHSSLNCPHFD 119		XX DT 19-AUG-1997 (first entry)
QY 121 LQNRGVSMALNVETQAGEYLLHHTQSERANYTLFTVNVROTQLYVLRPYPFRKWMNQ 180		XX DE Human flk-2 receptor.
DB 120 LQNRGVSMVILKWTQAGEYLLFTQSEATNTIIFTVSRNLTLYLRPYPFRKWMNQ 179		XX KW Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
QY 181 DALLCISEGVPEPTVEWVLCSSHRESCKEGPAVVRKEEKVLHFLFTDIRCCARNALGR 240		XX KW PTK; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
DB 180 DALVLCISESVPEPIVEWVLCDSQGESCKEESPAVVRKEEKVLHFLFTDIRCCARNELGR 239		XX KW haematopoietic hierarchy; extracellular domain; soluble form; ligand;
QY 241 ECTKLTIDLNQAPSTLPQLFLKVGEPWIRCKAHVNHGFLGTWELEKALBEGSYFE 300		XX KW proliferation; differentiation; mammalian; haematopoietic stem cell;
DB 240 ECTRLFTIDLNQPTLPQLFLKVGEPWIRCKAHVNHGFLGTWELEKALEEGNYFE 299		XX KW macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse.
QY 301 MGTYSTNRTMIRILLAFVSSVGRNDGYTCSSSKHPSQSALVTILEKGFINATSSOEY 360		XX OS Homo sapiens.
DB 300 MGTYSTNRTMIRILLAFVSSVGRNDGYTCSSSKHPSQSALVTIVKGFINATNSSEDY 359		XX FT Key 1..27 Location/Qualifiers
QY 361 EIDPYEKFCSVRFKAYPRIRCTWIFSQSFPCQEGLEDGYSISKPCDHKNKPGEIFY 420		XX FT Peptide /note= "Signal peptide"
DB 360 EIDPYEFCFSVRFKAYPQIRCTWTSRKSFPCEQGLDNGYISKFCNHKHQPGEIFH 419		XX FT Protein 28..993
QY 421 AENDDAQFTMTFLNTRKQPVLNANASQASCSGYPPLPSWTWKCDKSKPNCTEEIP 480		XX FT /note= "Mature flk-2"
DB 420 AENDDAQFTMTFLNTRKQPVLNANASQASCSGYPPLPSWTWKCDKSKPNCTEEIT 479		XX US US621090-A.
QY 481 EGVNKKANKRVFGQWSSSTLNMSAGKLLVKKCAVNSMGTSCETIFLNSPGPPFFIQ 540		XX PN 15-APR-1997.
DB 480 EGVNKKANKRVFGQWSSSTLNMSAIGFLVKCAVNSLGTSCETIFLNSPGPPFFIQ 539		XX PD 02-APR-1991; 91US-0679666.
QY 541 DNISFYATIGLCPFIIVLIVLICHYKKQFYESQLQMTQVTPLDNEYFYVDPRDYEY 600		XX PR 26-JUN-1992; 92US-0906397.
DB 540 DNISFYATIGVCLLFIVLTLICHYKKQFYESQLQMTQVTPLDNEYFYVDPRDYEY 599		XX PR 02-APR-1991; 91US-0679666.
QY 601 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISTGTGVSIOQAVKMLKEKADSCKEALM 660		XX PR 28-JUN-1991; 91US-0728913.
DB 600 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISTGTGVSIOQAVKMLKEKADSSREALM 659		XX PR 15-NOV-1991; 91US-0793065.
QY 661 SELKMTHLGHNDINVLGACTLSPGVYLIPEYCCYGDLLNLYRSKREKFEHTWTEIFK 720		XX PR 24-DEC-1991; 91US-0813593.
DB 660 SELKMTQLGSHENINVLGACTLSPGVYLIPEYCCYGDLLNLYRSKREKFEHTWTEIFK 719		XX (UYPR-) UNIV PRINCETON.
QY 721 EHNFSYPTFOAHNSMPSGSRVQLHPDQLDLSGFNGNSIHSEDETEYENQKRLAESEE 780		XX PI Lemischka IR;
DB 720 EHNFSYPTFOAHNSMPSGSRVQLHPDQLDLSGFNGNSIHSEDETEYENQKRLAESEE 777		XX DR WPI; 1997-235228/21.
QY 781 EDNLVLTFDLLCFAYQVAKGMFELBFKSCVHRDLAARNVLTHTGKVKVTCDFGLARDIL 840		XX DR N-PSDB; AAT72117.
DB 778 EDNLVLTFDLLCFAYQVAKGMFELBFKSCVHRDLAARNVLTHTGKVKVTCDFGLARDIM 837		XX XX Protein containing the extracellular domain of human flk-2 - used for identification of primitive haematopoietic cell proliferation and differentiation stimulatory ligands, e.g. for treating anaemia
QY 841 SDSSVYVRGNARLPVKWMAPESEFEGITYTKSDVNSGILLIWFISLVNYPYFGIPVDAN 900		XX PS Claim 1; Fig 1B; 55pp; English.
DB 838 SDSSVYVRGNARLPVKWMAPESEFEGITYTKSDVNSGILLIWFISLVNYPYFGIPVDAN 897		XX CC This sequence represents human fetal liver kinase 2 (flk2). flk-2 is a receptor protein tyrosine kinase (ptk) and is important in transducing putative self-renewal signals from the environment. flk-2 is expressed in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow, and it is thought that flk-2 is expressed in the entire primitive portion of the haematopoietic hierarchy. The invention concerns a recombinant nucleic acid, preferably mRNA, which encodes a protein containing only the extracellular domain of human flk-2 and lacking the flk-2 intracellular catalytic domain. The resultant protein represents a soluble form of flk-2 which is used to isolate specific ligands for flk-2. These ligands can be used to stimulate proliferation and/or differentiation of mammalian haematopoietic stem cells, in vivo or in vitro, e.g. for treatment of macrocytic or aplastic anaemia or bone marrow damage caused by cancer treatment or radiation.
QY 901 FYKLIOGFKMEOPFYATEGIYVWMSQWAFDGRKPSFNNLTSLFLGCOLAEAEAC-- 957		XX SQ Sequence 993 AA;
DB 898 FYKLIONGFKMDQPFYATEIYIIMOSQWAFDGRKPSFNNLTSLFLGCOLAEAEAMQN 957		XX Query Match 84.1%; Score 4429.5; DB 18; Length 993;
QY 958 ----IRTSIHLPKQAAPQQRG-GLRAQSPQORQVK 986		XX Best Local Similarity 84.1%; Pred. No. 0;
DB 958 VDRGVSECPHTYQNRPPFSRMDLGLLSPOAQVE 991		XX Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MRALAQSRDRRLLLLVLSVMILETVNQDLPVTKVLSHENNGSSAGKPSRYRMVGRS 60

Db 1 MPALA-RDAGTVLLVVFSAMIFGTTNQDLPVICKVLINHKNDSSVGKSSSYPNVSES 59
Qy 61 PEDLOCTPRQSGTVEAATVEAASGSITLOVQIATPGDLSCLWVFKHSSIGCOPHFD 120
Db 60 PEDLGCALRPQSGTVEAASGVDSASITLQVLDAPGNISCLWVFKHSSILNCOPHFD 119
Qy 121 LQNRGIVSMALNAVTOAGEYLLHQSERANYTVLTVNVRDTQLYVLRRPYFRKWNQ 180
Db 120 LQNRGVVSMILKOTETQAGEYLLFQSEATNTIILFTVSRNTLLYTLRRPYFRKWNQ 179
Qy 181 DALLCISEGVPEPTVEWVLCSSHRECKEEGPAVVRKEEKVLHELFGTDIRCARNALGR 240
Db 180 DALVCISESVPEPIVEWVLCDSGESCKEESPAVVKKEKVLHELFGTDIRCARNELGR 239
Qy 241 ECTKLTIDLNQAPQSTLPOLFLKVGEPWIRCKALHVNHGFLGTWELEDKALEBGSYFE 300
Db 240 ECTRLFTIDLNQTPOTTLPOLFLKVGEPWIRCKAVHNVHGFGLTWELENKALEBGSYFE 299
Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDGYTTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
Db 300 MSTYSTNRTMIRILFAFVSSVARNDGYTTCSSSKHPSQSALVTIIVKGFINATNSEDI 359
Qy 361 EIDPYEKFCSVRFKAYPRIRCTWIFQASFPCEQRGLEDGYISKFCDHKNKPGYIFY 420
Db 360 EIDQYBEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLONGYISKFCNHKHQPGYIFY 419
Qy 421 AENDDAQFTMFTLNIRKPKQVILANASQASCSGYPPLPSWTWKKCDKSPNCTEIP 480
Db 420 AENDDAQFTMFTLNIRKPKQVILANASQASCSGYPPLPSWTWKKCDKSPNCTEIT 479
Qy 481 EGVNKKANKKVFQGVSSSTLANSAGKLVKCCAYNSMGTSCETIPLNSPGPFFIQ 540
Db 480 EGVNKKANKKVFQGVSSSTLANSAGKLVKCCAYNSMGTSCETIPLNSPGPFFIQ 539
Qy 541 DNISFYATIGLCIPFIVLILVILCHYKQFRYESQLOMIQVTPGLDNEYFYVDFFRDY 600
Db 540 DNISFYATIGLCIPFIVLILVILCHYKQFRYESQLOMIQVTPGLDNEYFYVDFFREY 599
Qy 601 DLKWEPPRENLEFGKVLGSAFQVFNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
Db 600 DLKWEPPRENLEFGKVLGSAFQVFNATAYGISTGVSIQVAVKMLKEKADSSEREALM 659
Qy 661 SELKMTLGHNDNIYNLLGACTLSGPVYLIPEYCCYGDLLNLYRSKREKFRHTWTEIPK 720
Db 660 SELKMTLGHNDNIYNLLGACTLSGPVYLIPEYCCYGDLLNLYRSKREKFRHTWTEIFK 719
Qy 721 EHNFSYPTFQAHSNSMPSGSRVQLHPPLDQLSGFNGNSIHSEDEIYEYENQKRLAE 780
Db 720 EHNFSYPTFQAHSNSMPSGSRVQLHPPLDQLSGFNGNSIHSEDEIYEYENQKRLAE 777
Qy 781 EDNLVITFEDLLCFAYQVAKGMBFLFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIL 840
Db 778 EDNLVITFEDLLCFAYQVAKGMBFLFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIM 837
Qy 841 SDSYVVRGNARLPVKWMAPESEPIGTYITKSDVMSYGILLWEIFSLGVNPPYPIVDAN 900
Db 838 SDSYVVRGNARLPVKWMAPESEPIGTYITKSDVMSYGILLWEIFSLGVNPPYPIVDAN 897
Qy 901 FYKLIQSGFKWEPFFVATEGIYFVMSQWAFDSRKRPSFFNLTSFLGCQLAEEAEAC--- 957
Db 898 FYKLIQSGFKWEPFFVATEGIYFVMSQWAFDSRKRPSFFNLTSFLGCQLAEEAEAC--- 957
Qy 958 ----IRTSIHLPKOAPQQRG-GLRAQSPORQVK 986
Db 958 VDKRVSECPHTYQNRPRPFSREMDLGLLSPQAQVE 991

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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:59:30 ; Search time 40.9793 Seconds
(without alignments)
2400.704 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQSRDRLLLVLSV.....RGGLRAQSPQVQVIHRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pap.*
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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5264	100.0	992	10	US-09-919-408-2
2	5264	100.0	992	10	US-09-872-136-2
3	4429.5	84.1	993	10	US-09-919-408-4
4	4429.5	84.1	993	10	US-09-872-136-4
5	1223	23.2	975	9	US-10-192-867-2
6	1221.5	23.2	972	10	US-09-944-807-10
7	1196	22.7	976	9	US-10-099-895-32
8	1196	22.7	976	9	US-10-192-867-4
9	1152.5	21.9	1088	9	US-09-961-403-4
10	1152.5	21.9	1089	10	US-09-769-987-2
11	1152.5	21.9	1089	10	US-09-919-497-90
12	1152.5	21.9	1089	10	US-09-866-510-2
13	1150.5	21.8	1089	9	US-09-955-363-36
14	1149.5	21.8	1089	10	US-09-866-510-10
15	1148.5	21.8	1089	10	US-09-866-510-4
16	1147.5	21.8	1089	10	US-09-866-510-8
17	1146.5	21.8	1089	10	US-09-866-510-6
18	1078	20.5	1090	10	US-09-866-510-14
19	1078	20.5	1106	9	US-09-955-363-2

20	1078	20.5	1106	10	US-09-866-510-22	Sequence 22, Appl
21	1074	20.4	1106	10	US-09-866-510-16	Sequence 16, Appl
22	1073	20.4	1106	10	US-09-866-510-20	Sequence 20, Appl
23	1072	20.4	1106	10	US-09-866-510-18	Sequence 18, Appl
24	998.5	19.0	1338	9	US-10-059-585-44	Sequence 44, Appl
25	961.5	18.3	1356	9	US-10-022-939-2	Sequence 2, Appl
26	961.5	18.3	1356	9	US-10-100-405A-2	Sequence 2, Appl
27	960.5	18.2	1356	9	US-09-969-037-7	Sequence 7, Appl
28	954.5	18.1	1298	10	US-09-982-610-33	Sequence 33, Appl
29	954.5	18.1	1363	9	US-09-375-248-2	Sequence 2, Appl
30	952.5	18.1	1368	9	US-10-105-901-34	Sequence 34, Appl
31	952	18.1	1363	9	US-09-375-248-19	Sequence 19, Appl
32	943.5	17.9	1362	9	US-10-105-901-33	Sequence 33, Appl
33	941	17.9	386	9	US-09-939-833-6	Sequence 6, Appl
34	941	17.9	386	10	US-09-939-754-6	Sequence 6, Appl
35	941	17.9	386	10	US-09-939-832-6	Sequence 2, Appl
36	937.5	17.8	1367	10	US-09-766-678-2	Sequence 2, Appl
37	936.5	17.8	1363	9	US-10-105-901-32	Sequence 32, Appl
38	926.5	17.6	1367	10	US-09-919-408-6	Sequence 6, Appl
39	926.5	17.6	1367	10	US-09-872-136-6	Sequence 6, Appl
40	862	16.4	367	9	US-09-939-833-9	Sequence 9, Appl
41	862	16.4	367	10	US-09-939-754-9	Sequence 9, Appl
42	862	16.4	367	10	US-09-939-832-9	Sequence 9, Appl
43	856	16.3	367	9	US-09-939-833-12	Sequence 12, Appl
44	856	16.3	367	10	US-09-939-754-12	Sequence 12, Appl
45	856	16.3	367	10	US-09-939-832-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-919-408-2
; Sequence 2, Application US/09919408
; Patent No. US20020072077A1

GENERAL INFORMATION:

APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL RECEPTORS AND THEIR LIGANDS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated

STREET: 180 Varick Street

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/919,408

APPLICATION NUMBER: US 07/906,397

FILING DATE: 31-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,451

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/906,397

FILING DATE: 26-JUN-1992

APPLICATION NUMBER: US PCT/US92/05401

FILING DATE: 26-JUN-1992

APPLICATION NUMBER: TW 81102961

FILING DATE: 15-APR-1992

APPLICATION NUMBER: US PCT/US92/02750

FILING DATE: 02-APR-1992

APPLICATION NUMBER: US 07/813,593

FILING DATE: 24-DEC-1991

APPLICATION NUMBER: US 07/793,065

FILING DATE: 15-NOV-1991

APPLICATION NUMBER: US 07/728,913

FILING DATE: 28-JUN-1991

APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 5264; DB 10; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRSDRLLLVLSVMILETVNODLPVTKVLISHENNGSSAGKPSRYMVRGS 60
DB 1 MRALAQRSDRLLLVLSVMILETVNODLPVTKVLISHENNGSSAGKPSRYMVRGS 60
QY 61 PEDLOCTPRROSEGVYEAATVEAEGSITLQVLATPGDLCLVWFKHSLGCGPHD 120
DB 61 PEDLOCTPRROSEGVYEAATVEAEGSITLQVLATPGDLCLVWFKHSLGCGPHD 120
QY 121 LQNRGIVSMALNTVETOAGEYLLHIQSERANYTVLTVNVRDQLYVLRPYPFRKMEQ 180
DB 121 LQNRGIVSMALNTVETOAGEYLLHIQSERANYTVLTVNVRDQLYVLRPYPFRKMEQ 180
QY 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
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DB 241 ECTKLFTDLNQAQOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
QY 361 EIDPYEKFCSVRKAYPRIRCTWIFSOASPCQORGLDGYISIKFCDHKNKPGYEYFY 420
DB 361 EIDPYEKFCSVRKAYPRIRCTWIFSOASPCQORGLDGYISIKFCDHKNKPGYEYFY 420
QY 421 AENDDAQFTKMTNIRKKPOVLNANASQASCSDDGYPLSPWTKKCDKSPNCTEIP 480
DB 421 AENDDAQFTKMTNIRKKPOVLNANASQASCSDDGYPLSPWTKKCDKSPNCTEIP 480
QY 481 EGVWNNKANRVKFGOWSSSTLNSEAGKGLLVKCCAYNSMGTSCTETFLNSPGPPFIQ 540
DB 481 EGVWNNKANRVKFGOWSSSTLNSEAGKGLLVKCCAYNSMGTSCTETFLNSPGPPFIQ 540
QY 541 DNISFYATIGLCLPIVVLVILICHYKQFRYESQLQMIQVTPGLDNEYFYVDPFRDVEY 600
DB 541 DNISFYATIGLCLPIVVLVILICHYKQFRYESQLQMIQVTPGLDNEYFYVDPFRDVEY 600
QY 601 DLKWEFFRENLEFGVLGSGAFGRVWNNATAGISKTGYSIQAVKMLKEKADSCKEALM 660
DB 601 DLKWEFFRENLEFGVLGSGAFGRVWNNATAGISKTGYSIQAVKMLKEKADSCKEALM 660
QY 661 SELKMTHLGHHDNIVLLGACTLSGPPVLIPEYCCYGBDLNLYRSKREKFRHTWTWEIFK 720
DB 661 SELKMTHLGHHDNIVLLGACTLSGPPVLIPEYCCYGBDLNLYRSKREKFRHTWTWEIFK 720
QY 721 EHNFFSYPTFOAHNSNMPGSRVQLHPDQLSGFNNGSIHSEDEIYEYENQRLAESEE 780
DB 721 EHNFFSYPTFOAHNSNMPGSRVQLHPDQLSGFNNGSIHSEDEIYEYENQRLAESEE 780

QY 781 EDLNVLPEDLLCFAYOVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
DB 781 EDLNVLPEDLLCFAYOVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
QY 841 SDSSVYVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIPSLGVNYPGIPVDAN 900
DB 841 SDSSVYVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIPSLGVNYPGIPVDAN 900
QY 901 FYKLIOGFKMEOPFYATEGYIFVWQSCWAFDSRRKPSFPNLTSLGCOLAEAEACIRT 960
DB 901 FYKLIOGFKMEOPFYATEGYIFVWQSCWAFDSRRKPSFPNLTSLGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPQORGLRAQSPQORQVQKIHRS 992
DB 961 SIHLPKQAAPQORGLRAQSPQORQVQKIHRS 992

RESULT 2
US-09-872-136-2
Sequence 2, Application US/09872136
Patent No. US20020119545A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/208,786
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/021,324
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-872-136-2

Query Match 100.0%; Score 5264; DB 10; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRSDRRLLLVLSWILVTNQLDLPVTKCVLIHSHENNGSSAGKPSYRMVRGS 60
DB 1 MRALAQRSDRRLLLVLSWILVTNQLDLPVTKCVLIHSHENNGSSAGKPSYRMVRGS 60

QY 61 PEDLOCTPRQSEGTVEAATVEAEGSSITLQVLATPGDLSCLVWPKHSLGCGPHFD 120
DB 61 PEDLOCTPRQSEGTVEAATVEAEGSSITLQVLATPGDLSCLVWPKHSLGCGPHFD 120

QY 121 LQNRGIVSMALINVTQAGEYLLHIOSEANVTYVLTFTVNRDQLYVLRPYPFKMENQ 180
DB 121 LQNRGIVSMALINVTQAGEYLLHIOSEANVTYVLTFTVNRDQLYVLRPYPFKMENQ 180

QY 181 DALLCISEGVPEPTVENVLCSHRESCKEKGPAVVRKEEVLHFLGTDIRCCARNALGR 240
DB 181 DALLCISEGVPEPTVENVLCSHRESCKEKGPAVVRKEEVLHFLGTDIRCCARNALGR 240

QY 241 ECTKLFITDINOAPSTLPOLFLVKGPEPLATCKAIHVNHGFGLTWELEDKALEEGSYFE 300
DB 241 ECTKLFITDINOAPSTLPOLFLVKGPEPLATCKAIHVNHGFGLTWELEDKALEEGSYFE 300

QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSKSPQSALVTILEKGFINATSSOBEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSKSPQSALVTILEKGFINATSSOBEY 360

QY 361 EIDPYEKFCFSVPKAYPRIRCTWIFSOAGPCCQORLEDGYSISKFDHKNKPGYIFY 420
DB 361 EIDPYEKFCFSVPKAYPRIRCTWIFSOAGPCCQORLEDGYSISKFDHKNKPGYIFY 420

QY 421 AENDDAQTKMTFNTIRKPKQVLANASQASCSDDGYPSPWTWKCKSDKSPNCTEIP 480
DB 421 AENDDAQTKMTFNTIRKPKQVLANASQASCSDDGYPSPWTWKCKSDKSPNCTEIP 480

QY 481 EGVNWKANRKFVQOWSSSTLNNSEAGKLLVKCCAYNSMGTSCTIFLNSPGPFPIQ 540
DB 481 EGVNWKANRKFVQOWSSSTLNNSEAGKLLVKCCAYNSMGTSCTIFLNSPGPFPIQ 540

QY 541 DNISFYATIGLCLPFIIVLVILICHKYKQFRIESQLQMIQVTPGLDNEYFYVDFRDY 600
DB 541 DNISFYATIGLCLPFIIVLVILICHKYKQFRIESQLQMIQVTPGLDNEYFYVDFRDY 600

QY 601 DLKWEPPRENLEFGKVLGSAFGHVMNATYGISKTGVSQVAVKMLKEKADSCEKALM 660
DB 601 DLKWEPPRENLEFGKVLGSAFGHVMNATYGISKTGVSQVAVKMLKEKADSCEKALM 660

QY 661 SELKMTLGHNDINVLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK 720
DB 661 SELKMTLGHNDINVLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK 720

QY 721 EHNFSYPTFOAHNSMPSGSRVQLHPPLDQLSGFNGNSIHSDEIEYENQKRLABEEE 780
DB 721 EHNFSYPTFOAHNSMPSGSRVQLHPPLDQLSGFNGNSIHSDEIEYENQKRLABEEE 780

QY 781 EDNLVLTFFELLCFAYQAVKMEFLFKSCVHRDLARNVLVTHGKVKICDQGLARDIL 840
DB 781 EDNLVLTFFELLCFAYQAVKMEFLFKSCVHRDLARNVLVTHGKVKICDQGLARDIL 840

QY 841 SDSSYVVRGNARLPVKWAPESLPEGIYTTKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
DB 841 SDSSYVVRGNARLPVKWAPESLPEGIYTTKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900

QY 901 FYKLIOSGFKMEQPEYATGEGYFVWQSCWAFDSRPPSPNLTSLFGCOLAEACIET 960
DB 901 FYKLIOSGFKMEQPEYATGEGYFVWQSCWAFDSRPPSPNLTSLFGCOLAEACIET 960

QY 961 SIHLPKQAAPQORGGLRAQSPOROVKIHRS 992
DB 961 SIHLPKQAAPQORGGLRAQSPOROVKIHRS 992

RESULT 3
US-09-919-408-4
Sequence 4, Application US/09919408
Patent No. US2002072077A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/919,408
FILING DATE: 31-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,451
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-919-408-4

Query Match 84.1%; Score 4429.5; DB 10; Length 993;
Best Local Similarity 84.1%; Pred. No. 2.3e-297;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;


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QY 1 MRALAQRDRRLLLVLLVLSVMIETVTNQDLPVKCVLISHENNGSAGKPSYRMVGRS 60
Db 1 MPALA-RDAGTVPLLVVFSAMIFGTITNQDLPVKCVLINHKNDSSVGKSSYPMVSES 59
QY 61 PEDLOCTPRQSGTGYVEAATVEAASGSLTQVLATPGDLSCLVKFKHSSLCQPHFD 120
Db 60 PEDLGALRPSQSGTGYVEAAAVEVDVSASITLQVLDPAGNISCLVWFKHSSLCQPHFD 119
QY 121 LQNRGIVSMALNVETQAGEYLLHQTOSERANYTVLFTVNVVDTQLYVLRPRFKMENQ 180
Db 120 LQNRGVVSMVLLKMTETQAGEYLLFTQSEATNYTLFTVIRNLTLLYLRPRFKMENQ 179
QY 181 DALLCISEGPEPTVEVLVSSHRESCKEGPAVVRKEEVHLHELFGTDIRCCARNALGR 240
Db 180 DALVCLISESPEPIVEVLVCDSSGCKESPAVVKKEEVHLHELFGTDIRCCARNELGR 239
QY 241 ECTKLTFTIDUNQAPQSTLPOLFUKVEBPLWIRCKAIHVNHGFGLTWELEKALBEGSYFE 300
Db 240 ECTRLFTIDLNOTPOTTLPOLFLKVGEPWIRCKAVHVNHGFGLTWELENKALEEGNYFE 299
QY 301 MSTYSTNRTMIRILLAPVSSVGRNDGTGYTTCSSSKHPSQSALVTILEKGFINATSSOEY 360
Db 300 MSTYSTNRTMIRILLAPVSSVGRNDGTGYTTCSSSKHPSQSALVTIVGKGFINATNSSEDY 359
QY 361 EIDPYKFCFSVRFPKAYPRIRCTWIFSQASFPCEQRGLDEGYISIKFCDHKNKPGGEYIFY 420
Db 360 EIDQYEFCEFSVRFPKAYPOIRCTWTFSRKFPCEQKGLDGYISIKFCNHKHQGPGEYIFH 419
QY 421 AENDDAQFTKMTFLNIRKPKQVLANASASQASCSGDPYPLPSWTWKCSKSPNCTEIP 480
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QY 481 EGVNKKANRKFVQWSSVSTLNNSSEAGLLVKCCAYNSGTSCTIFLNSGCPFPFIQ 540
Db 480 EGVNKKANRKFVQWSSVSTLNNSSEAGLLVKCCAYNSGTSCTIFLNSGCPFPFIQ 539
QY 541 DNISFYATIGLCPLFFIVLLVILCHYKKGQFYESQLQMTQVGTPLDNEYFYVDPRDYEY 600
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QY 601 DLKWEPPRENLEFGKVLGSGAFQVMAATAYGKGTGVSQVAVMKLKEKADSCKEKALM 660
Db 600 DLKWEPPRENLEFGKVLGSGAFQVMAATAYGKGTGVSQVAVMKLKEKADSSEREALM 659
QY 661 SELKMTLHGHBNIVNLLGACTLSGPVYLIFECYCCYGDLLNLYRSKREKPHRTWTIEFK 720
Db 660 SELKMTLHGHBNIVNLLGACTLSGPVYLIFECYCCYGDLLNLYRSKREKPHRTWTIEFK 719
QY 721 EHNFSYPTTQAHNSNMPGSRVQLHPPLDQSLGFGNNGSIHSEDEIEYENQKRLABEEE 780
Db 720 EHNFSYPTTQAHNSNMPGSRVQLHPPLDQSLGFGNNGSIHSEDEIEYENQKRLABEEE 777
QY 781 EDNLVLTFFDLCLCFAYQVAKGMEFLPKSCVHRDLAARNVLTHGKVVKICDFGLARDIL 840
Db 778 EDNLVLTFFDLCLCFAYQVAKGMEFLPKSCVHRDLAARNVLTHGKVVKICDFGLARDIM 837
QY 841 SDSSYVVRGNARLPVKWAPESLPEGITTKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
Db 838 SDSSYVVRGNARLPVKWAPESLPEGITTKSDVWSYGILLWEIFSLGVNYPGIPVDAN 897
QY 901 FYKLIOGFKMEQPFYATGFIYFMQSCWAFDSKRSFPNLTSLFLGCOLAAEAEAC--- 957
Db 898 FYKLIOGFKMEQPFYATGFIYFMQSCWAFDSKRSFPNLTSLFLGCOLAAEAEAMYNQ 957
QY 958 ----IRTSIHLPKQAAPQQRG-GLRAQSPQRQVK 986
Db 958 VQGRVSECPHTYQNRPRPFSREMDLGLLSPOAQVE 991
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RESULT 4

US-09-872-136-4

; Sequence 4, Application US/09872136

; Patent No. US20020119545A1

```
GENERAL INFORMATION:
APPLICANT: Lemischka, Ibor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/208,786
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/021,324
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
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APPLICATION NUMBER: US 07/813,593
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APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-872-136-4
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Query Match 84.1%; Score 4429.5; DB 10; Length 993;

Best Local Similarity 84.1%; Pred. No. 2.3e-257;

Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

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QY 61 PEDLOCTPRQSGTGYVEAATVEAASGSLTQVLATPGDLSCLVKFKHSSLCQPHFD 120

Db 60 PEDLGALRPSQSGTGYVEAAAVEVDVSASITLQVLDPAGNISCLVWFKHSSLCQPHFD 119

QY 121 LQNRGIVSMALNVETQAGEYLLHQTOSERANYTVLFTVNVVDTQLYVLRPRFKMENQ 180

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Db 120 LQNRGVSVMLKMTQAGSYLLFIOSEATNYTLFTVSRNTLLYLRPPYRPMENQ 179
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Qy 241 ECTKLFTIDLNAQSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEBGSYFE 300
Db 240 ECTRLFTIDLNOTFTTLPQLFKVGEPLWIRCKAVHVNHGFGLTWELENKALEBGNFE 299
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Db 300 MSTYSTWTRMIRILAFVSSVARNDTGYYTCTSSKHPQSALVITVVGKFINATSSSEY 359
Qy 361 EIDYEFKFCFVRKAYPRIRCTWIFSOASPCPEORGELEDGYSISKFCDHKNKPEYIFY 420
Db 360 EIDYEFKFCFVRKAYPQIRCTWTFRSKSPCEOKGJNDGYSISKFCNKHQKPEYIFH 419
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Qy 481 EGVWVKANRKFVKGWSSSTLNMSKAGLLVKKCAVNSMGTSCTETFLNSPGPPFIQ 540
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Db 600 DLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGYSIQAVRMKLEKADSKSREALM 659
Qy 661 SELKMTHLGHHDNIVNLLGACTLGGPVLYIFCYCYGDLNVLTHGKWKICDFGLARDIL 840
Db 660 SELKMTQLGSHENIVNLLGACTLGGPVLYIFCYCYGDLNVLTHGKWKICDFGLARDIM 837
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Db 720 EHNFSYPTFOHNSMPPGREGVOLHPLDQSLGFGNCSHSEDEIEYENOKRLAESEE 777
Qy 781 EDNLVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIL 840
Db 778 EDNLVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIM 837
Qy 841 SDSYVVRGNARLPVKWMAPESLFEGITVTKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 838 SDSYVVRGNARLPVKWMAPESLFEGITVTKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
Qy 901 FYKLIOGFKMEOPYATEGYFMQSCWAFDSRKPSPNLTSLFGCOLABEAC--- 957
Db 898 FYKLIOGFKMDQPYATEEYIIMQSCWAFDSRKPSPNLTSLFGCOLADAEAEYQY 957
Qy 958 ----IRTSIHLPKQAAPOORG-GLRAQSPQROVK 986
Db 958 VDRGVSECPHTYQNRPPSRREMDGLLSPQAQVE 991
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RESULT 5

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US-10-192-867-2
; Sequence 2, Application US/10192867
; Publication No. US20030084466A1
; GENERAL INFORMATION:
; APPLICANT: BLUME-JENSEN, Peter
; APPLICANT: HUNTER, Tony
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
; FILE REFERENCE: SALKINS 002C1
; CURRENT APPLICATION NUMBER: US/10/192,867
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/175,625
; 2000-01-11
```

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; PRIOR APPLICATION NUMBER: PCT/US01/00573
; 2001-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 975
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-10-192-867-2
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Query Match 23.2%; Score 1223; DB 9; Length 975;

Best Local Similarity 32.1%; Pred. No. 4.3e-76; Matches 324; Conservative 172; Mismatches 331; Indels 182; Gaps 39;

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Qy 36 CVLISHENNGSAGKPSYRMVRGSPEDLOCTPRQSEGTVEAATVEVAESGSLTLQVQ 95
Db 12 CVLLVLLRGQTATPSA-----SPGEPSPSIHPAQSELIVEAGD-TL--- 54
Qy 96 LATPGDLSCL-----WVFKHSSLCQPHF-----DLQNRGIVSMAILNVTTQAGEYLL 144
Db 55 -----SLTCIDPDFVRWTFK-----TYFNEVMVENKKNWIOEKA-----EATRTGTTC 98
Qy 145 HIQSERANYTVLFTVNPVD-TQLYVLRBPYFRKMNQDALL-----CIS 187
Db 99 ---SNSNGLTSSIVYFVRDPAPKFLVGLPLFGK-EDSDALVRCPLTDPQVSNYSIECDG 154
Qy 188 EG-----VPEPTVWVLCSSHRESCKEEGPAVVRKEEVLHFGTDIRCCARNALGR 240
Db 155 KSLPTDLTFTVNP-----KAGITIKNVKRAYH-----RLCVRCAOR 191
Qy 241 ECTKL-----FTIDLNAQ-----POSTLPQL--FLKVGEPWIRCKAIHVNHGFGLTW--- 286
Db 192 DGTWLSKDFTLKVEAIKAIPIVSVSPETSHLLKKGDTFTVVTCTIKDVSTSVNMLWKN 251
Qy 287 -----BLEKALEEGSYFEMSTYSTNRTMIRILAFVSSVGRNDTGYYTCTSSSKHPQ 339
Db 252 PQQHIAQVKNHSMHRGDF-----NYEROETLT-----ISSARVDDSGVFMCAVNNTPGS 301
Qy 340 SALVT---ILEKGFINATS-SQEEYEIDPYEKFCFSVRPKAYPR-IRCTWIFSQASFPC 394
Db 302 ANVTTLKVEKGFINSIPVKNTTVFVDGENVDLVVEYEAYPEHQHQQWIYNRT--SA 359
Qy 395 ORGLE---DGYSISKFCDH-----KNKPGEYIFYAENDDAQFTKMTFLNIRKPKQVL 443
Db 360 NKGKDYVKNDSKNIRYVNLRLTLKLTGEGTGYTFLVSNSDASASVTENVVYNTKPEIL 419
Qy 444 A--NASASQSCSDGYPLPSWTWKCKSDKSPNCTEEI-PEGWVKKANRKFVQGWSS 500
Db 420 TYDRLINGMLOCAEGEPETIDWYFCTGAEQRCCTTPSPVDVQVQVNSVSPGKLVOGS 479
Qy 501 TLNMSEAGKLLVKKCAVNSMGTSCTETFLNSPGPPFIQDNI SFYATIGLCLPRTV--- 557
Db 480 SIDSVFRHNGTVECKASNDVGKS--SAFFN-----FAFKEQIOAHTLFTPLLIGFVVAAG 533
Qy 558 ---VLIVLICHYKKOPRYESOLOMI-QVTGPLDNEYFYVDPERDEYDLKWEFPRENLEF 613
Db 534 AMGIIIVMLTYKYLQKPMYEQWKVVEEING---NNYVVIDTQLPYDHKWEFPNRNLSF 590
Qy 614 GKVLGSGAFGRVMNATAYGISKTGYSIQAVRMKLEKADSKSEKALMSLKWMTHLGHHD 673
Db 591 GKTLGAGAFGKVEATAYGLIKSDAAMTVAVRMKLP SAHLTREALMSLKVLSYLGNHM 650
Qy 674 NIVNLLGACTLGGPVLYIFCYCYGDLNVLTHGKWKICDFGLARDIL 727
Db 651 NIVNLLGACTVGGPVLIVITEYCCYCGDLNVLNLRKRRKSDSFI FSQOEQOAEALYNLLHSTE 710
Qy 728 PTFQAHNSSM---PGSREVQLHPDLQSLGFGNCSHSEDEIEYENOKRLAESEEDLN 784
Db 711 PSCDS-SNEYMDMKEGVSVV-VPTKTDK-----RSARIDSYIERDVTVAIMEDDELAD 763
Qy 785 VLTPEDLICFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDILSDSS 844
Db 764 L---DDLLSFSYQVAKAMAFASKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSN 820
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QY 845 YVVRGNARLPVKWAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYKL 904
Db 821 YVVKGNARLPVKWAPESISCVYTFPSDVMSYGIFLWELFSLGSSYPGPNVDSKEYKM 880
QY 905 IQSGFMQEPYATEGIFYVMQSCWAFDSRKRFPNLTSLFGQLABA 953
Db 881 IKEGFRMVSPEHAPAEYDMVMTCDADPLKPTFKQVQVLIERQISDS 929
RESULT 6
US-09-944-807-10
; Sequence 10, Application US/09944807
; Patent No. US20020119494A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944, 807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-10
Query Match 23.2%; Score 1221.5; DB 10; Length 972;
Best Local Similarity 32.5%; Pred. No. 5.4e-76;
Matches 330; Conservative 152; Mismatches 331; Indels 201; Gaps 33;
QY 76 VYEAATVEAESGSIITLQVQLATPGDLSCLVWFKHSSILGQCPHFDLQNRGIVSMAIL--- 132
Db 22 VIEPSVELVVKPAT--VTILRCVNGSVWDGPPS-----PHWTLYSDG--SSSILSTN 72
QY 133 NVTEQAGEYLLHQTOSRANVTYVLTNNRDTQYLVRRPY-----FRKMNQDALL-C 185
Db 73 NATQNTGTYRCTEPGDPGLGSAIHLVYKDP-----ARPNVLAQEVVVPDQDALLPC 127
QY 186 ISEGVPEPTVWLVLCSSHRESCKEKGPAVVRKEK-----VLHE---LF 226
Db 128 L---LTDPEVL-----BAGVSLVRGRPLMRHTNYSFSPWHGTHIRAKPIQ 171
QY 227 GTDIRCCARNALGRECTKLTIDLNOAQPSLTP-----QLFLKVGPEPLMIRCKAI 276
Db 172 SODYQCSALMG-GR--KWSISIRLKVQKVIQPPALTLVPAELVRIRGEAAQIVCSAS 227
QY 277 HVNHGFGLTWELEKALEBGSYFEMSTYSTRNTRWIRILLAPVSVSGNRDNTGYTTCSSS-- 334
Db 228 SVDVNFDFVLQHNNTKL---AIPQSDPHNNRYQ-KVLTNLNDQVDFQHAGNYSVCVASNV 283
QY 335 --KHPSQALVTILEKFINATSQE-EYELDPYEKCFSVRFKAYPRIR-CTWIFSOAS 390
Db 284 QGKH-STSMFRVVEYAYLNLSSQNLIQEVTVGEGUNLKVMBEAYPGLOGFNWY----- 338
QY 391 FPCBQRGLEDGYSISKFDHKNKP-----GEYIFYAEN 423
Db 339 -----LQPSDHOPEPELANATTKDYRHTFTLSLRLKPEAGRYSFLARN 385
QY 424 DDAQTKMFTNIRKPKQV-----LANASQASCSGSDGYPLPSWTWKCKSDKSPNCTEE 478
Db 386 PGWRALTFELTLAYPPEVSVIWTFFINGSGT-LLCAASGYPOPNVTVLQCSGHTDRDEA 444
QY 479 LPEGVWN-----KKNRKFVQGWVSSSTLNMSEAGKLLVKKCAVNSMGTSCETIFLNSPG 534
Db 445 QVLQWDDDPYEVLSQBEFFHKVTYVQSLLTWTETLEHNTYECRAHNSVSGSWAFIPISAG 504
QY 535 PFPFIQDNISFYATIGLC---LPFIVVLVLICHKYKQFRYESOLOMIQVTPGLDNEYF 591

Db 505 AHTHPPDBFLTPVWVACMSIMALLLLLLLLLLLYKKQKPKYQVRWKIIE---SYEGNSYT 562
QY 592 YVDFRDYEDLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOAVAKMLKEKA 651
Db 563 FIDPTQLPYNEKWEFPFRNNIQFGKTLGAGAFKVVVEATAFGLGKEDDAVLKAVAKMLKSTA 622
QY 652 DSCKEALMSELKMTHLGHHDNIIVNLGACTLGGPVVLIPEYCCYGDLLNLYLSKRKRF 711
Db 623 HADEKEALMSELKMTSHLGHQHENIVNLGACTHGGPVLVITEYCCYGDLLNFLRKAB-- 680
QY 712 HRTWTEIFKHNFSYPTFOAHSSNMPGSGREVOLHPLDQLSGFNNGSIHSEDE----- 766
Db 681 -----AMLGP---SLSPQDPEGVDYKNIHLEKKYVRD 712
QY 767 -----IYENQKELAE--EEDLNVLTFEDLLCFAYOVAKMGFELEFK 808
Db 713 SGFSSQGVDTYVEMRPVSTNSDSFSEODLDKEDGRLELRDLHLFSQVQAQMAFLASK 772
QY 809 SCVHRDLAARNVLTHGKVKVICDFGLARDILSDSSVYVRGNARLPVKWMAPESEIFEGY 868
Db 773 NCIHROVAARNVLTNGHVAKIGDFGLARDIMDNSNIVKGNARLPVKWMAPESEIFDCVY 832
QY 869 TIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYKLIOGKPMEQPFYATEGIFYVMQSC 928
Db 833 TVQSDVMSYGILLWEIFSLGLNYPGILVNSKFYKLVKDGQYMAQAPAFAPKNIYSIMQAC 892
QY 929 WAFDSRKRPSFPNLTSLFGCOLAEAEACIRTSIHLKQAAPOQOGLRAQSPQ 982
Db 893 WALEPHTHPTFQIICSFL--QEQAQEDRRERDYNLNPSSS---RSGSGSSSSE 941
RESULT 7
US-10-099-895-32
; Sequence 32, Application US/10099895
; Patent No. US2002017166A1
; GENERAL INFORMATION:
; APPLICANT: BERNDT, Michael C
; APPLICANT: STOMSKI, Frank C
; APPLICANT: LOPEZ, Angel F
; APPLICANT: GUTHRIDGE, Mark A
; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
; FILE REFERENCE: 3991/0K379
; CURRENT APPLICATION NUMBER: US/10/099, 895
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/AU00/01118
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 32
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-099-895-32
Query Match 22.7%; Score 1196; DB 9; Length 976;
Best Local Similarity 31.4%; Pred. No. 3.1e-74;
Matches 312; Conservative 172; Mismatches 361; Indels 148; Gaps 32;
QY 36 CVLISHENNGSSAGKPSYRMVRGSPEDLQTPRRQSGTYVEAATVEAESGSIITLQVQ 95
Db 12 CVLLLLLRVQTSSQPS-----VSPGEPSPSIHPGKSDLIIVRVD-EIRLL 57
QY 96 LATFGDSLCLVWFKHSSILGQCPHFDLQNRGIVSMAILNVTEQAGEYLLHQTOSRANVT 155
Db 58 CTDPGFVK--WTFE---ILDETENKQNEWITEKA-----EATNCKYCTCTNKHGLNSIY 108
QY 156 LFTVNVDR-TOLYVLRPRYPRKMNQDALLCI-----SEG-----VPE 192
Db 109 VF-----VRDPAKFLVDRSLYKEDNDTLVRCLDPTDPEVTNYSKGCQCKPLPKDLRFPD 165
QY 193 PTVEWVLCSHRE-----SCKEGPAVVRKEKVLHLEFGTDIRCCARNALGRECTK 244

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Db 166 PKAGIMIKSVKRAVHRLCHLHCSVDQEG-----KSVLSEKFIKVRPAFK-----A 210
Qy 245 LFTIDLNOAPOSTLPQLFLKVGELWIRCKAIHNVHGFLTWELDK--ALEE----- 295
Db 211 VPVSVSKA-----SYLLREGEBEFTVCTIKDVSSSVYTWKRENSQTKLQEKYNSWH 264
Qy 296 GSYFEMSTYSTRNIMIRILLAFVSSVGRNDGYTCSSSKHPSQSALVTILE---KGFN 352
Db 265 GDF-----NYERQATLT-----ISSARVNDSGVFCYANNTFGSANVTITLVEVDKGFN 314
Qy 353 A-TSSQBEYEIDPVKEKFCFSVRKAYPR-IRCTWIFSOASF--PCEQRGLEDDGYISKFC 408
Db 315 IFPMINTTVFVNDGENVDLIVEYEAFFKPEHQOIMYMRFTFDKWDYPKSENESENIRYV 374
Qy 409 DHKN-----KPEGEYIFYAENDDAQFTKMTFLNIRKPKQVLA--NASASQASCSDDGYP 459
Db 375 SELHLTRLKGTGGTYTFLVNSDVNAIAFNVYVNTKPEILTYDRLVNGMLQCVAAAGFP 434
Qy 460 LPSWTWKCKSDKSNCTBEI-PEGVWKNKANKVFGQWSSSTLNMSEAGKLLVKCCAY 518
Db 435 EPTIDWYFCPTQRCASVLPVDVQTLNNSGPPFGKLVQSSIDSSAFKNGTVECKAY 494
Qy 519 NSMTGTCETIFLNSPGPPFIQDN-----ISFYATIGLCLPFIVLVILIC 564
Db 495 NDVGT--SAYFN-----FAFGNNKEQIHPHTLFTPLLIGFVIVAGM---MCIIVMILT 544
Qy 565 HKYKKQPRYESQLOMI-QVTGPLDNEYFYVDFRDYEDLKWEPFRENLEFGKVLGSGAFG 623
Db 545 YKYLQKPMYEVQWVVEING---NNVYIDPTQLPYDHWKWEFPNRNLSFGKTLGAGAFG 601
Qy 624 RVNMTAYGISTGVSIQVAVNMLKEKADSCKEALMSELKMTLGHHDNINVLGACT 683
Db 602 KVEATAYGLIKSDAAMTAVAKMLKPSAHLTEREALMSELKVLVSLGNHMINVLGACT 661
Qy 684 LSGPVYLIFECYCCGDLNLYLRSKREKHFRTWTETFEKHNFSSTYPTFOAHNSNMPGSR 743
Db 662 IGGTPLVITEYCCYCGDLNLFRRKRSDFICSKQEDHAAALYKNLLHKSKESSCDSTNEY 721
Qy 744 VOLHPPDLQL---SGFNNGSIHSEDEIEYENQKRLAEEDLNLVLTPEDLICFAYQVAK 800
Db 722 MDMPKGVSVVPTKADKRSVRIGSYIERDVTPTAMEDELALDL---EDLLSFYQVAK 778
Qy 801 GMEFLEPKSVHRDLAARNLVTHGKVKICDPGLARDILSDSSYVVRGNARLPVKWMAP 860
Db 779 GMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSNVYVKGARLPVKWMAP 838
Qy 861 ESLPEGIYTIKSDVWSYGIILLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEQPFYATEG 920
Db 839 ESIENCVYTFESDWSYGIIFLWELFSLGSSPYGMPVDSKFKYMIKEGFRMLSPHAPAE 898
Qy 921 IYFVWQSWAFDSRKRPSFPNLTSLFLGCQLAEA 953
Db 899 MYDIMKTCDADPLKRPFTFKQIVOLIEKQISES 931
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RESULT 8

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US-10-192-867-4
; Sequence 4, Application US/10192867
; Publication No. US20030084466A1
; GENERAL INFORMATION:
; APPLICANT: BLUME-JENSEN, Peter
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
; FILE REFERENCE: SALKINS.002C1
; CURRENT APPLICATION NUMBER: US/10/192,867
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/175,625
; 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US01/00573
; 2001-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
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; LENGTH: 976
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-192-867-4

Query Match      22.7%; Score 1196; DB 9; Length 976;
Best Local Similarity 31.4%; Pred. No. 3.1e-74;
Matches 312; Conservative 172; Mismatches 361; Indels 148; Gaps 32;

Qy 36 CVLISHENNGSSAGKPSYVRGSPEDLQCTPRQSGTGYVEAATVEVAESGSIITLQVQ 95
Db 12 CVLLLLLRVQTSSQPS-----VSPGEPSPSIHPGKSDLIIVRGD-EIRLL 57
Qy 96 LATPGDLSCLVFKHSLGCOQPHDLQNGRIVSMAILNVTFQAGEYLLHIOSEIRANYTV 155
Db 58 CTDPGFVK--WTFE---ILDETENKQNEWITEKA---EATNTGKYCTCTNKHGLNSIY 108
Qy 156 LFTVNVRD-TOLYVLRPRYFRKMNQDALLCT-----SEG-----VPE 192
Db 109 VF---VRDPKFLFLVDRSLYKGDNDTLVRCPLTDPEVTNYSLKGCQCKPLPKDLRFIPD 165
Qy 193 PTVEWVLCSSHRE-----SKEEGPAVVRKEBKVLHELFGTDIRCCARNALGRECTK 244
Db 166 PKAGIMIKSVKRAVHRLCHLHCSVDQEG-----KSVLSEKFIKVRPAFK-----A 210
Qy 245 LFTIDLNOAPOSTLPQLFLKVGELWIRCKAIHNVHGFLTWELDK--ALEE----- 295
Db 211 VPVSVSKA-----SYLLREGEBEFTVCTIKDVSSSVYTWKRENSQTKLQEKYNSWH 264
Qy 296 GSYFEMSTYSTRNIMIRILLAFVSSVGRNDGYTCSSSKHPSQSALVTILE---KGFN 352
Db 265 GDF-----NYERQATLT-----ISSARVNDSGVFCYANNTFGSANVTITLVEVDKGFN 314
Qy 353 A-TSSQBEYEIDPVKEKFCFSVRKAYPR-IRCTWIFSOASF--PCEQRGLEDDGYISKFC 408
Db 315 IFPMINTTVFVNDGENVDLIVEYEAFFKPEHQOIMYMRFTFDKWDYPKSENESENIRYV 374
Qy 409 DHKN-----KPEGEYIFYAENDDAQFTKMTFLNIRKPKQVLA--NASASQASCSDDGYP 459
Db 375 SELHLTRLKGTGGTYTFLVNSDVNAIAFNVYVNTKPEILTYDRLVNGMLQCVAAAGFP 434
Qy 460 LPSWTWKCKSDKSNCTBEI-PEGVWKNKANKVFGQWSSSTLNMSEAGKLLVKCCAY 518
Db 435 EPTIDWYFCPTQRCASVLPVDVQTLNNSGPPFGKLVQSSIDSSAFKNGTVECKAY 494
Qy 519 NSMTGTCETIFLNSPGPPFIQDN-----ISFYATIGLCLPFIVLVILIC 564
Db 495 NDVGT--SAYFN-----FAFGNNKEQIHPHTLFTPLLIGFVIVAGM---MCIIVMILT 544
Qy 565 HKYKKQPRYESQLOMI-QVTGPLDNEYFYVDFRDYEDLKWEPFRENLEFGKVLGSGAFG 623
Db 545 YKYLQKPMYEVQWVVEING---NNVYIDPTQLPYDHWKWEFPNRNLSFGKTLGAGAFG 601
Qy 624 RVNMTAYGISTGVSIQVAVNMLKEKADSCKEALMSELKMTLGHHDNINVLGACT 683
Db 602 KVEATAYGLIKSDAAMTAVAKMLKPSAHLTEREALMSELKVLVSLGNHMINVLGACT 661
Qy 684 LSGPVYLIFECYCCGDLNLYLRSKREKHFRTWTETFEKHNFSSTYPTFOAHNSNMPGSR 743
Db 662 IGGTPLVITEYCCYCGDLNLFRRKRSDFICSKQEDHAAALYKNLLHKSKESSCDSTNEY 721
Qy 744 VOLHPPDLQL---SGFNNGSIHSEDEIEYENQKRLAEEDLNLVLTPEDLICFAYQVAK 800
Db 722 MDMPKGVSVVPTKADKRSVRIGSYIERDVTPTAMEDELALDL---EDLLSFYQVAK 778
Qy 801 GMEFLEPKSVHRDLAARNLVTHGKVKICDPGLARDILSDSSYVVRGNARLPVKWMAP 860
Db 779 GMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSNVYVKGARLPVKWMAP 838
Qy 861 ESLPEGIYTIKSDVWSYGIILLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEQPFYATEG 920
Db 839 ESIENCVYTFESDWSYGIIFLWELFSLGSSPYGMPVDSKFKYMIKEGFRMLSPHAPAE 898
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QY 921 IYFVMSQWAFDGRKRPSPNLTSLFGLQCLAE 953
Db 899 MYDIMKTCDADPLKRTFTFKQIVQLIEKQISE 931

RESULT 9

US-09-961-403-4
; Sequence 4, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-4

Query Match 21.9%; Score 1152.5; DB 9; Length 1088;
Best Local Similarity 32.1%; Pred. No. 3.6e-71;
Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;
QY 94 VOLATPGDLSCLWVFKHSSLCQPHFDLQNRGIVSMALNVTTQAGEY--LLHIQSRA 151
Db 39 VOLNSSFSLR---FGESEVSWQ--YPMSEESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNVDRDQLYVLRPRFKMENODALLCISG-----VPEPTV-----EW 197
Db 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYVVPDPAFVPLGMDTY 136
QY 198 VLCSHRES---CK---EEGPAVVRKEEVL-----HELFGDIRCCARNALGR 240
Db 137 LVIVEDDDSAIPCRITDPTPTVTLHNSGVVPSYDSRQSGFNGFTTVPVCEATVKGK 196
QY 241 ECTKLFIDLNQAPQSTLPQLFL-----KVGPELWIRCKAIHVNHGFLTW-----E 287
Db 197 ---KFOTIPFNVAALKATSELDLEMEALKTVYKSGETIVVTC-AVFNVVVDLQWTPGE 252
QY 288 LEDKALEGSGYFEMSTYSTNRMTIR-----ILLAFVSSVGR---NDTGYVTCSSSK--- 335
Db 253 VKGKI-----TMDEETKVPISIKULVTLTVPDEATVKOSGDYECARQATR 297
QY 336 --HPSQALVITLKEGF--INATSSQBEYEDPYKFCFSVRFKAYPRIRCTWIFSQASF 391
Db 298 EVKEMKVTLSVHEKGFIEIKPTFSQLE-AVNLHEVKHFVVEVAYPPRISLWLNLT 356
QY 392 PCBORGLEDGYSIKFCD-----HKVK-----PGYIIFYAENDDAQFTMTFLN 435
Db 357 -----IENLTETITDVEKIQEIRYRSKLIIRAKEEDSGHYTTVAQMEDAVKSYTFELL 410
QY 436 IRKFPQVL-----ANASASQACSSDGYPLPSWTWKCKSDKSPNCTEELPEGVWNKKA 488
Db 411 TQVPESSILDVDDHHGSGTGQVTRCAEGTLPDIEWMICKD-IKKCNNETS-----WILA 466
QY 489 NRKVFQGWSS-----STLNMSEAGKGLIVKCCAYNSMGTSCTETIFLNSPG 534
Db 467 NN-----VSNIIIEHSRDRSTVEGRVTFPAKVETTAVRCLAKNLLGAENRELKVA-- 518
QY 535 PFPPIQDNISFYATIGLCLPFIVLVILCHIKYKQFRESQLOMIQVTPGLDNEYFYVD 594
Db 519 --PTLRSELTVAAAVLLVIVILISLIVLVVIMVKQKPRYERMRVIESISPDGHEYIYVD 576

QY 595 FRDYEDLKWFEFFRENLEFGKVLGSGAFGRVMNATAYIGISKTGVSIOVAVMVKLEKADSC 654
Db 577 PMQLPYDSRWEPFRDGLVLRGVLGSGAFGRVVEGTAYGLSRQSPVMKVAVKMLKPTARSS 636
QY 655 EKEALMSELKQWTHLGHHDNIVNLLGACTLSGPVYLIFCYCCYGGDLNLYLSRKEKF---- 711
Db 637 EKOALMSELKIMTHLGHPLNIVNLLGACTKSGPIYIITEYCFYGGDLNLYLHKNRDSFLSH 696
QY 712 -----HRTWTEIFKBNFSSYPTFOAHNSNSMP--GSREVQLHPP 749
Db 697 HPEKPKKELDIFGLNPADESTRSYVILSFENGDYMDMKQADTTQYVPMLEKESVSKSD 756
QY 750 LDQLSGFNGNSIHSEDEIYEYENQKRLAEEDDNLVLTFFDLFCAYQVAKGMFLBPKFS 809
Db 757 IQRSLYDRPASYYKKSMULDSEVNKLLSDNNSGLTLL---DLSFTYQVARGMEFLASKN 813
QY 810 CVHRDLAARNVLTGHKVKVICKDFGLARDILSDSSYVVRGNARLPVKWMAPESEFEGIYT 869
Db 814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYSYVSKGSTFLPVKWMAPESEFDNLYT 873
QY 870 IKSDVWSYGILLMEIFSLGIVNYPGIPVDANFYKLIQSGFKMEOPFYATEGIIYFVMQSCW 929
Db 874 TLDVWSYGILLMEIFSLGIVNYPGIPGMVMDSTFYNNKISGRMAKPDHATSEVYIEMVKCW 933
QY 930 AFDSRKRPSPNLTSL 946
Db 934 NSEPEKRPSPVHLSEIV 950

RESULT 10

US-09-769-987-2
; Sequence 2, Application US/09769987
; Patent No. US20020055129A1
; GENERAL INFORMATION:
; APPLICANT: Matsui, Toshimitsu
; APPLICANT: Aaronson, Stuart A.
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
; FILE REFERENCE: 14014, 026602
; CURRENT APPLICATION NUMBER: US/09/769,987
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 08/460,656
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/439,095
; PRIOR FILING DATE: 1995-05-11
; PRIOR APPLICATION NUMBER: US 07/915,884
; PRIOR FILING DATE: 1992-07-20
; PRIOR APPLICATION NUMBER: US 07/308,282
; PRIOR FILING DATE: 1989-02-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1e =
; OTHER INFORMATION: synthetic construct
US-09-769-987-2

Query Match 21.9%; Score 1152.5; DB 10; Length 1089;

Best Local Similarity 32.1%; Pred. No. 3.6e-71;
Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;
QY 94 VOLATPGDLSCLWVFKHSSLCQPHFDLQNRGIVSMALNVTTQAGEY--LLHIQSRA 151
Db 39 VOLNSSFSLR---FGESEVSWQ--YPMSEESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNVDRDQLYVLRPRFKMENODALLCISG-----VPEPTV-----EW 197
Db 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYVVPDPAFVPLGMDTY 136
QY 198 VLCSHRES---CK---EEGPAVVRKEEVL-----HELFGDIRCCARNALGR 240

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Db 137 LVIVEDDDSAIIPCKTTDPETPTVTLHNSGVVPASYSRQGNFGTFTVGPYICEATVKGK 196
Qy 241 ECTKLTIDLNAQPOSTLPQLFL-----KVGELWIRCKAIHVNHGFLTW---E 287
Db 197 ---KFQITPFNVYALKATSELDLEMEALKTVYKSETIVTTC-AVFNNVVDLQWYTPGE 252
Qy 288 LEDKALBEGSYFEMSTYSTNMTIR-----ILLAFVSSVGR---NDTGYTTCSSK--- 335
Db 253 VKGKI-----TMLKEIKVPSIKLYTTLTVPETATVKDSGDYECARQATR 297
Qy 336 --HPSQSALVITILEKGF--INATSSOEYEIDPYEKFCSVRFKAYPRIRCTWIFSQASF 391
Db 298 EVKEMKVTISVHEKGFIEIKPTFSQLE-AVNLEHVHFVVEVRAYPPIRISWLKNLTL 356
Qy 392 PCEQGLDGYSGISKFC-----HKNK-----PGEYIFAENDDAQFTKMTFLN 435
Db 357 -----IENLTETITDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEADVKSFTFELL 410
Qy 436 IRKQPQVL-----ANASASQASCSGYPPLPSWTWKCKSDKSPNCTEETIEPEGVWNKA 488
Db 411 TQVPSSILDVDDHHGSGGTGCTAGTPLPDIEWMICKD-IKKCNNETS---WTILA 466
Qy 489 NRKVFQGWSS-----STLNMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPG 534
Db 467 NN-----VSNIIETIHSRDRSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKVA-- 518
Qy 535 PFPFIQDNISFYATIGLCLPFIIVLILCHIKKOPRYESQLOMIQVTPGLDNEFYVD 594
Db 519 --PFLRSELTVAAAVLVLLVILVILVWVKQPRYERWRVIESISPDGHEIYVD 576
Qy 595 FRDYEYDLKWEFPRENLEFGKVLGSGAGFGRVMNATAYGISKTGVSQVAVKMLKEKADSC 654
Db 577 PMQLPYDSRWEFPDGLVGLRVLGSGAFKVGVEGTAYGLRSQPMKVAVKMLKPTARSS 636
Qy 655 EKEALMSELKMTLGHHDNIVNLLGACTLSGPVYLIFEYCYGDLLNLYRSKREKF--- 711
Db 637 EKQALMSELKMTLGHPLNIVNLLGACTKSGPIIITEYCFYGLDVLNLYLHKNRDSFLSH 696
Qy 712 -----HRTWTEIFKEHNFSSYPTFFQAHSSNMP--GSRVQLHPP 749
Db 697 HPEKPKKELDIFGLNPADESTRSYILSFENNQDYMMDKQADTTQYVPMLEKREKYSKYD 756
Qy 750 LDQLSGFNGNSIHSEDEIEYENQKRLAEBEEDLNVLTFEDLLCFAYQVAKGMEFLPFKS 809
Db 757 IQRSLYDRPASYKKKMLDSEVNKLLSDNSEGLTLL---DLLSFTYQVAKGMEFLASKN 813
Qy 810 CVHRDLAARNVLVTHGKVKIKCDFGLARDILSDSYVVRGNARLPVKWMAPESEIFEGIYT 869
Db 814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPLVKWMAPESEIFDNL 873
Qy 870 IKSDVWSYGILLWEIFSLGVNPPYGPIDANFYKLIQSGFKMEQPFYATEGIFYFMQSCW 929
Db 874 TLDVWSYGILLWEIFSLGTPYGMWVDSTFYNKIKSGYRMAKPDHATSEIVEIMVKCW 933
Qy 930 AFSRKRKPSFNLTSFL 946
Db 934 NSRPEKPSFVHLSEIV 950
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RESULT 11

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US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; FILE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
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; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 90

; LENGTH: 1089

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-919-497-90

Query Match 21.9%; Score 1152.5; DB 10; Length 1089;

Best Local Similarity 32.1%; Pred. No. 3.6e-71;

Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;

Qy 94 VOLATPGDLSCLLWPKHSLGCPHFIDLQNRGIVSMALNVTTETQAGEY--LLHIQSERA 151

Db 39 VQLNSSFSFLRC---PGESEVSMQ--YPMSEBESSDVEIRN-EENNSGLFVTVLVSVSSASA 92

Qy 152 NYTVLFTVNRDQLYLVLRPFYFRKMNQDALLCISEG-----VPEPTV-----EM 197

Db 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYIYVDPDPAFVPLGMDTY 136

Qy 198 VLCSSHRES---CK---EEGPAVVRKEEKVL-----HELFGTDIRCCARNALCR 240

Db 137 LVIVEDDDSAIIPCKTTDPETPTVTLHNSGVVPASYSRQGNFGTFTVGPYICEATVKGK 196

Qy 241 ECTKLTIDLNAQPOSTLPQLFL-----KVGELWIRCKAIHVNHGFLTW---E 287

Db 197 ---KFQITPFNVYALKATSELDLEMEALKTVYKSETIVTTC-AVFNNVVDLQWYTPGE 252

Qy 288 LEDKALBEGSYFEMSTYSTNMTIR-----ILLAFVSSVGR---NDTGYTTCSSK--- 335

Db 253 VKGKI-----TMLKEIKVPSIKLYTTLTVPETATVKDSGDYECARQATR 297

Qy 336 --HPSQSALVITILEKGF--INATSSOEYEIDPYEKFCSVRFKAYPRIRCTWIFSQASF 391

Db 298 EVKEMKVTISVHEKGFIEIKPTFSQLE-AVNLEHVHFVVEVRAYPPIRISWLKNLTL 356

Qy 392 PCEQGLDGYSGISKFC-----HKNK-----PGEYIFAENDDAQFTKMTFLN 435

Db 357 -----IENLTETITDVEKIQEIRYRSKLIRAKEEDSGHYTIVAQNEADVKSFTFELL 410

Qy 436 IRKQPQVL-----ANASASQASCSGYPPLPSWTWKCKSDKSPNCTEETIEPEGVWNKA 488

Db 411 TQVPSSILDVDDHHGSGGTGCTAGTPLPDIEWMICKD-IKKCNNETS---WTILA 466

Qy 489 NRKVFQGWSS-----STLNMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPG 534

Db 467 NN-----VSNIIETIHSRDRSTVEGRVTFPAKVEETIAVRCLAKNLLGAENRELKVA-- 518

Qy 535 PFPFIQDNISFYATIGLCLPFIIVLILCHIKKOPRYESQLOMIQVTPGLDNEFYVD 594

Db 519 --PFLRSELTVAAAVLVLLVILVILVWVKQPRYERWRVIESISPDGHEIYVD 576

Qy 595 FRDYEYDLKWEFPRENLEFGKVLGSGAGFGRVMNATAYGISKTGVSQVAVKMLKEKADSC 654

Db 577 PMQLPYDSRWEFPDGLVGLRVLGSGAFKVGVEGTAYGLRSQPMKVAVKMLKPTARSS 636

Qy 655 EKEALMSELKMTLGHHDNIVNLLGACTLSGPVYLIFEYCYGDLLNLYRSKREKF--- 711

Db 637 EKQALMSELKMTLGHPLNIVNLLGACTKSGPIIITEYCFYGLDVLNLYLHKNRDSFLSH 696

Qy 712 -----HRTWTEIFKEHNFSSYPTFFQAHSSNMP--GSRVQLHPP 749

Db 697 HPEKPKKELDIFGLNPADESTRSYILSFENNQDYMMDKQADTTQYVPMLEKREKYSKYD 756

Qy 750 LDQLSGFNGNSIHSEDEIEYENQKRLAEBEEDLNVLTFEDLLCFAYQVAKGMEFLPFKS 809

Db 757 IQRSLYDRPASYKKKMLDSEVNKLLSDNSEGLTLL---DLLSFTYQVAKGMEFLASKN 813

Qy 810 CVHRDLAARNVLVTHGKVKIKCDFGLARDILSDSYVVRGNARLPVKWMAPESEIFEGIYT 869

Db 814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPLVKWMAPESEIFDNL 873

Qy 870 IKSDVWSYGILLWEIFSLGVNPPYGPIDANFYKLIQSGFKMEQPFYATEGIFYFMQSCW 929

Db 874 TLDVWSYGILLWEIFSLGTFPGMVMVDSTFYNNKIKSGYRMAKPDHATSEVVEIMVKCW 933
QY 930 AFDSRKRPSPNLTSL 946
Db 934 NSEPEKRPSPHYLSEIV 950
RESULT 12
US-09-866-510-2
; Sequence 2, Application US/09866510
; Patent No. US2002011304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-2
Query Match 21.9%; Score 1152.5; DB 10; Length 1089;
Best Local Similarity 32.1%; Pred. No. 3.6e-71;
Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;
QY 94 VQLATPGDLCLWVFKHSLGCPHFDLQNRGIVSMAILNVTETQAGEY--LLHIQSRA 151
Db 39 VQLNSSPSLRCL--FGSEVSWQ--YPMSEESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYVLFTVNRDQLVLRFRYFRKMNQDALLCISEG-----VPEPTV-----EW 197
Db 93 AHTGLYTCYNNHTQ-----TEENE-----LEGRHYIYVDPDPVAFVPLGMMDY 136
QY 198 VLLCSSHRES---CK---EEGPAVVRKEEKL-----HELFGTDIRCCARNALGR 240
Db 137 LVIVEDDSALIPCKTDPETVTLHNSGVVPASYSRQGFNGFTTGVGPICEATVKGK 196
QY 241 ECTKLFTIDLNAQPOSTLQFL-----KVGELWIRCKAIHVNHGFLTW---E 287
Db 197 ---KFQTFPNNYALKATSELDLEMEALKTVYKSGETIIVTC-AVFNEVVDLQWTPGE 252
QY 288 LEDKALEGSGYFEMSTYNTNTRMIR-----ILLAFVSVGR---NDGYTCSKK--- 335
Db 253 VKGKI-----TMLBEIKVPSIKLYTLTVPEATVKDGDYECARQATR 297
QY 336 --HPSQSALVTILEKGF--INATSSQEEYEDPYEKFCSVRKFAYPRIKRTWIFESQASF 391
Db 298 EVKEMKKTIVSHKGFIEIKFTFSLQLE-AVNLHEVHFVVEVRAYPPIRSLWKNLTL 356
QY 392 PCEQRLGDDGYSISKFC-----HNK-----PGEYIFYAENDDAQFTKMTFLN 435
Db 357 -----IENLTITDVEKIQIRVRSKLIRAKEEDSGHYTIQAQNEADAVKSYTFELL 410
QY 436 IRKKEQVL-----ANASASQSCSDGYPPLSPWTWKCDKSNCTEETIEPEGVWNKA 488
Db 411 TQVPSSILDVDDHRRGGTQVRCATGTPLEDEWICKD-IKKCNETS---WTILA 466
QY 489 NRKVGQWSS-----STLNMSEAGKGLVKCCAYNSMGTSCETIFLNSPG 534
Db 467 NN-----VSNITTEIHSRDRSTVGRVTFATKEETIAVRCUAKNLLGAENRELKVA-- 518
QY 535 PPFPTQDNISFYATIGLCIPFTVWLIVLICHYKFKQFYESQLQMTQVTPGLDNEYFYVD 594
Db 519 --PTLSELTVAANVLVLVLIISLIVLWIKQKPRVIEIRWRVIESIPDGHEVIYVD 576

QY 595 FRDYEDLKWPEPRENLEFGKVLGSGAFGRVMNATAYGISKTYGSIQAVKMLKEKADSC 654
Db 577 PMQLPYDSRWEPFRDGLVLRVLSGAFGVVEGTAYGLRSQPMKVAVKMLKPTARSS 636
QY 655 EKEALMSELKQMTHLGHHDNIVNLLGACTLSGPPVLYFFCYCCYDGLLNLRLSKREKF--- 711
Db 637 EKQALMSELKIMTHLGHPLNIVNLLGACTKSGPIIITEYCFYGDVNLVHLKNRDPSLSH 696
QY 712 -----HRTWTEIFKEHNFSSYTFQAHNSNSMP--GSRREVQLHPP 749
Db 697 HPEKPKKELDI FGLNPADESTRSYVLSFNNGDYMOMKQADTTQYVPMLEKREKVSYSD 756
QY 750 LDQLSGFNGNSIHSEDEIEYENOKRLAEEDLNVLTFEDLLCFAYQVAKMGFEFLPFKS 809
Db 757 IQRSLYDRPASYYKKSLMDSEVNKLLSDDNSEGLTLL--DLSFTYQVARGMEFLASKN 813
QY 810 CVHRDLAARNVLYTHGKVKICDFGLARDILSSSYVVRGNARLPVKWMAPESLFEGIYT 869
Db 814 CVHRDLAARNVLLAQQKIKVICDFGLARDIMHDSNYYVSKGSTFLPVKWMAPESIFDNLTY 873
QY 870 IKSDVWSYGILLWEIFSLGVNPPYPCIPVDANFYKLIQSGFKMEQPFYATEGIYFVMQSCW 929
Db 874 TLDVWSYGILLWEIFSLGTFPGMVMVDSTFYNNKIKSGYRMAKPDHATSEVVEIMVKCW 933
QY 930 AFDSRKRPSPNLTSL 946
Db 934 NSEPEKRPSPHYLSEIV 950

RESULT 13

US-09-955-363-36
; Sequence 36, Application US/09955363
; Patent No. US20020173621A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/955,363
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELE: 3723836
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-955-363-36

Query Match 21.9%; Score 1150.5; DB 9; Length 1089;
Best Local Similarity 32.2%; Pred. No. 5e-71;
Matches 313; Conservative 154; Mismatches 327; Indels 177; Gaps 32;

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QY 94 VOLATPGDLSLWFKHSSLCQPHFDLQNGRIGVSMALNVTETQAGEY--LLHIQSER 151
DB 39 VOLNSFSFLRC---FGSEVSWQ--YPMSEBESDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNRDQLYVLRPRFRKMNQDALLCISEG-----VPEPTV-----EW 197
DB 93 AHTGLTYCYNHTQ-----TEENE-----LEGRHIYVDPDPAFVPLGMDTY 136
QY 198 VLSHRES-----CK---BEGAVVRKEEKL-----HELFGTDIRCCARNALGR 240
DB 137 LVIVEDDDSAIIPCKTDPETVTLHNSGVVPASVDSRQGFNGFTVGPVCEATVKGK 196
QY 241 ECTKLTIDLNOAQOSTLPQLFL-----KVEPLWIRCKAIHVHNGFGLTW----E 287
DB 197 ---KFQTIPTFNVAALKATSELDLEMEALKTVYKSGETIVVTC-AVFNNVVDLQWTPGE 252
QY 288 LEDKALEEGSYFENSTYNTIRILLAFVSSVGR---NDTGYVTCSSSK-----HPSQ 339
DB 253 VKGKI-----TILEEIKVSIKLVYTLTVPATVKDGSYECARQATREVKEMK 303
QY 340 SALVTILEKGF--INATSSQEEYIDPYEKFCSVRFKAYPRIRCTWIFSQAQSPCEQ 397
DB 304 KVTISVHEKGFIEIKPTFSQLE-AVNLHEVKGHFVEVRAYPPIPRISLKNLTL----- 356
QY 398 LEDGYSTSKPCD-----HKWK-----PGEYIFYAENDDAQFTMTFLNIRKPKQ 441
DB 357 IENLTITTDVEKIQEIRYRSKLIIRAKEDSDGHYTTVAQNEADAVKSYTFELLTQVPS 416
QY 442 VL-----ANASASQASCSDDGYPLPSWTWKCKSDKSPNCTEIEPEGVMKANKRVFG 494
DB 417 ILDLVDHSGTGQVTRCTAEGTLPDIEWIKCD-IKKCNNETS-----WTLANA 468
QY 495 QWVSS-----STLNMSAGKGLLVKCCAYNSMGTSCTETFLNSPGFPPIQ 540
DB 469 --VSNIIIEHSRDRSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVA----PTLR 522
QY 541 DNISFYATIGLCLPFIIVLIVLICHYKQKPRYSOLOMIQVTPGLDNEYFVDFRDY 600
DB 523 SELTVAAAVLLVIVLIVLIVLIVVWIKQPRYRIRWRVIESISPDGHEIYVDPMLPY 582
QY 601 DLKWEFFRENLEFGKVLGSGAGFVGMNATAYGISKTGYSIOAVKMLKEKADSCKEALM 660
DB 583 DSRWEFFRDGLVLGVLGSGAGFVGEVGTAYGLSRQVPMKVAVKMLKPTARSEKQALM 642
QY 661 SELKQWTHLGHNDHIVNLLGACTLSGVPYLIFEYCYGDLNLYRSKREKF----- 711
DB 643 SELKIMTHLGHPLNIVNLLGACTSGPIYIITEYCFYGLDLYNHLKNDRLSLSHPEKPK 702
QY 712 -----HRTWTEIFKEHNFSSYPTFOAHNSNMP--GSRVQLHPPLDQLSG 755
DB 703 KELDIFGLNPADESTRSVILSFENNNGDYMOMQADTTQYVPMLEKESVSKYSDIORS 762
QY 756 FNGNSIHSEDEIEYENOKRLAESEEDLNLTFEDLLCFAYQAVAKMEFLFKSCVHEDL 815
DB 763 DRPASVKKKGMLESEVKNLLSDDDNSEGLTLL---DLSFTYQVARGMEFLASKNCVHEDL 819
QY 816 AARNVLVTHGKVKVICDFGLARDILSDSYVVRGNARLPVKWMAPESEFEGYITIKSDVW 875
DB 820 AARNVLAQGIKVIKICDFGLARDIMHDSNYVSKGSTFLPKWMAPESEFDNLYITLSDVW 879
QY 876 SYGILLWEIFSLGVPYGPVDANFYKLIQSGFKMEQPFYATEGIYFVMSQWAFDSRK 935
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Db 880 SYGILLWEIFSLGVPYGPYGMVVDSTFYNNKISGYRNAKPDHATSEYVEIMVKWNSEPEK 939
QY 936 RPSFENLTSEFL 946
Db 940 RPSFYHLSEIV 950
RESULT 14
US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: EM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-10

Query Match 21.8%; Score 1149.5; DB 10; Length 1089;
Best Local Similarity 32.0%; Pred. No. 5.8e-71;
Matches 313; Conservative 155; Mismatches 320; Indels 189; Gaps 33;

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QY 94 VOLATPGDLSLWFKHSSLCQPHFDLQNGRIGVSMALNVTETQAGEY--LLHIQSER 151
DB 39 VOLNSFSFLRC---FGSEVSWQ--YPMSEBESDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNRDQLYVLRPRFRKMNQDALLCISEG-----VPEPTV-----EW 197
DB 93 AHTGLTYCYNHTQ-----TEENE-----LEGRHIYVDPDPAFVPLGMDTY 136
QY 198 VLSHRES-----CK---BEGAVVRKEEKL-----HELFGTDIRCCARNALGR 240
DB 137 LVIVEDDDSAIIPCKTDPETVTLHNSGVVPASVDSRQGFNGFTVGPVCEATVKGK 196
QY 241 ECTKLTIDLNOAQOSTLPQLFL-----KVEPLWIRCKAIHVHNGFGLTW----E 287
DB 197 ---KFQTIPTFNVAALKATSELDLEMEALKTVYKSGETIVVTC-AVFNNVVDLQWTPGE 252
QY 288 LEDKALEEGSYFENSTYNTIRMIIR-----ILLAFAVSSVGR---NDTGYVTCSSSK 335
DB 253 VKGKI-----TMLBEIKVPSIKLVYTLTVPATVKDGSYECARQATR 297
QY 336 --HPSQSALVTILEKGF--INATSSQEEYIDPYEKFCSVRFKAYPRIRCTWIFSQAQSF 391
DB 298 EVKEMKVTISVHEKGFIEIKPTFSQLE-AVNLHEVKGHFVEVRAYPPIPRISLKNLTL 356
QY 392 PCEQRLGDEGYSISKPCD-----HKWK-----PGEYIFYAENDDAQFTMTFLN 435
DB 357 -----IENLTITTDVEKIQEIRYRSKLIIRAKEDSDGHYTTVAQNEADAVKSYTFELL 410
QY 436 IRKKPQVL-----ANASASQASCSDDGYPLPSWTWKCKSDKSPNCTEIEPEGVMKKA 488
DB 411 TQVPSIILDLVDHSGTGQVTRCTAEGTLPDIEWIKCD-IKKCNNETS-----WTLA 466
QY 489 NRKVPQWVSS-----STLNMSAGKGLLVKCCAYNSMGTSCTETFLNSPG 534
DB 467 NN-----VSNIIIEHSRDRSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVA-- 518
QY 535 PFPFIQDNISFYATIGLCLPFIIVLIVLICHYKQKPRYSOLOMIQVTPGLDNEYFYVD 594
DB 519 --PTLRSELTVAAAVLLVIVLIVLIVLIVVWIKQPRYRIRWRVIESISPDGHEIYVD 576
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QY 595 FRDYEDLKWEPPRENLEFGKVLGSGAFGRVMNATAYGISKTVGSIQVAVKMLKEKADSC 654
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Db 577 PMQLPYDSRWKFRDGLVLRVLGSGAFGVVEGTAYGLSRSQPMKVAVKMLKPTARSS 636
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QY 655 EKEALMSELKQWTHLGHHDNIVNLLGACTLSGPVLIIFYCCYGDLLNLYLRSKREKF--- 711
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 637 EKOALMSELKIMTHLGHPLNIVNLLGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSH 696
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 712 -----HRTWTEIFKHNPFSSYPTFOAHNSNMP--GSREVQLHPP 749
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Db 697 HPEKPKXELDIFGLNPADESTRSYVLSFENNNGDYMMDKQADTTQYVPMLEKVEVSYSD 756
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QY 870 IKSDVMSYGILLWEIFSLGVNYPYGPVDANFYKLIQSGFKMEOPFYATEGIIYFMQSCW 929
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RESULT 15
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; Sequence 4, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-866-510-4
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Query Match 21.8%; Score 1148.5; DB 10; Length 1089;
Best Local Similarity 32.0%; Pred. No. 6.8e-71;
Matches 313; Conservative 155; Mismatches 320; Indels 189; Gaps 33;

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Search completed: May 24, 2003, 17:10:16
Job time : 46.9793 secs

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Db 757 IQRSLYDRPASYYKKKMLDSEVNKLLSDNSEGLTLL---DLLSFTYQVARGMEFLASKN 813
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QY 810 CVHRDLAARNVLTGHKVKIKCDPLGLARDILSDSSYVVRGNARLPVKWMAPESEFEGIYT 869
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Db 874 TLDVMSYGILLWEIFSLGGTPYGMVMDSTFYNNKIKSGYRMAKPDHATSEVYEIMVKCW 933
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GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:54:10 ; Search time 13.9929 Seconds
(without alignments)
2085.875 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQSRDRLLLLLVLSV.....RGGLRAQSPORQVKIHRERS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5264	100.0	992	1	US-07-977-451-2
3	5264	100.0	992	1	US-07-946-507-2
4	5264	100.0	992	1	US-08-252-517-2
5	5264	100.0	992	1	US-07-906-397A-2
6	5264	100.0	992	1	US-08-601-891-2
7	5264	100.0	992	2	US-09-021-324-2
8	5264	100.0	992	5	PCT-US92-02750-2
9	5264	100.0	992	5	PCT-US92-05401-2
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17	4430.5	84.2	1160	5	PCT-US92-05401-4
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22	4429.5	84.1	993	2	US-09-021-324-4
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25	4408.5	83.7	993	5	PCT-US95-00176A-2
26	2240.5	42.6	481	4	US-07-912-122-4
27	2240.5	42.6	481	5	PCT-US93-06404-4

28 1221.5 23.2 972 3 US-08-750-141A-2
29 1196 22.7 976 3 US-08-750-141A-1
30 1152.5 21.9 1089 1 US-08-168-917-4
31 1152.5 21.9 1089 2 US-08-460-510-4
32 1152.5 21.9 1089 2 US-08-460-490-4
33 1152.5 21.9 1089 3 US-08-462-728-2
34 1152.5 21.9 1089 4 US-08-461-917-2
35 1152.5 21.9 1089 5 PCT-US92-00730-4
36 1152.5 21.9 1089 5 PCT-US92-00862-4
37 1150.5 21.9 1089 1 US-08-180-195-36
38 1150.5 21.9 1089 1 US-08-477-329-36
39 1150.5 21.9 1089 2 US-08-475-458-36
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42 1150.5 21.9 1089 4 US-09-583-210-36
43 1150.5 21.9 1089 4 US-09-583-449A-36
44 1150.5 21.9 1089 4 US-09-435-059-36
45 1078 20.5 1106 1 US-08-180-195-2

ALIGNMENTS

RESULT 1
US-07-813-593-2
; Sequence 2, Application US/07813593
; Patent No. 5185438
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,593
; FILING DATE: 19920415
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-813-593-2
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Qy	481	EGVWNKXKARKVFCQWSSSTLNSEAGKLLVKKCAYNMGTSCTETIFLNSPGPPFIQ	540		
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Qy	721	EHNFSYPTFOAHNSNMPGSRVQLHPPLDQSGFNGNSIHSDEITEYENOKRLAEBEE	780		
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Qy	781	EDNLVTFEDLLCFAYQVAKGWEFLPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL	840		
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Qy	901	FYKLIQSGFKMEQPFYATGEGYFVMSQWAFDSRKRPSPFNLTSLGCOLAEBEACIRT	960		
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RESULT 2					

US-07-977-451-2
; Sequence 2, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-977-451-2

Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRALAQRSDRLRLLLVLSVMILETVTNQDLPVKCVLI SHENNGSSAGKPSSSYRMVRGS	60
Db	1	MRALAQRSDRLRLLLVLSVMILETVTNQDLPVKCVLI SHENNGSSAGKPSSSYRMVRGS	60

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QY 61 PEDLQCTPRRQSEGVVYEAATVEAEGSITLQVQLATPGDLSCLWFKHSSLGCPHFD 120
DB 61 PEDLQCTPRRQSEGVVYEAATVEAEGSITLQVQLATPGDLSCLWFKHSSLGCPHFD 120
QY 121 LQNRGIVSMAILNVTQAGSYLLHIQSERANYTVLFTVNRDITQVLRPRYFRKMNQ 180
DB 121 LQNRGIVSMAILNVTQAGSYLLHIQSERANYTVLFTVNRDITQVLRPRYFRKMNQ 180
QY 181 DALLCISGEVPEPTVEVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISGEVPEPTVEVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLFITDLNQAQOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
DB 241 ECTKLFITDLNQAQOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
QY 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASPPCORGLEDGYSISKFCDHKNKPGYIFY 420
DB 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASPPCORGLEDGYSISKFCDHKNKPGYIFY 420
QY 421 AENDDAQFTKMTFLNIRKKQVLANASASQSSDGYPLPSWTWKCKSDKSPNCTEIP 480
DB 421 AENDDAQFTKMTFLNIRKKQVLANASASQSSDGYPLPSWTWKCKSDKSPNCTEIP 480
QY 481 EGWNKANKRVKQWVSSSTLNSEAGKLLVKCCAYNSMGTSCTETIFLNSPGFFPIQ 540
DB 481 EGWNKANKRVKQWVSSSTLNSEAGKLLVKCCAYNSMGTSCTETIFLNSPGFFPIQ 540
QY 541 DNISFYATIGLCLPFIWVLIHVKYKOPRYESQLOMIQVTPGLDNEYFYVDFRDY 600
DB 541 DNISFYATIGLCLPFIWVLIHVKYKOPRYESQLOMIQVTPGLDNEYFYVDFRDY 600
QY 601 DLKWEFPRENLEFGKVLGSGAGFGRVMNATAGISKTGVSIOVAVKMLKEKADSCKEKALM 660
DB 601 DLKWEFPRENLEFGKVLGSGAGFGRVMNATAGISKTGVSIOVAVKMLKEKADSCKEKALM 660
QY 661 SELKQMTHLGHHDNIIVNLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK 720
DB 661 SELKQMTHLGHHDNIIVNLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK 720
QY 721 EHNFSYPTFOAHNSNMPGSRREVQLHPPLDOLSGFNGNSIHSDETEIYENOKRLABEE 780
DB 721 EHNFSYPTFOAHNSNMPGSRREVQLHPPLDOLSGFNGNSIHSDETEIYENOKRLABEE 780
QY 781 EDNLVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
DB 781 EDNLVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
QY 841 SDSSYVVRGNARLPVKWMAPELSEFLGYITIKSDVMSYGILLWEIFSLGWNYPGIPVDAN 900
DB 841 SDSSYVVRGNARLPVKWMAPELSEFLGYITIKSDVMSYGILLWEIFSLGWNYPGIPVDAN 900
QY 901 FYKLIQSGFKMEQPFYATEGIFVWQSCWAFDSKRSPFNLTSLFGCOLAEAEACIRT 960
DB 901 FYKLIQSGFKMEQPFYATEGIFVWQSCWAFDSKRSPFNLTSLFGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPQORGGLRAQSPQOVKIHRS 992
DB 961 SIHLPKQAAPQORGGLRAQSPQOVKIHRS 992
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RESULT 3

US-07-946-507-2
; Sequence 2, Application US/07946507
; Patent No. 5283354
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,507
FILING DATE: 19920917
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/913,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-946-507-2

Query Match 100.0%; Score 5264; DB 1; Length 992;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRALAQRSDRRLILLVLSVMILETVTNQDLPVVKCVLI SHENNGSSAGKPSSSYRMVRGS 60
DB 1 MRALAQRSDRRLILLVLSVMILETVTNQDLPVVKCVLI SHENNGSSAGKPSSSYRMVRGS 60
QY 61 PEDLQCTPRRQSEGVVYEAATVEAEGSITLQVQLATPGDLSCLWFKHSSLGCPHFD 120
DB 61 PEDLQCTPRRQSEGVVYEAATVEAEGSITLQVQLATPGDLSCLWFKHSSLGCPHFD 120
QY 121 LQNRGIVSMAILNVTQAGSYLLHIQSERANYTVLFTVNRDITQVLRPRYFRKMNQ 180
DB 121 LQNRGIVSMAILNVTQAGSYLLHIQSERANYTVLFTVNRDITQVLRPRYFRKMNQ 180
QY 181 DALLCISGEVPEPTVEVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISGEVPEPTVEVWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLFITDLNQAQOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
DB 241 ECTKLFITDLNQAQOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
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Qy 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAGPFCBQGLEDDGYSISKFCDHKNKPGYIFY 420
Db 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAGPFCBQGLEDDGYSISKFCDHKNKPGYIFY 420
Qy 421 AENDDAQFTKMTLIRKPKOVLANASASQASCSDDGYPLPSWTWKCSKSPNCTBEIP 480
Db 421 AENDDAQFTKMTLIRKPKOVLANASASQASCSDDGYPLPSWTWKCSKSPNCTBEIP 480
Qy 481 EGVWVKANRKFVQOWSSSTLNNSSEAGKLLVKCCAYNSMGTSCTETIFLNSRGPFPPIQ 540
Db 481 EGVWVKANRKFVQOWSSSTLNNSSEAGKLLVKCCAYNSMGTSCTETIFLNSRGPFPPIQ 540
Qy 541 DNISFYATIGLCLEPFIVVLVILCHYKKQPRYESQLOMIQVOTGFLDNEYFYVDFRDY 600
Db 541 DNISFYATIGLCLEPFIVVLVILCHYKKQPRYESQLOMIQVOTGFLDNEYFYVDFRDY 600
Qy 601 DLKWEFFRENLEFGKVLGSGAGFGRVMNATAYGISTGVSIOVAVKMLKEKADSCEKEALM 660
Db 601 DLKWEFFRENLEFGKVLGSGAGFGRVMNATAYGISTGVSIOVAVKMLKEKADSCEKEALM 660
Qy 661 SELKQWTHLGHHDINVLNLLGACTLSGPVYLIFBYCCYGDLLNLYLSRKEKPHRTWTEIFK 720
Db 661 SELKQWTHLGHHDINVLNLLGACTLSGPVYLIFBYCCYGDLLNLYLSRKEKPHRTWTEIFK 720
Qy 721 EHNFSYPTFOAHNSNMPGSGREVQLHPDLQSGFNGNSIHSDEIEYENOKRLAESEE 780
Db 721 EHNFSYPTFOAHNSNMPGSGREVQLHPDLQSGFNGNSIHSDEIEYENOKRLAESEE 780
Qy 781 EDLNLVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 781 EDLNLVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Qy 841 SDSSVYVRGNARLPVKWMAPELSLEGITIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
Db 841 SDSSVYVRGNARLPVKWMAPELSLEGITIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
Qy 901 FYKLIQSGFKMEQPPYATGEGYFVWQSCWAFDSRKRPSFPNLTSLGCOLAEAEACIRT 960
Db 901 FYKLIQSGFKMEQPPYATGEGYFVWQSCWAFDSRKRPSFPNLTSLGCOLAEAEACIRT 960
Qy 961 SIHLPKQAAPQORGLRAQSPQQRVKIHRERS 992
Db 961 SIHLPKQAAPQORGLRAQSPQQRVKIHRERS 992

RESULT 4
US-08-252-517-2
; Sequence 2, Application US/08252517
; Patent No. 5548065
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,517
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451
; FILING DATE: 19-NOV-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-252-517-2

Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRLLLLVLSVMILETVTNQDLPVKLVLSHENNGSSAGKPSYRWVRGS 60
Db 1 MRALAQRSDRLLLLVLSVMILETVTNQDLPVKLVLSHENNGSSAGKPSYRWVRGS 60
Qy 61 PEDLQCTPRQSEGTVEAATVEVAESGSI TLQVQLATPGDLSCLVWPKHSLGCGPHFD 120
Db 61 PEDLQCTPRQSEGTVEAATVEVAESGSI TLQVQLATPGDLSCLVWPKHSLGCGPHFD 120
Qy 121 LQNRGIVSMALNVTQAGBYLLHIQSERANYTVLFTVNVDTQLYVLRPPYFRKMNQ 180
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Qy 181 DALLCISGVPEPTVEWVLCSSHRESCKEKP VAVRKEEVLHFGTDIRCCARNALGR 240
Db 181 DALLCISGVPEPTVEWVLCSSHRESCKEKP VAVRKEEVLHFGTDIRCCARNALGR 240
Qy 241 ECTKLFITDLNQAQOSTLPQLFLKVGEPFLWIRCKAIHVNHGFGLTWELEDKALESGSYFE 300
Db 241 ECTKLFITDLNQAQOSTLPQLFLKVGEPFLWIRCKAIHVNHGFGLTWELEDKALESGSYFE 300
Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
Qy 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAGPFCBQGLEDDGYSISKFCDHKNKPGYIFY 420
Db 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAGPFCBQGLEDDGYSISKFCDHKNKPGYIFY 420
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Db 424 AENDDAQFTKMTLNIRKKPQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
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Db 481 EGVNKKANRKFVQGWSSSTLNSEAGKLLVKKCAVNSMGTSCTIFLNSPGPFPIQ 540
Qy 541 DNISFYATIGLCLPFIIVLIVLI CHYKQKQRYESQLOMIQVTPGLDNEYFYVDRDYEY 600
Db 541 DNISFYATIGLCLPFIIVLIVLI CHYKQKQRYESQLOMIQVTPGLDNEYFYVDRDYEY 600
Qy 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIOVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIOVAVKMLKEKADSCKEALM 660
Qy 661 SELKXMTLGHHDNIVNLLGACTLSGPPVYLIFEXCCYGDLLNLRKSKREKFRHTWTEIFK 720
Db 661 SELKXMTLGHHDNIVNLLGACTLSGPPVYLIFEXCCYGDLLNLRKSKREKFRHTWTEIFK 720
Qy 721 EHNFSYPTFOAHNSNMPGSGREVQLHPPLDOLSGFNGNSIHSEDEIEYENOKRLAESEE 780
Db 721 EHNFSYPTFOAHNSNMPGSGREVQLHPPLDOLSGFNGNSIHSEDEIEYENOKRLAESEE 780
Qy 781 EDLNVLPFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
Db 781 EDLNVLPFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
Qy 841 SDSSVYVVRGNARLPVKWMAPELSEFEGYITIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 841 SDSSVYVVRGNARLPVKWMAPELSEFEGYITIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Qy 901 FYKLIOGFKMEQPFYATEGYIFVWQSCWAFDSRKRPSFNLTPFLGQLAEBEACIRT 960
Db 901 FYKLIOGFKMEQPFYATEGYIFVWQSCWAFDSRKRPSFNLTPFLGQLAEBEACIRT 960
Qy 961 SIHLPKQAAPQOGLRAQSPQOVKIHRES 992
Db 961 SIHLPKQAAPQOGLRAQSPQOVKIHRES 992

RESULT 5
US-07-906-397A-2
; Sequence 2, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920626
; APPLICATION NUMBER: US/07/906,397A
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-906-397A-2

Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRRLLLLVLSVMILLETVTNODLPVVKCVLISHENNGSSACKPSSYBMRVGS 60
Db 1 MRALAQRSDRRLLLLVLSVMILLETVTNODLPVVKCVLISHENNGSSACKPSSYBMRVGS 60
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Db 61 PEDLOCTPRROSEGTVEAATVEVAESGSI TLQVQLATPGDLSCLWVPKHSLSGCGPHFD 120
Qy 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNVVDTOLYVLRPFRMENQ 180
Db 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNVVDTOLYVLRPFRMENQ 180
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Db 181 DALLICISGEVPEPTVEWVLCSSHRESCKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
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Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCCSSKHPQSALVTILEKGFINATSSQEEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCCSSKHPQSALVTILEKGFINATSSQEEY 360
Qy 361 EIDPYEKECFSVRFKAYPRICTWIFSOASPCBQORGLDGYISKFCDHKNKPGEYIFY 420
Db 361 EIDPYEKECFSVRFKAYPRICTWIFSOASPCBQORGLDGYISKFCDHKNKPGEYIFY 420
Qy 421 AENDDAQFTKMTLNIRKKPQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
Db 421 AENDDAQFTKMTLNIRKKPQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
Qy 481 EGVNKKANRKFVQGWSSSTLNSEAGKLLVKKCAVNSMGTSCTIFLNSPGPFPIQ 540
Db 481 EGVNKKANRKFVQGWSSSTLNSEAGKLLVKKCAVNSMGTSCTIFLNSPGPFPIQ 540
Qy 541 DNISFYATIGLCLPFIIVLIVLI CHYKQKQRYESQLOMIQVTPGLDNEYFYVDRDYEY 600
Db 541 DNISFYATIGLCLPFIIVLIVLI CHYKQKQRYESQLOMIQVTPGLDNEYFYVDRDYEY 600
Qy 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIOVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIOVAVKMLKEKADSCKEALM 660
Qy 661 SELKXMTLGHHDNIVNLLGACTLSGPPVYLIFEXCCYGDLLNLRKSKREKFRHTWTEIFK 720
Db 661 SELKXMTLGHHDNIVNLLGACTLSGPPVYLIFEXCCYGDLLNLRKSKREKFRHTWTEIFK 720
Qy 721 EHNFSYPTFOAHNSNMPGSGREVQLHPPLDOLSGFNGNSIHSEDEIEYENOKRLAESEE 780
Db 721 EHNFSYPTFOAHNSNMPGSGREVQLHPPLDOLSGFNGNSIHSEDEIEYENOKRLAESEE 780

QY 781 EDNLVTFEDLLCFAYQVAKGMEFLEKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
Db 781 EDNLVTFEDLLCFAYQVAKGMEFLEKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 841 SDGSYVVRGNARLPVKWAPESLFEIGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 841 SDGSYVVRGNARLPVKWAPESLFEIGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
QY 901 FYKLIQSGFKMEQPFYATEGIFYFMQSCWAPDSKRSPFNLTSLFGCOLAEEACIRT 960
Db 901 FYKLIQSGFKMEQPFYATEGIFYFMQSCWAPDSKRSPFNLTSLFGCOLAEEACIRT 960
QY 961 SIHLPKQAAPQORGLRAQSPQORVKIHRRS 992
Db 961 SIHLPKQAAPQORGLRAQSPQORVKIHRRS 992

RESULT 6
US-08-601-891-2
Sequence 2, Application US/08601891
Patent No. 5747651
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: InClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-891-2

Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVKVLI SHENNGSSAGKSSYRMVRGS 60
Db 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVKVLI SHENNGSSAGKSSYRMVRGS 60
QY 61 PEDLOCTPROSEGTVEAATVEAEGSITLOVQLATPGDLSCLVFKHSLGCPHFD 120
Db 61 PEDLOCTPROSEGTVEAATVEAEGSITLOVQLATPGDLSCLVFKHSLGCPHFD 120
QY 121 LQNRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNVVRDTQLYVLRFPYFRKMNQ 180
Db 121 LQNRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNVVRDTQLYVLRFPYFRKMNQ 180
QY 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEEKLHELFGTDIRCCARNALGR 240
Db 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEEKLHELFGTDIRCCARNALGR 240
QY 241 ECTKLFTIDLNOAQOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSGYFE 300
Db 241 ECTKLFTIDLNOAQOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSGYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
QY 361 EIDPYEKPCFSVRPKAYPRICRTWIFSOASPCBORGLEDGYSISKFCDHKNKPGYEIPY 420
Db 361 EIDPYEKPCFSVRPKAYPRICRTWIFSOASPCBORGLEDGYSISKFCDHKNKPGYEIPY 420
QY 421 AENDDAQFTKMTLINIRKKPOVLANASASQASCSGDPVLPBSWTWKCSKSDSPNCTEIP 480
Db 421 AENDDAQFTKMTLINIRKKPOVLANASASQASCSGDPVLPBSWTWKCSKSDSPNCTEIP 480
QY 481 EGVNKKANRVFGQWVSSSTLNMSSEAGKLLVKCCAYNSMGTSCTETFLNSPGPPFIQ 540
Db 481 EGVNKKANRVFGQWVSSSTLNMSSEAGKLLVKCCAYNSMGTSCTETFLNSPGPPFIQ 540
QY 541 DNISFYATIGLCLPFIIVLILVLI CHYKQKQRYESQLOMIQVTGPDLDNEYFVDFRDVEY 600
Db 541 DNISFYATIGLCLPFIIVLILVLI CHYKQKQRYESQLOMIQVTGPDLDNEYFVDFRDVEY 600
QY 601 DLKWEFFRENLEFGKVLGSGAGFGRVMNATAYGISKTGYSIOVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFRENLEFGKVLGSGAGFGRVMNATAYGISKTGYSIOVAVKMLKEKADSCKEALM 660
QY 661 SELKWMTHLGHHDNIVLLGACTLSGPVLIIFEYCCYGDLLNLYRSKREKPHRTWTETPK 720
Db 661 SELKWMTHLGHHDNIVLLGACTLSGPVLIIFEYCCYGDLLNLYRSKREKPHRTWTETPK 720
QY 721 EHNFSYPTFOAHNSNMPGSRVQLHPPLDQSGFNCSIHSEDEIEYENOKRLAEEEEE 780
Db 721 EHNFSYPTFOAHNSNMPGSRVQLHPPLDQSGFNCSIHSEDEIEYENOKRLAEEEEE 780
QY 781 EDNLVTFEDLLCFAYQVAKGMEFLEKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
Db 781 EDNLVTFEDLLCFAYQVAKGMEFLEKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 841 SDGSYVVRGNARLPVKWAPESLFEIGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900

Db 841 SSSSVVGRNARLPVKWAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 900
Qy 901 FYKLIQSGFKMEQPFYATGEGYFVMSQWAFDSRKRPSPFNLTSLFLGCOLABAEAEACIRT 960
Db 901 FYKLIQSGFKMEQPFYATGEGYFVMSQWAFDSRKRPSPFNLTSLFLGCOLABAEAEACIRT 960
Qy 961 SIHLPKQAAPQORGGLRAQSPORQVKIHRERS 992
Db 961 SIHLPKQAAPQORGGLRAQSPORQVKIHRERS 992

RESULT 7

US-09-021-324-2
; Sequence 2, Application US/09021324
; Patent No. 5912133
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ithor R.
; TITLE OF INVENTION: TOPIOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,324
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 1992-11-19
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 992 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-021-324-2
Query Match 100.0%; Score 5264; DB 2; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRALAQRSDRRLLLLVLSVMILETVTNODLPVICKVLISHENNGSSAGKPSRYRVRGS 60
Db 1 MRALAQRSDRRLLLLVLSVMILETVTNODLPVICKVLISHENNGSSAGKPSRYRVRGS 60
Qy 61 PEDLOCTPRRQSEGTVEAATVEAEGSITITQVQLATPGDLSCLVKVFVSHSSLCGCPHFD 120
Db 61 PEDLOCTPRRQSEGTVEAATVEAEGSITITQVQLATPGDLSCLVKVFVSHSSLCGCPHFD 120
Qy 121 LQNRGIVSMAILNVTTQAGEYLLHHTQSEBRANYTVLFTVNVRTDQLYVLRPPYFRKWMENQ 180
Db 121 LQNRGIVSMAILNVTTQAGEYLLHHTQSEBRANYTVLFTVNVRTDQLYVLRPPYFRKWMENQ 180
Qy 181 DALLCISEGVPRPTVEWVLCSSHRESCKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
Db 181 DALLCISEGVPRPTVEWVLCSSHRESCKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
Qy 241 ECTKLTIDLNQAPQSTLPQLFKVGEPLWIRCKAIVNVHGFGLTWELDKALEEGSYFE 300
Db 241 ECTKLTIDLNQAPQSTLPQLFKVGEPLWIRCKAIVNVHGFGLTWELDKALEEGSYFE 300
Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYVTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYVTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
Qy 361 EIDPYEKFCSVRFKAYPRICTWIPSOASFPCEQRGBLEDGYSISKFDHKNKPGYIFY 420
Db 361 EIDPYEKFCSVRFKAYPRICTWIPSOASFPCEQRGBLEDGYSISKFDHKNKPGYIFY 420
Qy 421 AENDDAQFTKMTFLNIRKPKQVLANASASQSSDGYPLPSWTWKKCDKSPNCTEIP 480
Db 421 AENDDAQFTKMTFLNIRKPKQVLANASASQSSDGYPLPSWTWKKCDKSPNCTEIP 480
Qy 481 EGVNKKANRKYFGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETILNSPFPFIQ 540
Db 481 EGVNKKANRKYFGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETILNSPFPFIQ 540
Qy 541 DNISFYATTIGLCLPFIVLVILVILCHYKQFRIESOLQMIQVTPGLDNEYFYVDFRDYEY 600
Db 541 DNISFYATTIGLCLPFIVLVILVILCHYKQFRIESOLQMIQVTPGLDNEYFYVDFRDYEY 600
Qy 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
Qy 661 SELKMMTHLGHHDNIIVNLGACTLSGPVYLIPEYCCYGDLLNLYRSKREKFRHTWTETEFK 720
Db 661 SELKMMTHLGHHDNIIVNLGACTLSGPVYLIPEYCCYGDLLNLYRSKREKFRHTWTETEFK 720
Qy 721 EHNFSYPTFOAHSNSMPGSRREVQLHPDLQSGPNGNSIHSEDEIEYENOKRLAEBEE 780
Db 721 EHNFSYPTFOAHSNSMPGSRREVQLHPDLQSGPNGNSIHSEDEIEYENOKRLAEBEE 780
Qy 781 EDNLVLTREDLLCFAYQVAKGMEFEFKSCVHRDLAARNVLVTHGKVKVLCDFGLARDIL 840
Db 781 EDNLVLTREDLLCFAYQVAKGMEFEFKSCVHRDLAARNVLVTHGKVKVLCDFGLARDIL 840
Qy 841 SDSYVVRGNARLPVKWAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 900
Db 841 SDSYVVRGNARLPVKWAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 900
Qy 901 FYKLIQSGFKMEQPFYATGEGYFVMSQWAFDSRKRPSPFNLTSLFLGCOLABAEAEACIRT 960
Db 901 FYKLIQSGFKMEQPFYATGEGYFVMSQWAFDSRKRPSPFNLTSLFLGCOLABAEAEACIRT 960


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Qy 961 SIHLPKQAAPQORGLRAQSPQORQVQKIHRS 992
Db 961 SIHLPKQAAPQORGLRAQSPQORQVQKIHRS 992

RESULT 8
PCT-US92-02750-2
; Sequence 2, Application PC/TUS9202750
; GENERAL INFORMATION:
; APPLICANT: LEMISCHKA, IHOR R.
; TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
; TITLE OF INVENTION: Receptors And Their Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: US
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02750
; FILING DATE: 19920402
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FEIT, IRVING N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02750-2

Query Match 100.0%; Score 5264; DB 5; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRRLLLLVLSVMIETVTNQDLPVVKCVLISHENNGSSAGKPSRYRMVRGS 60
Db 1 MRALAQRSDRRLLLLVLSVMIETVTNQDLPVVKCVLISHENNGSSAGKPSRYRMVRGS 60

Qy 61 PEDLQCTPRRSEGTGYEAATVEVAESGITLQVQLATPGDLSCLVFKHSLGCGQPHD 120
Db 61 PEDLQCTPRRSEGTGYEAATVEVAESGITLQVQLATPGDLSCLVFKHSLGCGQPHD 120

Qy 121 LQNRGIVSMALNVTETQAGEVLLIHQSERANYTVLFTVNVVDTOLYVLRPRYFRKMNQ 180
Db 121 LQNRGIVSMALNVTETQAGEVLLIHQSERANYTVLFTVNVVDTOLYVLRPRYFRKMNQ 180

Qy 181 DALLCISEGVPEPTVEWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
Db 181 DALLCISEGVPEPTVEWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240

Qy 241 ECTKLFTIDLNAQOSTLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALERSGYFE 300
Db 241 ECTKLFTIDLNAQOSTLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALERSGYFE 300

Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTSCSSKHPSQSALVTILEKGFINATSSQEEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTSCSSKHPSQSALVTILEKGFINATSSQEEY 360

361 EIDPYEKFCFSVRFKAYPRIRCTWIFSOASPPCORGLEDGYISKFCPDHKNKPGCEYIF 420
361 EIDPYEKFCFSVRFKAYPRIRCTWIFSOASPPCORGLEDGYISKFCPDHKNKPGCEYIF 420
421 AENDDAQFTKMTNIRKKPOVLNANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
421 AENDDAQFTKMTNIRKKPOVLNANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
481 EGVNKKANRKFVQGWSSSTLNMSSEAGKLLVRCCAYNSMGTSCTETIFLNSPGPFPIQ 540
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541 DNISFYATIGLCLPPIVVLIVLICHYKKQPRYESQLOMIQVTPGLDNEYFVDRDY 600
601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGYSIOVAVKMKLKEKADSCKEALM 660
601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGYSIOVAVKMKLKEKADSCKEALM 660
661 SELKXMTLGHHDNIVNLLGACTLSGPVYLIFCYCCYGDLLNLYLSKREKPHRTWTEIFK 720
661 SELKXMTLGHHDNIVNLLGACTLSGPVYLIFCYCCYGDLLNLYLSKREKPHRTWTEIFK 720
721 EHNFSYPTFOAHNSNMPGSRREVQLHPDLQSLGFGNSIHSEDEIEYENQKRLAESEE 780
721 EHNFSYPTFOAHNSNMPGSRREVQLHPDLQSLGFGNSIHSEDEIEYENQKRLAESEE 780
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781 EDNLVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDPGLARDIL 840
841 SDSSYVVRGNARLPVKWMAPELPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
841 SDSSYVVRGNARLPVKWMAPELPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
901 FYKLQSGFKMEQPFYATEGYIVMQSCWAFDSRKRPFNLTSLFGCOLABAEACIRT 960
901 FYKLQSGFKMEQPFYATEGYIVMQSCWAFDSRKRPFNLTSLFGCOLABAEACIRT 960
961 SIHLPKQAAPQORGLRAQSPQORQVQKIHRS 992
961 SIHLPKQAAPQORGLRAQSPQORQVQKIHRS 992

RESULT 9
PCT-US92-05401-2
; Sequence 2, Application PC/TUS9205401
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05401
; FILING DATE: 19920626
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPTPT
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05401-2

Query Match 100.0%; Score 5264; DB 5; Length 992;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVKCVLISHENNGSSAGKPSRYMRVRS 60
Db 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVKCVLISHENNGSSAGKPSRYMRVRS 60
Qy 61 PEDLOCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVFKHSSLGCPHFD 120
Db 61 PEDLOCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVFKHSSLGCPHFD 120
Qy 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNRDITQYVLRPRYFRKMEQ 180
Db 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNRDITQYVLRPRYFRKMEQ 180
Qy 181 DALLCISGVEPTVEWVLCSSHRESCKEGBPAVVRKEKVLHFGTDIRCCARNALGR 240
Db 181 DALLCISGVEPTVEWVLCSSHRESCKEGBPAVVRKEKVLHFGTDIRCCARNALGR 240
Qy 241 ECTKLTIDLNAQPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
Db 241 ECTKLTIDLNAQPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
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Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSKHPSQSALVTILEKGFNATSSQBEY 360
Qy 361 BIDPYKECFVSRPKAYPRICRTWIFSOAPCEORGELEDGYSISKFDHKNKPGEYIFY 420
Db 361 BIDPYKECFVSRPKAYPRICRTWIFSOAPCEORGELEDGYSISKFDHKNKPGEYIFY 420
Qy 421 AENDDAQFTKMTLIRKKPOVLANASQASCSDDGYPLPSWTWKCSKSPNCTEIP 480
Db 421 AENDDAQFTKMTLIRKKPOVLANASQASCSDDGYPLPSWTWKCSKSPNCTEIP 480
Qy 481 EGVNWKANRKFVQGWVSSSTLNMSAEGKLLVKKCAVNSMGTSCTETPLNSPGPFPIQ 540
Db 481 EGVNWKANRKFVQGWVSSSTLNMSAEGKLLVKKCAVNSMGTSCTETPLNSPGPFPIQ 540
Qy 541 DNISFYATIGLCLPIVVLIVLICHYKKQRYESQLOMIQVTPGLDNEYFVVDPRDYEY 600
Db 541 DNISFYATIGLCLPIVVLIVLICHYKKQRYESQLOMIQVTPGLDNEYFVVDPRDYEY 600
Qy 601 DLKWEFFRENLEFQKVLGSGAFGRVMNATAYGISKTGVSIOAVKMLKEKADSCEKEALM 660
Db 601 DLKWEFFRENLEFQKVLGSGAFGRVMNATAYGISKTGVSIOAVKMLKEKADSCEKEALM 660
Qy 661 SELKQMTHLGHHDNIUNLLGACTLSGPVYLIFEYCCYGDLLNLRSKREKTHRTWTEIFK 720
Db 661 SELKQMTHLGHHDNIUNLLGACTLSGPVYLIFEYCCYGDLLNLRSKREKTHRTWTEIFK 720
Qy 721 EHNFSYPTFOAHNSNMPGSRVOLHPDLQSLGFGNSIHSDEIEIYENQKRLAESEE 780
Db 721 EHNFSYPTFOAHNSNMPGSRVOLHPDLQSLGFGNSIHSDEIEIYENQKRLAESEE 780
Qy 781 EDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 781 EDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Qy 841 SDSSTVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGWNVPYGPVDAN 900
Db 841 SDSSTVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGWNVPYGPVDAN 900

RESULT 10

PCT-US92-09893-2

Sequence 2, Application PC/TUS9209893

GENERAL INFORMATION:

APPLICANT: Lemischka, Ihor R.

TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: ImClone Systems Incorporated

STREET: 180 Varick Street

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/09893

FILING DATE: 19921116

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Feit, Irving N.

REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: LEM-3-7PT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405

TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 992 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-09893-2

Query Match

Best Local Similarity 100.0%; Score 5264; DB 5; Length 992;

Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVKCVLISHENNGSSAGKPSRYMRVRS 60
Db 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVKCVLISHENNGSSAGKPSRYMRVRS 60
Qy 61 PEDLOCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVFKHSSLGCPHFD 120
Db 61 PEDLOCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVFKHSSLGCPHFD 120
Qy 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNRDITQYVLRPRYFRKMEQ 180
Db 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNRDITQYVLRPRYFRKMEQ 180
Qy 181 DALLCISGVEPTVEWVLCSSHRESCKEGBPAVVRKEKVLHFGTDIRCCARNALGR 240
Db 181 DALLCISGVEPTVEWVLCSSHRESCKEGBPAVVRKEKVLHFGTDIRCCARNALGR 240
Qy 241 ECTKLTIDLNAQPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
Db 241 ECTKLTIDLNAQPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300

301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFNATSSOBEY 360
301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFNATSSOBEY 360
361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCQORGLDGYISKFCDHKNKPGGEYIF 420
361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCQORGLDGYISKFCDHKNKPGGEYIF 420
421 AENDDAOFTKMTNIRKPOVLNANASQSCSDGYPLPSWTWKCSKSPNCTEIP 480
421 AENDDAOFTKMTNIRKPOVLNANASQSCSDGYPLPSWTWKCSKSPNCTEIP 480
481 EGVNKKANRKFQOWSSSTLNSEAGKLLVKKCAYNMGTSCTETIFLNSPGFPFIQ 540
481 EGVNKKANRKFQOWSSSTLNSEAGKLLVKKCAYNMGTSCTETIFLNSPGFPFIQ 540
541 DNISFYATIGLCLPFIIVLIVLICHYKQKOPRYESQLOMIQVTPGLDNEYFYVDFRDEY 600
541 DNISFYATIGLCLPFIIVLIVLICHYKQKOPRYESQLOMIQVTPGLDNEYFYVDFRDEY 600
601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
661 SELKQMTLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLRSKREKPHRTWTIFK 720
661 SELKQMTLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLRSKREKPHRTWTIFK 720
721 EHNFSYPTFOAHNSMPSGREGVOLHPPDLQSLGFGNNGSIHSEDEIYENOKRLABEE 780
721 EHNFSYPTFOAHNSMPSGREGVOLHPPDLQSLGFGNNGSIHSEDEIYENOKRLABEE 780
781 EDNLVTFEDLLCFAYQVAKMELEKSCVHRDLAARNVLTGKVVKICDFGLARDIL 840
781 EDNLVTFEDLLCFAYQVAKMELEKSCVHRDLAARNVLTGKVVKICDFGLARDIL 840
841 SDSVYVRGNARLPVKWAPESLPEGIYTIKSDVMSYGILLWEI FSLGWNYPGIPVDAN 900
841 SDSVYVRGNARLPVKWAPESLPEGIYTIKSDVMSYGILLWEI FSLGWNYPGIPVDAN 900
901 FYKLIQSGFKMEQFPYATEGYIFVWQSCWAFDSRKRPSPNLTGFLGQLAEEACIRT 960
901 FYKLIQSGFKMEQFPYATEGYIFVWQSCWAFDSRKRPSPNLTGFLGQLAEEACIRT 960
961 SIHLPKQAPQORGLRAQSPQOVKIHRS 992
961 SIHLPKQAPQORGLRAQSPQOVKIHRS 992

RESULT 11
US-08-222-299-2
; Sequence 2, Application US/08222299
; Patent No. 5635388
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Susan D.
; APPLICANT: Matthews, William
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-299-2

Query Match 96.9%; Score 5102; DB 1; Length 1000;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;

Qy 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVIKCVLISHENNGSSAGKPSVYRMVRGS 60
Db 1 MRALAQRSDRRLLLVLSVMILETVTNQDLPVIKCVLISHENNGSSAGKPSVYRMVRGS 60
Qy 61 PEDLOCTPRQSEGTVEAATVEAEGSITLQVOLATPGDLSCLVKPSHSLGQCPHFD 120
Db 61 PEDLOCTPRQSEGTVEAATVEAEGSITLQVOLATPGDLSCLVKPSHSLGQCPHFD 120
Qy 121 LQNRGIVSMALNVETQAGEYLLHIQSERANYTVLTVNVTRDTQLYVRRPYFRKMEQ 180
Db 121 LQNRGIVSMALNVETQAGEYLLHIQSEAAANYTVLTVNVTRDTQLYVRRPYFRKMEQ 180
Qy 181 DALLCISEGPEPTVEVWVLCSSHRESCKECPAVVRKEEVLHFGTDIRCCARNALQR 240
Db 181 DALLCISEGPEPTVEVWVLCSSHRESCKECPAVVRKEEVLHFGTDIRCCARNALQR 240
Qy 241 ECTKLFTIDLNAQPSLTLPQLFLKVGEPWIRCKAIHVNHGFGLTWELEDKALEBSYFE 300
Db 241 ESTKLFTIDLNAQPSLTLPQLFLKVGEPWIRCKAIHVNHGFGLTWELEDKALEBSYFE 300
Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFNATSSOBEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFNATSSOBEY 360
Qy 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCQORGLDGYISKFCDHKNKPGGEYIF 420
Db 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCQORGLDGYISKFCDHKNKPGGEYIF 420
Qy 421 AENDDAOFTKMTNIRKPOVLNANASQSCSDGYPLPSWTWKCSKSPNCTEIP 480
Db 421 AENDDAOFTKMTNIRKPOVLNANASQSCSDGYPLPSWTWKCSKSPNCTEIP 480
Qy 481 EGVNKKANRKFQOWSSSTLNSEAGKLLVKKCAYNMGTSCTETIFLNSPGFPFIQ 540
Db 481 EGVNKKANRKFQOWSSSTLNSEAGKLLVKKCAYNMGTSCTETIFLNSPGFPFIQ 540
Qy 541 DNISFYATIGLCLPFIIVLIVLICHYKQKOPRYESQLOMIQVTPGLDNEYFYVDFRDEY 600
Db 541 DNISFYATIGLCLPFIIVLIVLICHYKQKOPRYESQLOMIQVTPGLDNEYFYVDFRDEY 600
Qy 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
Qy 661 SELKQMTLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLRSKREKPHRTWTIFK 720
Db 661 SELKQMTLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLRSKREKPHRTWTIFK 720

Qy	721	EHNPSYPTQAHNSNMPGSRVQVUHPPLDQLSGFNGNSIIHSEDEIYEYENQKRLAESEE	780
Db	721	EHNFSYPTQAHNSNMPGSRVQVUHPPLDQLSGFNGNSIIHSEDEIYEYENQKRLAESEE	780
Qy	781	EDNLVITFEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL	840
Db	781	EDNLVITFEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL	840
Qy	841	SDSSYVVRGNARLPVKWMAPESELEFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN	900
Db	841	SDSSYVVRGNARLPVKWMAPESELEFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN	900
Qy	901	FYKLIOSGFKNQEPFYATGEGIFVWQSCWAFOSRKPSPNLTSLFGCOLAEAEACIRI	960
Db	901	FYKLIOSGFKNQEPFYATGEGIFVWQSCWAFOSRKPSPNLTSLFGCOLAEAEACIRI	960
Qy	961	-----SIHLPKAAAPQGRGLRAQSPQRQVKTIRRS	992
Db	961	MGNVPSEPHSIYQNRNPLSREAGS-EPPSPQACVKTIRRS	1000

RESULT 12
US-08-434-878-2
; Sequence 2, Application US/08434878
; Patent No. 5997865
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Susan D.
; APPLICANT: Matthews, William
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

Query Match 96.9%; Score 5102; DB 2; Length 1000;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;
 QY 1 MRALQSRDRLLLVLSVMILETTVTNQDLPTKCVLISHENNNGSSAGKPSSRYMVRGS 60
 |||||

Db	1	MR	A	Q	S	D	R	R	L	L	L	L	L	L	V	S	M	I	L	E	T	V	N	Q	D	L	P	V	I	K	V	L	I	S	H	E	N	G	S	A	K	P	S	Y	M	R	V	G	S	60							
Qy	61	P	E	D	I	O	C	T	P	R	R	O	S	E	G	T	Y	E	A	A	T	V	E	A	S	G	S	I	T	L	Q	V	A	T	P	D	G	I	S	L	C	L	M	V	F	K	H	S	L	G	C	O	P	H	E	120	
Db	61	P	E	D	I	O	C	T	P	R	R	O	S	E	G	T	Y	E	A	A	T	V	E	A	S	G	S	I	T	L	Q	V	A	T	P	D	G	I	S	L	C	L	M	V	F	K	H	S	L	G	C	O	P	H	E	120	
Qy	121	L	O	N	G	I	V	S	M	A	I	N	T	E	T	O	A	G	E	Y	I	L	L	H	T	O	S	E	B	A	N	T	V	L	F	T	V	N	R	D	T	Q	L	Y	V	L	R	P	F	R	K	E	N	Q	180		
Db	121	L	O	N	G	I	V	S	M	A	I	N	T	E	T	O	A	G	E	Y	I	L	L	H	T	O	S	E	B	A	N	T	V	L	F	T	V	N	R	D	T	Q	L	Y	V	L	R	P	F	R	K	E	N	Q	180		
Qy	181	D	A	L	L	C	I	S	E	G	P	E	P	T	V	E	M	L	C	S	H	R	E	S	K	E	B	E	G	P	A	V	R	K	E	K	V	L	H	E	L	F	G	T	D	I	R	C	C	A	R	N	A	L	G	R	240
Db	181	D	A	L	L	C	I	S	E	G	P	E	P	T	V	E	M	L	C	S	H	R	E	S	K	E	B	E	G	P	A	V	R	K	E	K	V	L	H	E	L	F	G	T	D	I	R	C	C	A	R	N	A	L	G	R	240
Qy	241	E	C	T	K	L	F	I	D	N	O	A	P	O	S	T	L	P	O	L	F	K	V	G	E	P	L	W	I	R	C	A	I	H	V	N	H	G	L	T	W	E	L	D	K	A	L	E	G	S	Y	E	300				
Db	241	E	C	T	K	L	F	I	D	N	O	A	P	O	S	T	L	P	O	L	F	K	V	G	E	P	L	W	I	R	C	A	I	H	V	N	H	G	L	T	W	E	L	D	K	A	L	E	G	S	Y	E	300				
Qy	301	M	S	T	Y	T	N	R	T	M	I	R	L	L	A	P	V	S	S	V	G	R	N	D	T	G	Y	T	C	S	S	K	H	P	S	O	S	A	L	V	T	L	E	K	G	F	I	N	A	T	S	S	O	E	Y	E	360
Db	301	M	S	T	Y	T	N	R	T	M	I	R	L	L	A	P	V	S	S	V	G	R	N	D	T	G	Y	T	C	S	S	K	H	P	S	O	S	A	L	V	T	L	E	K	G	F	I	N	A	T	S	S	O	E	Y	E	360
Qy	361	E	I	D	P	E	K	F	C	F	S	V	R	F	K	A	P	R	I	C	T	W	I	E	S	O	A	S	F	C	P	C	E	O	R	G	L	E	D	G	S	I	S	K	F	C	D	H	K	N	K	P	E	Y	E	420	
Db	361	E	I	D	P	E	K	F	C	F	S	V	R	F	K	A	P	R	I	C	T	W	I	E	S	O	A	S	F	C	P	C	E	O	R	G	L	E	D	G	S	I	S	K	F	C	D	H	K	N	K	P	E	Y	E	420	
Qy	421	A	E	N	D	D	A	O	F	T	K	M	F	L	N	I	R	K	K	P	O	V	L	A	N	A	S	O	A	C	S	D	G	Y	P	L	S	W	T	M	K	K	S	D	K	S	P	N	C	T							

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RESULT 13
PCT-US95-03718-2
; Sequence 2, Application PC/TUS9503718
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE ELK2/ELT3 RECEPTOR AND USES T

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 879PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-03718-2

Query Match 96.9%; Score 5102; DB 5; Length 1000;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;
QY 1 MRALAQRDRLLLLVLSWMILETVNQDLPVVKVLI SHENNGSSAGKSSYRMVRGS 60
DB 1 MRALAQRDRLLLLVLSWMILETVNQDLPVVKVLI SHENNGSSAGKSSYRMVRGS 60
QY 61 PEDLOCTPRQSGTVYEAATVEVAESGSLTQVQLATPGDLSCLWVFKHSLGCGQPHD 120
DB 61 PEDLOCTPRQSGTVYEAATVEVAESGSLTQVQLATPGDLSCLWVFKHSLGCGQPHD 120
QY 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVVDTQLYVLRPPYFRKMENQ 180
DB 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVVDTQLYVLRPPYFRKMENQ 180
QY 181 DALLCISEGVPEPTVEVWLCSSHRESCKEGPAVVRKEEVKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISEGVPEPTVEVWLCSSHRESCKEGPAVVRKEEVKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLFITDINOAPQSTLPOLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
DB 241 ESTKLFITDINOAPQSTLPOLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILBKGFINATSSQEEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILBKGFINATSSQEEY 360
QY 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASFPCEORGLDGYISKSCDHKNKPGGEYIFY 420
DB 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASFPCEORGLDGYISKSCDHKNKPGGEYIFY 420
QY 421 AENDDAQFTKMTLINIRKKQVLANASASQSCSDGYPLPSTWTKCKSDKSPNCTEIP 480
DB 421 AENDDAQFTKMTLINIRKKQVLANASASQSCSDGYPLPSTWTKCKSDKSPNCTEIP 480
QY 481 EGVNKKANRKFQGVQWSSSTLNNSEAGKGLLVKCCAYNSMGTSCTIFLNSPGFPFFIQ 540

DB 481 EGVNKKANRKFQGVQWSSSTLNNSEAGKGLLVKCCAYNSMGTSCTIFLNSPGFPFFIQ 540
QY 541 DNISFYATIGLCPLFFIWLIVLICHYKQFRYESOLOMIQVTPLDNNEYFYVDVFRDYEY 600
DB 541 DNISFYATIGLCPLFFIWLIVLICHYKQFRYESOLOMIQVTPLDNNEYFYVDVFRDYEY 600
QY 601 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIOQAVKMLKEKADSCKEKALM 660
DB 601 DLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIOQAVKMLKEKADSCKEKALM 660
QY 661 SELKMMTHLGHNDNIYNLLGACTLSGPPVLIPEYCCYGDLLNLVLSRSEKPHRTWTIEFK 720
DB 661 SELKMMTHLGHNDNIYNLLGACTLSGPPVLIPEYCCYGDLLNLVLSRSEKPHRTWTIEFK 720
QY 721 EHNFSYPTFOAHSNSMPCGSRVQLHPPDQLSGFNGNSIHSEDETEYENQKRLAEEEE 780
DB 721 EHNFSYPTFOAHSNSMPCGSRVQLHPPDQLSGFNGNSIHSEDETEYENQKRLAEEEE 780
QY 781 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
DB 781 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
QY 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVVDAN 900
DB 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVVDAN 900
QY 901 FYKLIOGPKMEQPEYATEGIIYFMOSCAWAFDSKRPSPNLTSLFCGLAEEAEACIRT 960
DB 901 FYKLIOGPKMEQPEYATEGIIYFMOSCAWAFDSKRPSPNLTSLFCGLAEEAEACIRT 960
QY 961 -----SIHLPKQAAPQOGRGLRAQSPQROVKIHRERS 992
DB 961 MCGNVPEHPSPSIQYNNRRLPSREAGS-BPPSPQAQVKIHRERS 1000

RESULT 14
US-08-222-299-4
Sequence 4, Application US/08222299
Patent No. 5635388
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES T
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
PRIOR APPLICATION: 435
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haesk, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 993 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-222-299-4

Query Match 84.3%; Score 4436.5; DB 1; Length 993;
 Best Local Similarity 84.0%; Pred. NO. 0;
 Matches 836; Conservative 59; Mismatches 87; Indels 13; Gaps 4;

Qy 1 MPAALQSDRRLLLVLSVMTLETTNODLPVVKVLSHENNGSSACKPSRYMVRGS 60
 Db 1 MPAALQSDRRLLLVLSVMTLETTNODLPVVKVLSHENNGSSACKPSRYMVRGS 59
 Qy 61 PEDLOCTPRRQSEGTVEAATVEAESGSIITQVOLATPGDLSCLWVFKHSSLCQPHFD 120
 Db 60 PEDLGALRPQSSGTVYEAADVEVDVASITLQVLADPAGNISCLWVFKHSSLCQPHFD 119
 Qy 121 LQNRGIVSMALNVTTQAGEYLLHQSERANYTVLFTVNVVDTQLYVLRPFYFRMENO 180
 Db 120 LQNRGIVSMALNVTTQAGEYLLHQSERANYTVLFTVNVVDTQLYVLRPFYFRMENO 179
 Qy 181 DALLCISEGVPEPTVEWVLCSSHRSCKEEGPAVVRKEEKLHFLPGTDIRCCARNALGR 240
 Db 180 DALVCISEGVPEPTVEWVLCSSHRSCKEEGPAVVRKEEKLHFLPGTDIRCCARNALGR 239
 Qy 241 ECTKLFTIDLNOAQPOSTLPOLFLKGEPLWIRCKAIVHNVHGFGLTWELEDKALEGSYFE 300
 Db 240 ECTRLFTIDLNOAQPOSTLPOLFLKGEPLWIRCKAIVHNVHGFGLTWELEDKALEGSYFE 299
 Qy 301 MSTYSTNRTMIRILAFVSSVGRNDTGYTSSCKHPQSALVTILEKGFINATSSQEEY 360
 Db 300 MSTYSTNRTMIRILAFVSSVGRNDTGYTSSCKHPQSALVTILEKGFINATSSQEEY 359
 Qy 361 EIDPYKECFSVRPKAYRIRCTWTFSQASPCBORGLEDGYSISKFCDHKKKPGYEYIPY 420
 Db 360 EIDQYEEFCFSVRPKAYRIRCTWTFSRSPCEQGLDNGYSISKFCNHKHPQGEYIPH 419
 Qy 421 AENDDAQFTKFTNIRKPOVLANASQASCSDDGYPPLSPMTWKKCSKSPNCTEIP 480
 Db 420 AENDDAQFTKFTNIRKPOVLANASQASCSDDGYPPLSPMTWKKCSKSPNCTEIP 479
 Qy 481 EGVNKKANRVKFGOWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETPLNSPGFPPIQ 540
 Db 480 EGVNKKANRVKFGOWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETPLNSPGFPPIQ 539
 Qy 541 DNIIFYATIGCLPIVVLVILCHYKQRYESQLOMIQVGTGLDNEFYFVDPREDY 600
 Db 540 DNIIFYATIGCLPIVVLVILCHYKQRYESQLOMIQVGTGLDNEFYFVDPREDY 599
 Qy 601 DLKWEFFRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIQAVKMLKEKADSCKEALM 660
 Db 600 DLKWEFFRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIQAVKMLKEKADSCKEALM 659
 Qy 661 SELKQWTHLGHHDNVLNLLGACTLSGPVYLIFEYCCYGDLLNLYSKREKFRHTWTETFK 720
 Db 660 SELKQWTHLGHHDNVLNLLGACTLSGPVYLIFEYCCYGDLLNLYSKREKFRHTWTETFK 719
 Qy 721 EHNFSYPTFOAHNSMPGREGVOLHPLDQLSFGNNGSIHSEDEIEYENQKRLAESEE 780
 Db 720 EHNFSYPTFOAHNSMPGREGVOLHPLDQLSFGNNGSIHSEDEIEYENQKRLAESEE 777
 Qy 781 EDLNVLTPEDLICFAYQVAKGMEFEFFKSCVHRDLAARNVLVTHGVKVKICDPLGARDIL 840
 Db 778 EDLNVLTPEDLICFAYQVAKGMEFEFFKSCVHRDLAARNVLVTHGVKVKICDPLGARDIL 837
 Qy 841 SDSYVVRGNARLPVKWMAPESLFEGITTIKSDVMSYIGILLWEIFSLGWNYPGIPVDAN 900
 Db 838 SDSYVVRGNARLPVKWMAPESLFEGITTIKSDVMSYIGILLWEIFSLGWNYPGIPVDAN 897
 Qy 901 FYKLIQSGFKMEQPPYATGYIFVWQSWAFDSRKRKSPFNLTSLGCOLAEAEACIRT 960
 Db 900 FYKLIQSGFKMEQPPYATGYIFVWQSWAFDSRKRKSPFNLTSLGCOLAEAEACIRT 956

Db 898 FYKLQNGPMDOFPFYATEBIIYIMQSWAFDSRKRKSPFNLTSLGCOLAEAEAMYQ- 956
 Qy 961 SIHLPKQAAP-----QORGGRAQSPQROVK 986
 Db 957 NVDPGVSECPHTYQNRPFSPREMDLGLLSPQAQVE 991

RESULT 15

US-08-434-878-4
 Sequence 4, Application US/08434878
 Patent No. 599785
 GENERAL INFORMATION:
 APPLICANT: Bennett, Brian D.
 APPLICANT: Broz, Susan D.
 APPLICANT: Matthews, William
 APPLICANT: Zeigler, Francis C.
 TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434,878
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: 879
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 993 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-434-878-4

Query Match 84.3%; Score 4436.5; DB 2; Length 993;
 Best Local Similarity 84.0%; Pred. NO. 0;
 Matches 836; Conservative 59; Mismatches 87; Indels 13; Gaps 4;

Qy 1 MPAALQSDRRLLLVLSVMTLETTNODLPVVKVLSHENNGSSACKPSRYMVRGS 60
 Db 1 MPAALQSDRRLLLVLSVMTLETTNODLPVVKVLSHENNGSSACKPSRYMVRGS 59
 Qy 61 PEDLOCTPRRQSEGTVEAATVEAESGSIITQVOLATPGDLSCLWVFKHSSLCQPHFD 120
 Db 60 PEDLGALRPQSSGTVYEAADVEVDVASITLQVLADPAGNISCLWVFKHSSLCQPHFD 119
 Qy 121 LQNRGIVSMALNVTTQAGEYLLHQSERANYTVLFTVNVVDTQLYVLRPFYFRMENO 180
 Db 120 LQNRGIVSMALNVTTQAGEYLLHQSERANYTVLFTVNVVDTQLYVLRPFYFRMENO 179
 Qy 181 DALLCISEGVPEPTVEWVLCSSHRSCKEEGPAVVRKEEKLHFLPGTDIRCCARNALGR 240
 Db 180 DALVCISEGVPEPTVEWVLCSSHRSCKEEGPAVVRKEEKLHFLPGTDIRCCARNALGR 239
 Qy 241 ECTKLFTIDLNOAQPOSTLPOLFLKGEPLWIRCKAIVHNVHGFGLTWELEDKALEGSYFE 300

Db 240 ECTRLFTIDLNOTPOTTLPOLFLKVGSLRCKAVHNRGFLTWELNKALEEGNYFE 299
Qy 301 MSTYSTNRMTIRILLAAVSSVGRNDTCYTCSSSKHPSQSALVTILEKGFINATSSOEY 360
Db 300 MSTYSTNRMTIRILFAFVSVARNDTCYTCSSSKHPSQSALVTIVEKGFINATSSDY 359
Qy 361 EIDPYEKFCSVRPKAYPRIRCTWIFSOASFPCCORGLDGYISKFCDHKNKPGYIFY 420
Db 360 EIDQYEEFCSVRPKAYPOIRCTWTFSRKFPCCQKGLDNGYSISKFCNKHQPGYIFH 419
Qy 421 AENDDAQFTKMTINIRKQVTLANASASQASCSDDGYPLPSWTWKKCSDKSPNCTEIP 480
Db 420 AENDDAQFTKMTINIRKQVTLAEASASQASCSDDGYPLPSWTWKKCSDKSPNCTEIT 479
Qy 481 EGVNKKANRKFQWYSSSTLNMSEAGKLLVKCCAYNSMTSCETIFLNSPGPPFIQ 540
Db 480 EGVNRRKANRKFQWYSSSTLNMSEAKGLVKCCAYNSLGTSCETILLNSPGPPFIQ 539
Qy 541 DNISFYATIGLCLPFIIVLIVLICHKYKQFRYESQLQMIQVGTPLDNEYFYVDFRDEY 600
Db 540 DNISFYATIGVCLLFIIVLILLICHKYKQFRYESQLQMIQVGTSSDNEYFYVDFREY 599
Qy 601 DLKWEFPRENLEFGKVLGSGAFKVMNATAYGISKTVSIQVAVKMLKEXADSCEKALM 660
Db 600 DLKWEFPRENLEFGKVLGSGAFKVMNATAYGISKTVSIQVAVKMLKEXADSEREALM 659
Qy 661 SELKOWTHLGHNDINVLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTBIFK 720
Db 660 SELKOWTQLGSHENIVNLLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTBIFK 719
Qy 721 EHNFSYPTFOAHNSMPSGSRVQLHPPDLDSGFNGNSIHSDEIYEYENOKRLAEEEE 780
Db 720 EHNFSYPTFOAHNSMPSGSRVQLHPPDLDSGFNGNSIHSDEIYEYENOKRLA--EE 777
Qy 781 EDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 778 EDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIM 837
Qy 841 SDSSYVVRGNARLKVWMAPELSEFEGYITIKSDVMSYGILLWEIIFSLGVNYPGIPVDAN 900
Db 838 SDSSYVVRGNARLKVWMAPELSEFEGYITIKSDVMSYGILLWEIIFSLGVNYPGIPVDAN 897
Qy 901 FYKLIQSGFKMEOPFYATEGYFVWQSWAFDSRPSFPNLTSLGCOLAEAEACIRT 960
Db 898 FYKLIQSGFKMEOPFYATEGYFVWQSWAFDSRPSFPNLTSLGCOLADAEAMYQ- 956
Qy 961 SIHLPKQAAP-----QORGLRAQSPQOVK 986
Db 957 NVDGFSVSECPHTYQNRFRPFREMDLGLLSPQAQVE 991

Search completed: May 24, 2003, 17:01:06
Job time : 18.9929 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:53:00 ; Search time 34.5174 Seconds
(without alignments)
2765.606 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVPLLVVFSAM.....PFSREMDLGLLSPOAQVEDS 993

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5238	99.3	993	2	A36873
2	4533.5	86.0	1000	2	S18827
3	4429.5	84.0	992	2	A39931
4	1286	24.4	977	2	I45877
5	1266	24.0	975	1	TVMSKT
6	1263.5	24.0	978	1	A49814
7	1251	23.7	976	1	TVHUKT
8	1226	23.2	954	2	I51703
9	1225.5	23.2	980	1	TVCTMD
10	1218	23.1	941	1	TVVMD
11	1216.5	23.1	972	1	TVHUMD
12	1215	23.0	960	1	JN0677
13	1213	23.0	975	2	T30816
14	1194	22.6	978	2	S16385
15	1183.5	22.4	976	1	TVMSMD
16	1176	22.3	1088	1	PPTHGA
17	1166	22.1	1089	1	PFHUGA
18	1146	21.7	1089	1	S33727
19	1128	21.4	1087	2	I51552
20	1105.5	21.0	1098	1	PFMSRB
21	1086.5	20.6	1106	1	PFHUGB
22	1080	20.5	1048	2	T30815
23	992	18.8	790	1	FOMVHZ
24	990	18.8	1338	2	S09982
25	959.5	18.2	1333	2	I78875
26	956	18.1	1336	2	I60598
27	944.5	17.9	1356	2	JCL402
28	939.5	17.8	1330	2	S49010
29	935	17.7	1348	2	S51656

30	932	17.7	1379	2	JC4954	vascular endotheli
31	923	17.5	1367	2	A41228	protein-tyrosine k
32	907.5	17.2	1363	2	I58375	protein-tyrosine k
33	904.5	17.2	1298	2	A48999	protein-tyrosine k
34	874.5	16.6	823	2	B35963	protein-tyrosine k
35	851	16.1	160	2	A39061	protein-tyrosine k
36	849	16.1	821	1	TVHUF2	fibroblast growth
37	842	16.0	813	1	A49123	fibroblast growth
38	841	15.9	824	2	S24108	protein-tyrosine k
39	836.5	15.9	822	2	A45081	fibroblast growth
40	832.5	15.8	824	2	S36439	fibroblast growth
41	828.5	15.7	769	2	S16236	fibroblast growth
42	828.5	15.7	822	2	A41794	keratinocyte growt
43	827	15.7	797	2	S38579	fibroblast growth
44	825	15.6	821	1	TVMSBK	fibroblast growth
45	823.5	15.6	822	2	B54846	fibroblast growth

ALIGNMENTS

RESULT 1

A36873

protein-tyrosine kinase (EC 2.7.1.112) STK-1 precursor - human

N:Alternate names: stem cell tyrosine kinase 1

C:Species: Homo sapiens (man)

C>Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 04-Feb-2000

C:Accession: A36873

R:Small, D.; Levenstein, M.; Kim, E.; Carow, C.; Amin, S.; Rockwell, P.; Witte, L.; F

Proc. Natl. Acad. Sci. U.S.A. 91, 459-463, 1994

A:Title: STK-1, the human homolog of Fik-2/Fik-3, is selectively expressed in CD34 (+)

A:Reference number: A36873; MUID:94119906; PMID:7507245

A:Accession: A36873

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-993 <SMA>

A:Cross-references: GB:U02687

A>Note: in the authors translation, an additional residue Ala is shown after 420-Ala

C:Genetics:

A:Map position: 13q12

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hon

C:Keywords: ATP; Glycoprotein; phosphotransferase; transmembrane protein; tyrosine-Sg

F:608-950/Domain: protein kinase homology <KIN>

F:616-624/Region: protein kinase ATP-binding motif

Query Match	99.3%;	Score 5238;	DB 2;	Length 993;
Best Local Similarity	99.7%;	Pred. NO. 2.3e-247;		
Matches 991:	Conservative	0;	Mismatches 1;	Indels 2;
				Gaps 2;

QY 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKVLIHKNNDSSVGKSSSYPMYSESP 60

Db 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKVLIHKNNDSSVGKSSSYPMYSESP 60

QY 61 EDLGCALRQSSGTVYAAAVDVVSASITLQVLDAPGNISCLVWFKHSLLNCQPHFDL 120

Db 61 EDLGCALRQSSGTVYAAAVDVVSASITLQVLDAPGNISCLVWFKHSLLNCQPHFDL 120

QY 121 QNRGVSVWLKMTQAGEYLLFTQSEATNTYTLFTVSRINTLLYTLRRPYRKMNQD 180

Db 121 QNRGVSVWLKMTQAGEYLLFTQSEATNTYTLFTVSRINTLLYTLRRPYRKMNQD 180

QY 181 ALVCISESVPEIWEVLCDQSGCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240

Db 181 ALVCISESVPEIWEVLCDQSGCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240

QY 241 CTRLFIDLNQPTQTLPLFLKVGEPILWIRCKAVHNVHFGTLWELENKALEEGNYFEM 300

Db 241 CTRLFIDLNQPTQTLPLFLKVGEPILWIRCKAVHNVHFGTLWELENKALEEGNYFEM 300

QY 301 STYSINRTMIRILFAFVSSVARNDTGYTCSSSKPQSALVTIVGKGFINATNSSDYE 360

Db 301 STYSINRTMIRILFAFVSSVARNDTGYTCSSSKPQSALVTIVGKGFINATNSSDYE 360

A;Reference number: A39931; MUID:91292518; PMID:1648448

A;Accession: A39931

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-992 <MAT>

A;Cross-references: GB:M64689; NID:g193327; PIDN:AAA37634.1; PID:g193328

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki

F;609-953/Domain: protein kinase homology <KIN>

F;617-625/Region: protein kinase ATP-binding motif

Query Match 84.0%; Score 4429.5; DB 2; Length 992;
Best Local Similarity 84.1%; Pred. No. 4.6e-208;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

Qy 1 MPALA-RDAGTVPLLVFAMIFGITNODLPVKVLINHNKNDSSVGKSSSPYMSVS 59

Db 1 MRALAQRRDRLLLVLSVMIETVTNODLPVKVCLISHENGGSSAGKPSRYMVRGS 60

Qy 60 PEDLGCALRPQSSGTYEAAAEVDSASITLQVLVDAPGNISCLVVFKHSSLNCPHPD 119

Db 61 PEDLQCTPRRQSEGTVEAATAVEAESGITLQVLATPGDLSCLVVFKHSSLGCCQHPD 120

Qy 120 LQNRGVSVMLKMTETQAGEYLLFIQSEATNYTLFTVSIINTLLYTLRRPFRKXENQ 179

Db 121 LQNRGIVSMAILNVTTETQAGEYLLFIQSERANYTLFTVNVDRDTQLVLRPFYFRKXENQ 180

Qy 180 DALVCISSEVPPIVVEWVLCDGSGESKEESPAVVKKEKVLHELFGTDIRCCARNEIGR 239

Db 181 DALLCISGVPPTVEWVLCSHRSCKEEGPAVVKKEKVLHELFGTDIRCCARNALGR 240

Qy 240 ECTRLFTDLNQTPTTLPLQLFKVGEPLWIRCKAVHNVHGFGLTWELNKALEEGNYFE 299

Db 241 ECTKLFTDLNAQPOSTLPQLFKVGEPLWIRCKAIHNVHGFGLTWELNKALEEGSYFE 300

Qy 300 MSTYSTNRTMIRILPAFVSVARNDTGYTSCSSKHPSOSALVTIVGKGFINATNSSEY 359

Db 301 MSTYSTNRTMIRILAFVSSVRNDTGYTSCSSKHPSOSALVTILEKGFINATSSQBEY 360

Qy 360 EIDQVEECFVSVRKAYPOIRCTWTTPSRKSFPCEOKGLDNGYSISKFCNKHKQPGYVIFH 419

Db 361 EIDPYKECFVSVRKAYPRICRTWTIPQSAFPCEQGLDNGYSISKFCDHKNKPGYVIFY 420

Qy 420 AENDDAQFTKMTLNIARRPQVLAEASQASCFDGYPLPSWTWKCKSDKSPNCTEET 479

Db 421 AENDDAQFTKMTLNIARKPQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEET 480

Qy 480 EGVNRRKANRKYFGQWVSSSTLNMSAIGKFLVKCCAYNSLGTSCBTILLNSPGPPFIQ 539

Db 481 EGVNRRKANRKYFGQWVSSSTLNMSAIGKFLVKCCAYNSMGTSCTIFLNSPGPPFIQ 540

Qy 540 DNISFYATIGVCLLFTVVLTLIICHYKKQRYESOLQWVQVGTGSSDNEYFYVDREYEX 599

Db 541 DNISFYATIGLCLPFTVVLVLIICHYKKQRYESOLQWVQVGTGPDNIFYVVDREY 600

Qy 600 DLKWEPPRENLEFQVILGSGAFQVNNATAYGISKTVGSIQVAVKMLKEKADSSREALM 659

Db 601 DLKWEPPRENLEFQVILGSGAFQVNNATAYGISKTVGSIQVAVKMLKEKADSSREALM 660

Qy 660 SELKQMTQLGSHENIVNLGACTLGGPIYLIIFYCCYGDLLNLYRSRKPKHRTWTETFK 719

Db 661 SELKQMTLGHHDNI VNLGACTLGGPVYLIIFYCCYGDLLNLYRSRKPKHRTWTETFK 720

Qy 720 EHNFSYPTFOQSHNSMPGSRVQHPDSDQISGLHGNFSHSEDIENQKRL--EE 777

Db 721 EHNFSYPTFOQSHNSMPGSRVQHPDQDLSGFGNGSIHSEDIENQKRLAEESE 780

Qy 778 EDNLVLTREDLLCFAYQVAKGMEFLFKSVHRDLAARNVLTGHKVKIKDQGLARDIM 837

Db 781 EDNLVLTREDLLCFAYQVAKGMEFLFKSVHRDLAARNVLTGHKVKIKDQGLARDIL 840

Qy 838 SDSNTYVVRGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897

Db 841 SDSYVVRGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900

Qy 898 FYKLIQNGFKMDQPFYATEEYIIMQSWAFDSRRKPSFPNLTSLFLGCLADAEAEAMYQN 957

Db 901 FYKLIQSGFKMDQPFYATEGIVFMQSWAFDSRRKPSFPNLTSLFLGCLADAEAEAC--- 957

Qy 958 VQGRVSECHTQVNRPPSPREMDLGLLSQAQVE 991

Db 958 ----IRTSIHLPKQAAPQORG-GLRAQSPQRQVK 986

RESULT 4

I45877

protein-tyrosine kinase (BC 2.7.1.112), receptor type kit precursor - aurochs

C;Species: Bos primigenius (aurochs)

C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Apr-2000

C;Accession: I45877

R;Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.

Gene 141, 305-306, 1994

A;Title: Sequence of a bovine c-kit proto-oncogene cDNA.

A;Reference number: I45877; MUID:94215924; PMID:7512939

A;Accession: I45877

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-977 <KUB>

C;Cross-references: GB:D16680; NID:g516659; PIDN:BAA04084.1; PID:g516660

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolc

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F;329-395/Domain: immunoglobulin homology <IMM>

F;588-932/Domain: protein kinase homology <KIN>

Query Match 24.4%; Score 1286; DB 2; Length 977;

Best Local Similarity 33.2%; Pred. No. 2.7e-55;

Matches 332; Conservative 172; Mismatches 344; Indels 152; Gaps 36;

Qy 47 VKSSSYPMWSSSPEDLGC-ALRPQSSGTYEAAAEVDSASITLQVLVDAPGNISCLW 105

Db 20 VQTGSSQPSV--SPGELSLPSIHPAKS-----ELIVSVGDEIRLLCTDQGFVK--W 66

Qy 106 VPKHSSLNCPHPDLQNRGVSVMLKMTETQAGEYLLFIQSEAT--NYTLFTVSIRN 162

Db 67 TFE-----ILGQLSEKTNPEWIT-EKAEATNTGNTCTNKGGLSS 105

Qy 163 TL-----LYTLRRPYFRKMENODALVCISESVPEPIVWVLCDGSGESCKEESPAV 213

Db 106 SIYVVRDPEKFLDIDLPLYGKEEN-DTLVRCPLTDE-VTVNYSLTGCEGKPLPKDLTFV 163

Qy 214 -----VKKEKVLHELFGTDIRC--CARNELGRE-CTRLFTID----LNQTPQTLTP 258

Db 164 ADPKAGITIRNVKREYHRL-----CLHCSANQRGKSMLSKKFTLVKRAAIKAVPVVSVS 217

Qy 259 Q--LFLKVGEPWLIRCKAVHNVHGFGLTWELNKALEEGNYFEMSTYSTNRTMIRILFAP 316

Db 218 KTSYLLREGEFAVTCILIKDVSSVSDSMWIKENSQOTKAQTKKNSHQGFDFSLQERLT 277

Qy 317 VGSVAANDGYTTCSSSKHPSOSALVT---IVGKGFINA-----TWSSEDIYDQY 364

Db 278 ISSARVNDGSGVFCYANNTFGSANVTITLEVVDKGFINIFPMNNTTVFVNDGENVDL--- 334

Qy 365 BEFCFSVRFKAYPQ-IRCTWTFSRKS-----FPCEQKGLDNGYSISKFCNKHK----- 411

Db 335 -----VVEEAYPKPVHRQWIYNNRTSTDKWDDYPKSE-----NESNIRYVNELHLTRLK 384

Qy 412 --OPGEYIIFHAENDDAQFTMFTLNIRRPQVLAESA--SQASCFSDGYPPLPSWTWKCC 467

Db 385 GTEGGTYTFHVSNDVNSSTVFNVVYNTKPEILTHDRLVNGLMLQCVAAGFPPEPTIDWYFC 444

Qy 468 SDKSPNCTEEI-TEGVNRRKANRKYFGQWVSSSTLNMSAIGKFLVKCCAYNSLGTSCET 526

Db 445 PGTEQRCSVPVGVVDVQIQNSSVSPFGKLVVYSTIDDSFTFKNGTVECRAYNDVGKSSAS 504

Qy 527 ILLNSPGPPP-----FTQDNISFYATIGVCLLFTVVLTLIICHYKKQRYESOLQM 578

Db 505 FNFAFGKSGKEQIHAHTLFTPLLLGVIAAGLMCFVMMILT----YKLLQKPMYEQWKV 560
Qy 579 V-QVTGSSDNFYVDPREYEDLQWEPRENLEFGKVLGSCAFGKVMNATAYGSKTGV 637
Db 561 VEEING--NNVYIDPTQLPYDHWKPEPRNLSFGKTLGAGAFKGVVATAYGLIKSDA 617
Qy 638 SIQAVKMLKEKADSSEREALMSLKMTQGLSHENIVNLLGACTLSGPIYLIIFYCCYVG 697
Db 618 AMTAVKMLKPSAHLTEREALMSLKVLKSYLGNHNVNLLGACTIGGPTLVITYCCYVG 677
Qy 698 DLLNVLRSKREKPHRTWTE-----IFKEHNFSFPTTPOSHNSM---PGSRVQIHPD 748
Db 678 DLLNFLRRKRDSFICSKQEDHAVALYKLLNLSKSSCNDSTNEYMDMKPGVSYV-VPTK 736
Qy 749 SDQISGLHNSPHSEDEIYENQKLEEREEDLNVLTFEDLLCFAYQVAKMGFLRPSKCV 808
Db 737 ADKRSARIGSY-----IERDVTPTAIMEDEL-ALDELLSFSYQVAKGMFLASKNCI 790
Qy 809 HRDLAARNVLVTHGKVKICDFGLARDIMSDSNVYVVRGNARLPVKWMAPESEFEGIYTIK 868
Db 791 HRDLAARNILLTHGRITKICDFGLARDIKDSDNVYVVRGNARLPVKWMAPESEFNCVYTFE 850
Qy 869 SDVWSYGILLWEIFSLGNVPYGPVANDANFYKLIQNGFKQDOPFYATEHIYIMOSWAF 928
Db 851 SDVWSYGIFLWELFSLGSPYGPMPVDSKFKYKWKIEGFRMLSPHAPAEYMDIMKTCWDA 910
Qy 929 DSRKPSFNLTSLFGCOLADAEABAMYNQVGRVSEC-PH 967
Db 911 DPLKRPFTKQIVOLIEKQISESTNNHIYSN-----LANCSPH 946

RESULT 5
TVMSKT
Protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - mouse
N;Alternate names: tyrosine kinase receptor c-kit
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text_change 31-Mar-2000
A;Accession: S00474; B44876; I49596
R;Qiu, F.; Ray, P.; Brown, K.; Barker, P.E.; Jhanwar, S.; Ruddle, F.H.; Besmer, P.
EMBO J. 7, 1003-1011, 1988
A;Title: Primary structure of c-kit: relationship with the CSF-1/PDGF receptor kinase fa
A;Reference number: S00474; PMID:88296403; PMID:2456920
A;Accession: S00474
A;Molecule type: mRNA
A;Residues: 1-975 <QIU>
A;Cross-references: GB:Y00864; NID:950423; PIDN:CAA8772.1; PID:g50424
R;Rossi, P.; Marzitali, G.; Albanesi, C.; Charlesworth, A.; Geremia, R.; Sorrentino, V.
Dev. Biol. 152, 203-207, 1992
A;Title: A novel c-kit transcript, potentially encoding a truncated receptor, originates
A;Reference number: A44876; MUID:92331813; PMID:1378413
A;Accession: B44876
A;Molecule type: DNA
A;Residues: 771-814 <ROS>
A;Note: sequence extracted from NCBI backbone (NCBIN:108837, NCBI:108840)
R;Yasuda, H.; Galli, S.J.; Geissler, E.N.
Biochem. Biophys. Res. Commun. 191, 893-901, 1993
A;Title: Cloning and functional analysis of the mouse c-kit promoter.
A;Reference number: I49596; MUID:93221533; PMID:7682073
A;Accession: I49596
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:L11358; NID:g293325; PIDN:AAA37420.1; PID:g293326
C;Genetics:
A;Gene: kit; c-kit
A;Map position: 5
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP, autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-975/Product: protein-tyrosine kinase kit #status predicted <KTC>
F;23-519/Domain: extracellular #status predicted <EXT>
F;51-100/Domain: immunoglobulin homology <IMM1>

F;130-189/Domain: immunoglobulin homology <IMM2>
F;227-295/Domain: immunoglobulin homology <IMM3>
F;331-397/Domain: immunoglobulin homology <IMM4>
F;426-496/Domain: immunoglobulin homology <IMM5>
F;520-542/Domain: transmembrane #status predicted <TM>
F;543-975/Domain: intracellular #status predicted <INT>
F;586-929/Domain: protein kinase ATP-binding motif
F;594-602/Region: 431-494/Disulfide bonds: #status predicted
F;58-98,137-187,234-293,431-494/Binding site: carbohydrate (Asn) (covalent) #status
F;146,296,303,323,355,370,466,489/Binding site: Lys, Glu, Asp #status predicted
F;622,639,790/Active site: magnesium (Asn, Asp) #status predicted
F;795,808/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 24.0%; Score 1266; DB 1; Length 975;

Best Local Similarity 33.2%; Pred. No. 2.5e-54;

Matches 336; Conservative 173; Mismatches 330; Indels 172; Gaps 41;

Qy 35 CVLINHKNDSVGVSSYPMVSESPEDLGICALRPOSSGTVVEAAAVDVDSITLQVL 94

Db 12 CVLLVLLRGQTATSPASPGSPSP-----SIHPAQ-----ELIVEAGDTL--- 54

Qy 95 VDAPGNISCL-----WVFKHSLNCQPHFDLQNRGVSVMLKMTETQAGEYLLFTQSE 148

Db 55 -----SLTICIDPDFVRWTFK-----TYFN-----EMVENKKNWIQ-EKAE 89

Qy 149 ATNYTILFTVSRNTL-----LYTLRRPYFRKMNQDALVCISESVSPPIVE 195

Db 90 ATR-TGTYTCNSNGLTSSIIYVVRDPKFLVGLPLFGK-EDSDALVRCPLTDPO-VSN 146

Qy 196 WVLCDQSGESKEESPAV-----VKKEKVLHLEFGTDIRCCARNELGRCTRL--- 244

Db 147 YSLIECDGKSLPTDLTFVDPNPKAGITIKVKKRAYHRLC---VRCAAQ-----RDGTWLHSD 199

Qy 245 -PTIDLNTQ-----PQTLPLQL--FLKVGELPLWIRCKAVHNVHGFGLTW-----E 286

Db 200 KFTLVKREAIKAPVSVSPETSHLLKKGDTFTVCTIKDVSTSVNSWLKKNPQPOHIAQ 259

Qy 287 LENKALEEGNPEMSTYSTNRTMIRILFAFVSSVARNDGYTYTSSSKHPSQSALVT--- 343

Db 260 VKHNSWHRGDF-----NYERQETLT-----ISSARVDDSGVFCVYANNTFGSANVTTLK 309

Qy 344 IVKGKGFNATN-SSBDEYIDQVEEFCFVRKAYPO-IRCTWTFSRKSPFCEOKGLD--- 398

Db 310 VVEKGFNINISPVKNTTVFTDGENVDLVVEYAYPKPEHQOYIMNRT--SANKGKDYVK 367

Qy 399 -NGYSISKECNKH-----OPGEYIHAENDDAQTKMFTLINIRKPOVLA--EASAS 448

Db 368 SDNKNIRYVYNQLRLTLKGTGGTYTFLVNSDASASVTFFVYVNTKPEILTYDRLING 427

Qy 449 QASCFSDGYPLPSWTWKCKSDKSPNCTEITE-GVMNRKANRVFGQWVSSSTLNKSEAI 507

Db 428 MLCQVAEGFPEPTIDWYFCTGAEQRTTPVSPVDVQVQVSVSPFCKLVVQSSIDSVFR 487

Qy 508 KGFVLKCCAYNSLGTSCETILLNSPGPPF---IQDN-----ISFYATIGVCLLPVIV 557

Db 488 HNGTVECKASNDVGKS--SAFFN-----PAFKEIQIQAHTLPTPLLIGFVVAAGAIIVMV 541

Qy 558 LTLICHYKQKFRYBSLOMV-QVTGSSDNEYFYDPREYEDLQWEPRENLEFGKVL 616

Db 542 LT-----YKLLQKPMYEQWKVVEEING---NNVYIDPTQLPYDHWKPEPRNLSFGKTL 594

Qy 617 GSGAFKVMNATAYGISKTVGSIOAVKMLKEKADSSEREALMSLKMTQGLSHENIVN 676

Db 595 GAGAFKGVVATAYGLIKSDAAMTAVKMLKPSAHLTEREALMSLKVLKSYLGNHNVN 654

Qy 677 LLGACTLSGFIYLIIFYCCYCGDLLNLYRSKREKF-----HRTWTEIFKEHNFSFYPTFQ 730

Db 655 LLGACTVGGTTLVITEYCCYCGDLLNFLRRKRDSFIFSKQEEQAEAAALYKLLHSTBSCD 714

Qy 731 SHPNSSM---PGSRVQIHPDSDQISGLHNSPHSEDEIYENQKLEEREEDLNVLTFED 787

Db 715 S-SNEYMDMKPGVSYV-VPTKTDKRRSARIDSY-----IERDVTPTAIMEDEL-ALDLD 766

Qy 788 LFCAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDNSVTVVRGN 847
Db LLSFSYQVAKAMFLASKNCHIRDLAARNILITHGRITKICDFGLARDIRNDSNVTVVRGN 826
Qy 848 ARLPVKMAPELSEFGIYITIKSDVWSYGILLWEIFSLGWNVPYGGIPVDANFYKLQNGPK 907
Db 827 ARLPVKMAPELSEFGIYITIKSDVWSYGILLWEIFSLGWNVPYGGIPVDANFYKLQNGPK 886
Qy 908 MDQPFYATYEEIYIMOSCAWFDSDRSPFNLTSLGQQLADAEAMYNQV 958
Db 887 MVSEPHAEAMVDVMTCDADPLKRPFTKQVQVQLIEKQISDSTKHIIYNSL 937
RESULT 6
A49814
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A49814; S49088
R:Tsujimura, T.; Hirota, S.; Nomura, S.; Niwa, Y.; Yamazaki, M.; Tono, T.; Morii, E.; Kitajima, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.
Blood 78, 1942-1946, 1991
A:Title: Characterization of Ws mutant allele of rats: a 12-base deletion in tyrosine kinase gene
A:Reference number: A49814; MUID:92003944; PMID:1912577
A:Accession: A49814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-978 <TSU>
A:Cross-references: GB:D12524; NID:g220707; PID:BAA02094.1; PID:g220708
R:Tsujimura, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.
submitted to the EMBL Data Library, October 1991
A:Description: Two isoforms of rat c-kit receptor tyrosine kinase.
A:Reference number: S49088
A:Accession: S49088
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511,516-978 <TS2>
A:Cross-references: EMBL:X62491; NID:G509135; PID:CAA44354.1; PID:G509136
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology
C:Keywords: ATP; autophosphorylation; phosphotransferase; tyrosine-specific protein kinase
F:129-188/Domain: immunoglobulin homology <IMH>
F:589-932/Domain: protein kinase homology <KIN>
F:597-605/Region: protein kinase ATP-binding motif

Query Match 24.0%; Score 1263.5; DB 1; Length 978;
Best Local Similarity 33.8%; Pred. No. 3.4e-54;
Matches 334; Conservative 171; Mismatches 361; Indels 121; Gaps 37;
Qy 35 CVLINHKNDSVSGKSSYPMVSESPDLGCLALPQSGTVYEAADVVDVVSASITLQVL 94
Db 12 CVLLVLLRGQTGTSQPSASPGPPSP-----SIQPAQS-----ELIVEAGDTIRLT 57
Qy 95 VDAPGNISCLMVFKHSLNCPHFLQNRGVVSVILKYTE--TQAGEYLLFIQSEATNYT 153
Db 58 CTDPAFVK--WTFE-----ILDVRIENKQSEWIREKAEATHYTKYTCVSGSGLRSSI 107
Qy 154 ILFTVSIIRN--TLTYLRPRYFRKMNQDALVCISVSPVPIVEWVLCDSQGSCKEESPA 212
Db 108 YVF---VSDPAVLFLVGLFLFK--EDNALVRCPLTDQ--VSNYSLEICDGLSLPTDLKF 162
Qy 213 V-----VVKBEKVLHLEFOTDIRCCARNELGRECTRLFTID-----LNQPTPTLQOL 260
Db 163 VNPKGAGITIKNVKAYHRLC---IRCAQREGKWMRSDKFTLKVRAAIKAIPIVVSVPET 219
Qy 261 --FLKVGELMTRCAVHVNHGFLTW-----ELENKALEEGNYFEMS--TYSTNRTMIR 311
Db 220 SHLLKEGDTFTVICTIKDVSTVSDVMWIKLNPQPOKQAKVNSHQGDGFNYEROETLT- 278
Qy 312 ILFAPVSSVARNDTGYYTCSSSKHPSQALVT---IVGKGFIN---ATNSSSDYIDQVE 365
Db 279 -----ISSARVNDSGVFWCYANTGSAVNTTLKVEKGFINIPVKNT--VFVTDGE 331
Qy 366 EFCFSVRFKAYPQ--IRCTWTFSRKSPCEQKGLD-----NGYSISKFCNKKH-----OP 413

Db 332 NVDLVVEFEAYPKPHQOQIYNMRT--PTNRGDEVKSNQSNIRYVNEIRLTRKLGTEG 389
Qy 414 GEYIIFHAENDDAQTKMFTLNIRRKPOVLA--EASASQACSFSDGYPLPSWTWKCSDKS 471
Db 390 GYITFLVNSDVASVTFDYYVNTKPEILTYDLNMRGLQCVAAAGPEPTIDWYFCTGAE 449
Qy 472 PNCETBEITE-GVMNRKANRKFQGWSSSTLNMBSAIGFLVKCCAYNSLGTSCETILLN 530
Db 450 QRCTVPVPVPDVQIQNASVSPGKLWVQSSIDSSVFRHNGTVECKASNAVGKS--SAFFN 507
Qy 531 SPGPFPF-----IODN-----ISFYATIGVCLLFIWVLTLLCHIKYKQFRYESOL 576
Db 508 ----FAFKGNSKQIQPHLTFTPLLIGFVVYTAG--LMGIIVMWL--AYKYLQKPMYEVQW 559
Qy 577 QMV-QVTSSDNEYFYDFREYEDLKWEFFRENLEFGKVLGSGAFGKVMNATAYGISTK 635
Db 560 KVEEING---NNYVYIDPTQLPYDHKWEFFRNRLSFGKTLGAGAFKGVKVEATAYGLIKS 616
Qy 636 GVSIOVAVKMLKEKADSSEREALMSELKMMTQGLGSHENIVNLLGACTLSGPIYLIFEYCC 695
Db 617 DAAMTVAVKMLKPSAHLTEREALMSELKVLVSLGNHNNIVNLLGACTVGGPTLVITEYCC 676
Qy 696 YGDLNLNLRKREKPHRTWTEIFKHNFSFYTFQSHPNSSMPGSRV-VQIHDPDSQISG 754
Db 677 YGDLNLFRRKDSF--IFSQEQEADAALYKNLLHSESSCDSSNMYMDMKFGVSYVVP 734
Qy 755 LHGNSFHS---EDEIYEYENQKRELEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRD 811
Db 735 TKTDKRSARIDSYIERDVTTPAIMEDEL-ADLELLSFSYQVAKGMAFLASKNCIHRD 793
Qy 812 LAARNVLVTHGKVKICDFGLARDIMSDNSVTVVRGNARLPVKWMAPELSEFGIYITIKSDV 871
Db 794 LAARNILLTHGRITKICDFGLARDIRNDSNVTVVRGNARLPVKWMAPELSEFGIYITIKSDV 853
Qy 872 WSYGILLWEIFSLGWNVPYGGIPVDANFYKLQNGKMDQPFYATEBIYIMOSCAWFDSDR 931
Db 854 WSYGIFLWELFSLGSPYGPMPVDSKFKYMKIEGFRMLSPHAPAAAYEVMKTCWDADPL 913
Qy 932 KRPSFENLTSFLGCOLADAEAMYNQV 958
Db 914 KRPTFKQVQLIEKQISDSSKHHIYNSL 940
RESULT 7
TVHUKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human
N:Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jul-2000
C:Accession: S01426; PC1015; A41815; B41815; C41815; I37948; I56954; I54336
R:Yarden, Y.; Kuang, W.J.; Yang-Feng, T.; Coussens, L.; Munemitsu, S.; Dull, T.J.; Ch-
EMBO J. 6, 3341-3351, 1987
A:Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for
A:Reference number: S01426; MUID:88111521; PMID:2448137
A:Accession: S01426
A:Molecule type: mRNA
A:Residues: 1-976 <YAB>
A:Cross-references: GB:X06182; NID:g34084; PIDN:CAA29548.1; PID:g34085
R:Hu, W.X.; Cornu, F.; Andre, C.; Gallibert, F.
Chinese Biochem. J. 7, 618-629, 1991
A:Title: Nucleotide sequence of two neighbouring fragments of human c-kit proto-oncoge-
A:Reference number: PC1015
A:Accession: PC1015
A:Molecule type: DNA
A:Residues: 412-713 <HUG>
A:Note: article in Chinese with English abstract
R:Spritz, R.A.; Giebel, L.B.; Holmes, S.A.
Am. J. Hum. Genet. 50, 261-269, 1992
A:Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cel-
A:Reference number: A41815; MUID:92133600; PMID:1370874
A:Accession: A41815
A:Molecule type: DNA
A:Residues: 579-583, 'L', 585-589 <SPR>

RESULT 8

151703
c-kit-related kinase 1 (Xkrkl) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C:Accession: I51703
R:Baker, C.V.; Sharpe, C.R.; Torpey, N.P.; Heasman, J.; Wylie, C.C.
Mech. Dev. 50, 217-228, 1995
A:Title: A Xenopus c-kit-related receptor tyrosine kinase expressed in migrating stem cells
A:Reference number: I51703; MUID:95344996; PMID:7619732
A:Accession: I51703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-954 <BAK>
A:Cross-references: EMBL:Z48770; NID:G763033; PIDN:CAA8688.1; PID:G763034
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP
F:575-915/Domain: protein kinase homology <KIN>
F:583-591/Region: protein kinase ATP-binding motif

Query Match 23.2%; Score 1226; DB 2; Length 954;
Best Local Similarity 33.1%; Pred. No. 2.2e-52;
Matches 305; Conservative 162; Mismatches 322; Indels 132; Gaps 30;

QY 107 FKHSLLNCPHDLQNRGVVS-----MVLKMTQAGEYLLFIQSEATNYTLTFTVSI 160
DB 52 FQKSLMKKPR-DLKSRLNNSETDQFFVIRKADLRHIGRYICTTQENTSV--SLFV 108
QY 161 RNTLLYTLRRPFRKMNEDALVCISVPEPIVENVLCDQSGESCKE-----ESPA 212
DB 109 KDPAPFLDIPIDVTEGADTVGMCFPTDPMIDIAIEKCD--GSPLENFTTTDIEAGI 166
QY 213 VYKKEKVLHFLGTDIRCCARNELR--BCTRLFTIDLNQTTLPQLFL-----KV 264
DB 167 TIKTQLAPDSCV-----VCSGNKSGTVKKSSTFSIHVKPVK-KVPTVFLSKSRVLVT 220
QY 265 GEPLMIRKAVVNHGFLTW-ELENKALEBNGYEMSTYSTNRTMIRILFAPVSSVARN 323
DB 221 GEFFETCAVLDFVSTFKAQMLDVKEGTVKQANFRSSNVFSYNLTLS-----DGVPS 274
QY 324 DTGYTCSSSKHPSO---SALVTIVKGFINAT--NSSEDEYDQVEEFCFSVRKAYPO- 378
DB 275 ESRTTQAEANAIGQVNAFTLDVLDVGVNLTUVENTTISVAGNVLKVIYIDAYHPH 334
QY 379 IRCTWTFRSPCKQKGLDNGYSISK-----FCNHKH-----QPGEYIFHAENDDA 425
DB 335 DGVVWTFNETHL---LNTSDHYVATKDEGNRYVSELHLRLKTEKGVYTFYTNSD 390
QY 426 QTKMPTNIRKPKQVLAESASQAS--CFSDGYPLPSWTWKCKSDKSNCTEETEGVM 483
DB 391 DASVFNIOQVTRPEILIAERTSEGLQCVATGFPVPAIQWYFCPGEQRCTDYPLSPV 450
QY 484 NRK--ANRKFQGVSSSTLWNSAIEKGLVKCCAYNSLGTSCETILLNSPGFPFP-1QD 540
DB 451 NEKFTQENSLGRIVVESTIDVNDLKKGTQVOCVASNEVESAYSV-----SFPAKE 502
QY 541 N-----ISFYATIGVCLLPIVLTLLIHKYKKQFRESQLOMV-OVTGSSDNE 588
DB 503 KLRTHTLTPLLIGIAAGLACIAVAVL---MYKLQKPKYELQWKVVEING--NN 555
QY 589 YFYVDPRYEYDLKWEPPRENLEFGKVLGSGAFGKVMNATAYGSKTGVSIQVAVKMLE 648
DB 556 YVYIDPTQLPDNKEFPRDLRCFGLKAGAFGKVEATAYGLLKEDSRLLTVAVKMLKP 615
QY 649 KADSSERAAKMTQGLSHENIVNLGACTLSGPIYLIIFYCCYGDLLNLYRSKRE 708
DB 616 SAHSTERAAKSELKVLGYLGHKKNVNLGACTVGGPLVITEYCCYGDLLNLYRRKRD 675
QY 709 KFHRTWTEIFKEHNFSTFOSHNS-----SMGPSREVQIHPDSDOI----- 752
DB 676 SF-----ICPKEDNSEAALYKNLLNTRDMGCEGMSEYIDMKPAVSIVVPT 721
QY 753 --SGLHNSFHSDEIEYENOKRLEEDLNVLTFEDLLCFAYQVAKGMFELEFKSCVHR 810

RESULT 9

TVCTMD

macrophage colony-stimulating factor 1 receptor precursor - cat

N:Contains: protein-tyrosine kinase (EC 2.7.1.112) csflr/fms

C:Species: Felis silvestris catus (domestic cat)

C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 13-Jun-1997

C:Accession: A31636

R:Woolford, J.; McAuliffe, A.; Rohrschneider, L.R.

Cell 55, 965-977, 1988

A:Title: Activation of the feline c-fms proto-oncogene: multiple alterations are req

A:Reference number: A31636; MUID:89077553; PMID:2849512

A:Accession: A31636

A:Molecule type: mRNA

A:Residues: 1-980 <WOO>

A:Cross-references: EMBL:X03663

C:Genetics:

C:Gene: fms

C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homol
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote
fic protein kinase

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-980/Product: macrophage colony-stimulating factor 1 receptor #status predicted <

F:24-509/Domain: extracellular #status predicted <EXT>

F:35-86/Domain: immunoglobulin homology <IMM1>

F:120-179/Domain: immunoglobulin homology <IMM2>

F:217-280/Domain: immunoglobulin homology <IMM3>

F:316-381/Domain: immunoglobulin homology <IMM4>

F:410-484/Domain: immunoglobulin homology <IMM5>

F:510-534/Domain: transmembrane #status predicted <TMW>

F:535-980/Domain: intracellular #status predicted <INT>

F:577-915/Domain: protein kinase homology <KIN>

F:585-593/Region: protein kinase ATP-binding motif

F:42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted

F:45,73,94,153,275,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #s

F:613,630,776/Active site: Lys, Glu, Asp #status predicted

F:781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 23.2%; Score 1225.5; DB 1; Length 980;

Best Local Similarity 33.5%; Pred. No. 2.4e-52;

Matches 321; Conservative 168; Mismatches 321; Indels 149; Gaps 34;

QY 83 VDVSAITLOVLVDAPGNISCLW---VFKHSSLNCOOP-----HFDLQNRGVSNMVL 131

DB 32 VEPGTTVTLRCV---GNGSVEMDGPISPHNLDLDPSSILTTNNATFQNTYHCT-- 85

QY 132 KMTETQAGEYL--LFTQSEATNYTL---FTVSIRNTLYTLRRPYFRKMNEDALV-CI 195

DB 86 EFGNFQGNATHLVKDPARPKVKLAQEVTV-----LEGODALLPCL 128

QY 186 SSVSPEPIVE--WVLCDQSGESCKEE-----SP---AVVKEEKVLHFLFGTDIRCCARN 235

DB 129 ---LTDPALEAGVSLVRGRVPLQTNYSFSPWHGFTTHKAKFIENHYV-----QCSARV 191

QY 236 ELGRCTRI-----FTIDLNTQPTTL-PQLFKV-GEPLWIRCKAVVNHGFLGTLWELE 288

DB 182 D-GRVTVSMIGLWKVKQKDISGPATLTLEPAELVRIQGEAAQVCSASNDVNFV---- 235

Qy 836 IMSDSNVVRGNARLPVKWMAPELFEIGYTIKSDVMSYGLLWELPSLGUNPYGPIVD 895
 Db 801 IMSDSNVYKGNARLPVKWMAPELFEIGYTIKSDVMSYGLLWELPSLGUNPYGPIVD 860
 Qy 896 ANFYKLIQNGFMKDOFFYATBIYIMOSWAFDSRKPSPNLTSLFGCLQADAEEMY 955
 Db 861 SKFYKLVKDGVCMAQAPAPKNIYSIMQACWALETRPTTQICSLQKQ---AQE--- 914
 Qy 956 QNVGRV---SECPTYQNR--RPF 975
 Db 915 ---DRRVENYTNLPSSSSSRLRPW 936

RESULT 11
 TVHMD
 macrophage colony-stimulating factor 1 receptor precursor - human
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
 C:Species: Homo sapiens (man)
 C>Date: 28-Dec-1987 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
 C:Accession: S08123; A24533; I56672; I57648; I59083; I52772
 R:Hampe, A.; Shamoon, B.M.; Gobet, M.; Sherr, C.J.; Galibert, F.
 Oncogene Res. 4, 9-17, 1989
 A:Title: Nucleotide sequence and structural organization of the human FMS proto-oncogene
 A:Reference number: S08123; UID:892339490; PMID:2524025
 A:Accession: S08123
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-972 <HAM>
 A:Cross-references: GB:U63963; EMBL:X14720; NID:G1915975; PIDN:AA851696.1; PID:G1915976
 A:Note: this sequence was submitted to the EMBL Data Library March 1989
 R:Cousens, L.; Van Beveren, C.; Smith, D.; Chen, E.; Mitchell, R.L.; Isacke, C.M.; Verma
 Nature 320, 277-280, 1986
 A:Title: Structural alteration of viral homologue of receptor proto-oncogene fms at carb
 A:Reference number: A24533; UID:86175013; PMID:2421165
 A:Accession: A24533
 A:Molecule type: mRNA
 A:Residues: 1-53, 'A', 55-972 <COU>
 A:Cross-references: GB:J03149
 A:Note: the authors translated the codon GCA for residue 54 as Pro
 R:Wheeler, E.F.; Roussel, M.F.; Hampe, A.; Walker, M.H.; Fried, V.A.; Look, A.T.; Retter
 J. Virol. 59, 224-233, 1986
 A:Title: The amino-terminal domain of the v-fms oncogene product includes a functional s
 sequences.
 A:Reference number: I56672; UID:86281820; PMID:3525854
 A:Accession: I56672
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RES>
 A:Cross-references: GB:M14002; NID:G182676; PIDN:AAA35849.1; PID:G553292
 R:Visvader, J.; Verma, I.M.
 Mol. Cell. Biol. 9, 1336-1341, 1989
 A:Title: Differential transcription of exon 1 of the human c-fms gene in placental troph
 A:Reference number: I57648; UID:89261741; PMID:2524648
 A:Accession: I57648
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-16 <RES>
 A:Cross-references: GB:M25786; NID:G349454; PIDN:AAA58421.1; PID:G553224
 R:Browning, P.J.; Bunn, H.F.; Cline, A.; Shuman, M.; Nienhuis, A.W.
 Proc. Natl. Acad. Sci. U.S.A. 83, 7800-7804, 1986
 A:Title: Replacement of COOH-terminal truncation of v-fms with c-fms sequences markedly
 A:Reference number: I59083; UID:87017034; PMID:3532121
 A:Accession: I59083
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 874-972 <RES>
 A:Cross-references: GB:M14193; NID:G182521; PIDN:AAA35834.1; PID:G182522
 R:Nienhuis, A.W.; Bunn, H.F.; Turner, P.H.; Gopal, T.V.; Nash, W.G.; O'Brien, S.
 Cell 42, 421-428, 1985
 A:Title: Expression of the human c-fms proto-oncogene in hematopoietic cells and its del
 A:Reference number: I52772; UID:85282599; PMID:4028159
 A:Accession: I52772
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 244-295 <RE4>
 A:Cross-references: GB:M11067; NID:G182674; PIDN:AAA35848.1; PID:G442423
 C:Genetics:
 A:Gene: GDB:CSF1R; FMS
 A:Cross-references: GDB:120600; OMIM:164770
 A:Map position: Sq33.2-Sq33.3
 A:Introns: 17/1; 103/1; 198/1; 243/3; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homol
 C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote
 fic protein kinase
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-972/Product: macrophage colony-stimulating factor 1 receptor #status predicted <
 F:24-512/Domain: extracellular #status predicted <EXT>
 F:35-86/Domain: immunoglobulin homology <IMM1>
 F:120-179/Domain: immunoglobulin homology <IMM2>
 F:217-280/Domain: immunoglobulin homology <IMM3>
 F:316-383/Domain: immunoglobulin homology <IMM4>
 F:412-487/Domain: immunoglobulin homology <IMM5>
 F:513-537/Domain: transmembrane #status predicted <TMM>
 F:538-972/Domain: intracellular #status predicted <INT>
 F:580-917/Domain: protein kinase homology <KIN>
 F:588-596/Region: protein kinase ATP-binding motif
 F:42-84,127-177,224-278,419-485/Disulfide bonds: #status predicted
 F:45,73,153,240,275,302,335,412,428,480/Binding site: carbohydrate (Asn) (covalen
 F:1616,633,778/Active site: Lys, Glu, Asp #status predicted
 F:783,796/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 23.1%; Score 1216.5; DB 1; Length 972;
 Best Local Similarity 32.8%; Pred. No. 6.4e-52;
 Matches 325; Conservative 156; Mismatches 316; Indels 195; Gaps 33;

Qy 75 VYAAAEVDV--SASITQLQVLVDAPGNISCLWPKHSLNQPHFDLQNRGVSMVLK 132
 Db 22 VIEPSVPELVKPGATVILRCV-----GNGSVWDGPPS-----PHTLVSDGSSLSLTN 72
 Qy 133 MTE-----TQAGEYL-----LFIQSEATNTILFTVSIIRNTLYTLRRPYFRKM 176
 Db 73 NATFQNTGYRCTECPDPLGGSAALHLVKDPAPRWNL-----AQEVVVF----- 118
 Qy 177 ENODALV-CISESPEPIVEVWVLCDSQESKEESPANVVKEEK-----VLHE--- 223
 Db 119 EDQDALPCL---LTDPVLE-----AGSLVVRGRFLMRHTNYSFSPWHGFTTHRAKF 169
 Qy 224 LFGTDIRCARNELGRECTFLTIDLNOTPTTL-----OLFLKVEPLWIRCK 273
 Db 170 IQSQDYQCSALMG-GR---KVMISIRLKVKQVPGPPALTLPVPAELVIRGEAAQIVCS 225
 Qy 274 AVVNHGFLTWELNKALEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTSCSS 333
 Db 236 ASSVDVNFDFVLQHNNTKLA---IPQSDFNRRYQ-KVLTNLNQDQDFQHAGNYSQVAS 281
 Qy 334 ---KHPQSQALVTIVGKGFNATNNSSED---YEIDVEEFCFSVRFKAYPOIR-CTWTF 385
 Db 282 NVQGHK-STSMFFRVVYESAYLNL--SSEQLTIQVTVGEGNLKVMVEAYPGLOGFNMTY 338
 Qy 386 SRKSPCEQKGLDNGYSISKFNHGHQ-----GEYIF 418
 Db 339 -----LGPFSDHQPEKLANATKYRHTFTLSLRLKPESEAGRYSF 381
 Qy 419 HAENDDAQFTKMTLNIIRKPKVLAESAASQAS-----CFSDGYPLPSWTWKCSKSPNC 474
 Db 382 LARNPGGWRALTFTLTLPPEVSVIWTIFNGSGTLTLLCAASGYPPQPNVTWLOCSGHTDRC 441
 Qy 475 TEEITEGVN---RKANRKFVGQWSSSTLNMSBAIKGFLVKCCAYNSLGTSCTILN 530
 Db 442 DEAQVLQWDDPYPEVLVSQEPFKVTVQSLTTLTETLEHNTQVECRAHNSVSGSGWAFPI 501
 Qy 531 SPGPPFPFDQINISFATIGVC---LLFVLVTLTLLCHYKKQFVYESQLQWQVTVGSSDN 587
 Db 502 SAGATHPPDBFLFTPVVAVCMSTNALLLLLLLYLYKKQPKYQVRWKIIE--SYEGN 559
 Qy 588 EYFYVDFREYEDLKWPEPPRENLEFGVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLK 647

Db 560 SYTFIDPTQLPYNEKWEPPRNLFQKXTLGAGAFKGVVEATAFGLGKEDAVLKVAVRMLK 619
Qy 648 EKADSSREALMSKLMKMTOLGSHENIVNLGACTLSPVILIEYCCYGLDLNLYLSKR 707
Db 620 STAHADKEALMSKLMKMTOLGSHENIVNLGACTHGPVLVITIEYCCYGLDLNLYLSKR 679
Qy 708 E-----KFHRTWTEIFKEHNFYFPTFQSHPNSSMPGSEVQIHP 747
Db 680 EAMLGPSLPQDPGEGVDYKNIHLEKKYVRDGSF-----SQGVDYV 724
Qy 748 DSDOISGLHNSHSEDEIEYENOKRLEBEDNLVLFEDLLCFAYQVAKWMEFLFKSC 807
Db 725 EMRPVSTSSNDSF-SEQDLKEDGRPLE-----LRDLHFSSOVAQMAFLASKNC 774
Qy 808 VHRDLARNVLVTHGKVKICDFGLARDIMSDSNVVRGNARLPVKMAPELSEGYTI 867
Db 775 IHRDVAARNVLLTNGHAKIGDGLARDIMSDSNVVRGNARLPVKMAPELSEGYTI 834
Qy 868 KSDVWSYGILLWEIFSLGVPNPYGPVDANFYKLIQNGKMDQPFYATEEYIIMQSCWA 927
Db 835 QSDVWSYGILLWEIFSLGVPNPYGPILVNSKFLVKGQYMAQAFAPKNIYSIMQACWA 894
Qy 928 FDSKRPSFNLTSFLGCOL-ADAEAEAMQNV 958
Db 895 LEPTHRPTFOQCSFLOEQAOEDRRERYTNL 926

RESULT 12
JN0677
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken
N;Alternate names: tyrosine kinase receptor kit
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JN0677
R;Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Naito, M.; Sakurai, M.
Gene 128, 257-261, 1993
A;Title: Cloning and expression of the chicken c-kit proto-oncogene.
A;Reference number: JN0677; MUID:93292995; PMID:7685729
A;Accession: JN0677
A;Molecule type: mRNA
A;Residues: 1-960 <SAS>
A;Cross-references: DDBJ:D13225; NID:g303532; PIDN:BAA02506.1; PID:g303533
A;Experimental source: brain
A;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
retein kinase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-960/Product: tyrosine kinase receptor #status predicted <MAT>
F;314-380/Domain: immunoglobulin homology <IMM>
F;573-916/Domain: protein kinase homology <KIN>
F;581-589/Region: protein kinase ATP-binding motif
F;76,135,149,269,286,306,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)

Query Match 23.0%; Score 1215; DB 1; Length 960;
Best Local Similarity 32.3%; Pred. No. 7.5e-52;
Matches 314; Conservative 165; Mismatches 370; Indels 124; Gaps 34;

Qy 66 ALRQSGSTVVEAAAEVDVDSASTLQVLVDAPGNISCLVWFKSS-----LNCQPHFD 119
Db 18 SLIPAGGSVPHESSLVNKGEEELKCNKEGP-----VTWNFQNSDPSAKTRISKEKWH 73
Qy 120 LQNGV--VSMVLKMTQAGEVLLFTQSEATNYTLFTVSIKNTLTYLTLRRPYFRKWE 177
Db 74 TKNATIRDIGYECKSGKSVNSFVFKDP-----NVLFV---DSLIV-----GKED 119
Qy 178 NQDALVCISEVPBP-IVEWVLCDSSQGSCKEESPAVVYKKEE-----KVLHFLFGTDIRCC 232
Db 120 SDILLVC---PLTDPDLNFTLRCKDGRPLKPNMTFIENPKQGIILKVNQSFKCYCQL 176
Qy 233 AR-NELGRECTRLFTIDNQTP-QTTLPOL-----FLKVGEPILWIRCKAVVNHGFL 283
Db 177 AKHNGVEKISEHIF---LNVKPVHVKALPVITLSKSYELLKEGEEPEVTCIITDVDSVKA 233

Qy 284 TWLENKALBEGNYFEMSTYSTRNTRMIRILFAFVSSVARNDTYTTCSSKHP--SOSAL 341
Db 234 SWISYSAIVTSKSRNLGDYGERK----LTNIRSVDNSGEGFTC-QAENPFCKTNAT 288
Qy 342 VTI--VKGGIN---ATNSSEDEIDQYBEFCFVRKAYQAIR-CTWTFKRKSPCEOK 395
Db 289 VTKALAKGVRVLPATNTTIDINAGQNG--LTVEYEAYPKPKKEEVMYMNTEL---ON 343
Qy 396 GLDNGYSISKFCNHK-----QPGEYIFHAENDDAQFTKMTLIRRKQVOLA 443
Db 344 SSHYVVKFTVGNNSYTSSELHLFLKGTGGIYTFVSNSSDASSVTENVYVKPEILT 403
Qy 444 EASASQ--ASCFSQGYPLPSWTKKCDKSPNCTEITEGVNMRKANRKFVGQWSSSTL 501
Db 404 LDMGLNDILQCVATGFPAPTYVYFCPTQECORCLDPSITSPMDVKVS-----YTNSSVP 457
Qy 502 NMSEAIKGLVKCCAYNSLGTSCETILLNSGPPFF-----IQDNISFYA-----TGV 550
Db 458 SPERILVESTVNASMFKSTGTICCEASNGDKSSVFNFAIKEQIRHTLTPLLIAFGV 517
Qy 551 CLLFIVVLTLLICHYKKOPREYEQLOMV-OVTGSSDNEYFYVDPREYEDLKWEFFREN 609
Db 518 AAGLMCIIVMLVYIYLOKPKYEVQWKVEING---NNYVYIDPTQLPYDHKWEFFRNR 574
Qy 610 LEFGKVLGSGAFGKVMNATAYGISKTGVSIOVAVKMLKEKADSSEREALMSKLMTOIG 669
Db 575 LSPGKTLGAGAFKGVVEATAYGLFKSDAAMTVAVKMLKPSAHLTEREALMSKLVSLG 634
Qy 670 SHENIVNLGACTLSPVILIEYCCYGLDLNLYLSKRKEP-----HRTWTEIFKSHNSF 725
Db 635 NHINIVNLGACTTGGTLPVITEYCCYGLDLNLYLSKRKEP-----VTLSMLEDE 746
Qy 726 YPTQSHPS-----SMPGSRVQIHPDSDOISGLHNSHSEDEIEYENOKRELEE 778
Db 693 --LHQAEPTADAVNEYMDKPGVYAVPPKADKRPVKSQSYTDQD-----VTLSMLEDE 746
Qy 779 DLNVLTFEDLLCFAYQVAKWMEFLFKSCVHRDLARNVLVTHGKVKICDFGLARDIMS 838
Db 747 --LALDVEDLLSFSYQVAKGMSFLASKNCIHRDLARNVLLTHGRITKICDFGLARDIRN 804
Qy 839 DSNVVRGNARLPVKMAPELSEGYTIKSDVWSYGILLWEIFSLGVPNPYGPVDFANF 898
Db 805 DSNVVRGNARLPVKMAPELSEGYTIKSDVWSYGILLWEIFSLGVPNPYGPVDFANF 864
Qy 899 YKLQNGFQMDQPFVATEEYIIMQSCWAFDPSRKPSPNLTSLFLGCOLADAEAEAMQNV 958
Db 865 YKMLKEGTRMFPSCPPPEMDIMKSCWDADPLQRPITFKQIVQLIEQQQLSDNAPRYAN- 923
Qy 959 DGRVSECPHTYQN 971
Db 924 --FSTPPSTQGN 933

RESULT 13
T30816
macrophage colony-stimulating factor receptor - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
R;How, G.F.; Venkatesh, B.; Brenner, S.
Genome Res. 6, 1185-1191, 1996
A;Title: Conserved linkage between the pufferfish (Fugu rubripes) and human genes for I
A;Reference number: Z20882; MUID:97129405; PMID:8973913
A;Accession: T30816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-975 <HOW>
A;Cross-references: EMBL:U63926; NID:g1752706; PID:g1752708; PIDN:AAC60063.1
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology

Query Match 23.0%; Score 1213; DB 2; Length 975;
Best Local Similarity 31.7%; Pred. No. 9.6e-52;

Matches 325; Conservative 177; Mismatches 333; Indels 190; Gaps 37;

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Qy 33 IKCVLINHNKNDSSVGKSSYP---MVSESPEDLGC--ALRP--QSSCT---VTEAAAV 81
Db 47 LKC-----GGDPVNWQTRLPKHKYMSRSPGNLRTIRVAPRTAEFTGTYKCFYSAWAQ 100
Qy 82 EVDVSAITLQVLVDAPGNISCLWFKHSSLCNCPHFDLQNGVGVVSWILKMTWTOAGEY 141
Db 101 HRLHTSSV--HVVYKDPNRV--FW-----TSSTSLRVVRKEGEDY 136
Qy 142 L--LFIQSEATNYTLTVSRNTLLYTLRPPYFRKMENQDALVCISESPEPVEVWL 198
Db 137 LPLCLLTDPTEADLGL-----RMDN-----GTVVP--PENNYTV 168
Qy 199 CDSQGESCKEESPAAVVKKEEVLHFLGTDIRCCARNELGRECTRLFTIDLNTQPTILP 258
Db 169 YHRGILRSIQPS-----FNADYVCTAKVGVEKTSFTSINVILQKLRFP-P 215
Qy 259 QLFK-----VGEPLMIRCKAVNHVHGFLTWLEKNA-----LBEGNYFEMSTYSTNRT 308
Db 216 YVFLMEDEYVRIVGBELQIRCMTHNPNFNVNTYTKSRVTIEE---RVRSSGENRL 271
Qy 309 MIRILFAFVSSVARNDTGYTSSCKHP---SQSALVTIVGKFI-----NATNSE 357
Db 272 DIQSILT--ISAVDLADTGNHSCIGTNEAGVNSSNTYLLVVEKPYIRLWPQLIPKLASOGL 330
Qy 358 DYEIDQEEFCFSVRFKAYPOLR--CTWTFSRKSPFCEOKGLDNGVYSISKFCNKHQPOGEY 416
Db 331 SVEVNEGEDLELGVNVEAYPOLDIRHWHTPTSPSTMSQEHYHARLQLKRWMAQEQ--QY 389
Qy 417 IFAENDDAQFTKMTLNIIRKP--QVLAAASQASQCSFSDGVPPLPSWTWKKCSKSPNCT 475
Db 390 TFYAKSNLANGISPHVKMYQKPIAVVRWENTITLTCTSGFYPAPOIIWYQCSGIRPTCN 449
Qy 476 BEITEGVNR-----KANRKGQVQVSSSTLNMSEAIGFLVKCCAYNSLGTSCETI 527
Db 450 GNNT--GLPKQNHQALTEVQREYGEVSESVFTVGLSNHRTMTEVCAFNVLGVSSDTF 508
Qy 528 LNSGPPFPFTQDNISFVATI---GVCLLFTVTLTLICHYKQKQFVYESQLQWQVGTG 583
Db 509 TVE-----VSDKI--FTSTLIGAGVLAIFLLLVLL--YKKOKPFEIRWKIIE--A 557
Qy 584 SSDNEYFYVDREYEDLWKEFPRENLEFGKVLGSGAFGKVMNATAYGISK--TGVSIQVA 642
Db 558 REGNNYTFIDPTQLPYNEKEWEPFRDKLKLGVLAGAGFGKVVEATAFGLGEDKDNTRVA 617
Qy 643 VKMLKEKADSSEREALMSELKMTOLGSHENIVNLLGACTLSGPYILFPCYCGDLLNY 702
Db 618 VKMLKANAHSDEREALMSELKILSHLGHQNTVNLGACTYGGPVLVITEYCSLGLDLNF 677
Qy 703 LRSKREKTHRTWTEIFKEHNFSFYPTFQSHPN-----SSMPGSRREVQ 744
Db 678 LQKAEFTFNLVWNI-----PEIMENSNDYKNICQKVIYRSDGISSTSSSTYLE 728
Qy 745 IHPDSQISGLHGNFSHSEDEIEYENQKRLBEEDLNVLTFEDLLCFAYQVAKGMFELEF 804
Db 729 MRPS-----QOSHIEASGRKSLCEDNGDWPLDIDDLRFSIQVAQGLDFLAS 775
Qy 805 KSCVHRDLAARNVLVTHGKVKVICDFGLARDIMSDNSYVVRGNARLPVKWMAPESLFEG 864
Db 776 RNCIHRDVAARNVLLTDKRVAKICDFGLARDIMSDNSYVVRGNARLPVKWMAPESLFDCV 835
Qy 865 YTIKSDVMSYGLLWEIFSLGNVPYGPVPDANFYKLQNGFKMDOPPFVATEIYIMOS 924
Db 836 YTVQSDVMSYGLLWEIFSLGKSPYSMAVDVSFRFYKWKRGYQMSQOPFALPEIYIMKOM 895
Qy 925 CWAFDSRKRPPFNLTSLFGCOLA---DAEEAMYNQV-----DGRVSECPHTYQNRFP 975
Db 896 CWNLEPTERTFMSIQMINRLLGGQDQGEKLIYRNQVPEQVABEACDEPKRYD--PPC 953
Qy 976 SREMD 980
Db 954 ERSKD 958
```

```
RESULT 14
S16385
macrophage colony-stimulating factor 1 receptor precursor - rat
Nt contains: protein-tyrosine kinase (EC 2.7.1.112) CSF-1R
C.Species: Rattus norvegicus (Norway rat)
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Jun-2000
C.Accession: I60321; S16385
R.Borycki, A.G.; Guillier, M.; Leibovitch, M.P.; Leibovitch, S.A.
Growth Factors 6, 209-218, 1992
A.Title: Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence analysis ar
A.Reference number: I60321; MUID:93001225; PMID:1389227
A.Accession: I60321
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-978 <RES>
A.Cross-references: EMBL:X61479; NID:G57543; PID:CAA43706.1; PID:G57544
A.Note: in Genbank entry RRCFS1, release 113.0, the source is designated as Rattus r
A.Note: submitted to the EMBL Data Library, August 1991
C.Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolc
C.Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; kinase-re
protein; tyrosine-specific protein kinase
F.1-19/Domain: signal sequence #status predicted <SIG>
F.20-978/Product: macrophage colony-stimulating factor 1 receptor #status predicted <EXT>
F.20-515/Domain: immunoglobulin #status predicted <IM1>
F.120-179/Domain: immunoglobulin homology <IM2>
F.217-280/Domain: immunoglobulin homology <IM3>
F.316-381/Domain: immunoglobulin homology <IM4>
F.410-485/Domain: immunoglobulin homology <IM5>
F.516-535/Domain: transmembrane #status predicted <TM>
F.536-978/Domain: intracellular #status predicted <INT>
F.578-915/Domain: protein kinase homology <KIN>
F.586-594/Region: protein kinase ATP-binding motif
F.42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
F.45.73.302.335.389.410.449.478.491/Binding site: carbohydrate (Asn) (covalent) #stat
F.614.631.776/Active site: Lys, Glu, Asp #status predicted
F.781.794/Binding site: magnesium (Asn, Asp) #status predicted
```

Query Match 22.6%; Score 1194; DB 2; Length 978;

Best Local Similarity 33.1%; Pred. No. 86-51;

Matches 321; Conservative 154; Mismatches 332; Indels 164; Gaps 32;

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Qy 83 VDVSAITLQVL---VDAPGNISCLWFKHSSLCNCPHFDLQNGV---SMWLKM 133
Db 32 VEGFTVTLRUCVNSGVWDGFIPIYWLDPES---POSTLTRNATPKNTGYRCTL 87
Qy 134 TETQAGEYL--LFIQSEATNYTL---FTVSIRNTLLYTLRPPYFRKMENQDALVCISES 188
Db 88 EDPMAGSTIHLVVKDPAHSHWNLQAQEVTV-----VEQEA----- 124
Qy 189 VPEPIVWVLCDSQGESCKEESPAAVVKK-----EEKVLHELFGTDIRCCAR 234
Db 125 LPLCLITDPALKDSV--SLMREGGRQVLRKTVYFFSAWRGFIIRKAKVL---DSNTVYCKT 179
Qy 235 NELGRECTEL--FTIDLN---QTPQTTL--POLFLV--GEPLMIRCKAVNHVHGFGTLWEL 287
Db 180 MYNGRESTSTGTLWKNVRVHPEPQIKLEPSKLVIRGSAQAQIVCSATNAEVGNILKR 239
Qy 288 ENKALE-----EGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTC--SSSKHPSOS 339
Db 240 GTKLEIPLNSDFQNYK-----KVRALSLNAVDFQDAGIYCSVASNDVGTRT 288
Qy 340 ALVT--IVGKGFINATN--SSDYEDIDQVEEFCFSVRFKAYPOLR--CTWTFSRKSPFCEQK 395
Db 289 ATMNQWVESAVLNTLSEOSLLQEVSGVDSLILTVHADAYPSIQHYNWTYLVGPFPS--DQR 347
Qy 396 GLD-----NGYSISKFCNH--KHQPGYIIFAENDDAQFTKMTLNIIRKQVLAES 446
Db 348 KLEFITQIRAIYRTFKLFLNLRVKASEGQYFLMAQNKAGMNNLTFFELTLRYPPEVSTM 407
Qy 447 ASQAS-----CFSDGYPLPSWTWKKCSKSPNCTEETEGVNV---RKANRKYFGQWVSS 498
```

Db 408 PVNGSDVLCFCDVSGYQPSQVPMWECRGHTDRCDCAQAQLQVWNDTHPEVLSQKPFQKVIQ 467
 Qy 499 STANMSEAIKGFVLYKCCAYNSLGTSCETILLNSGPPFFIOONISFYATIGVC---LLPI 555
 Db 468 SOLPIGLKHNWYFCKTHNSGVNSQYFRAVLSGQSKQLEDLSFTPVVACHMSVMSLL 527
 Qy 556 VVLTILLICHYKKQFRYBSQJQVQVGTSSDNEYFYVDREYEDLKWEFPRENLEFGKV 615
 Db 528 VLLLLLLLYKKQPKYQVRWKIIE--RYEGNSYTFIDPTQLPYNEKWEFPNNLQFCKT 585
 Qy 616 LGSAGFGKMNATAYGSKTGVSIQAVAKMEFLFKSCVHRDLAARNVLTGHGKVKICDFGLARD 835
 Db 586 LGAGAFGVBEATAFGLKEDAVLKVAVMLKSTAHADKEALMSSELKIMSHLGQHENIV 645
 Qy 676 NLGACTLSGPIYLIFECYCGDILLNLSKRE-----KEPRTWT 715
 Db 646 NLGACTHGGVPLVITEYCCYGDLLNFURKAAEAMGLPSLSPGQDSGSSYKNILHLEKK 705
 Qy 716 BIFKEHNSFYPTFQSHNSMPSGSRVQIHPDSDQISGLHGNSPHSDEIEYENQKRIE 775
 Db 706 YVRDSGFS-----SQGVDTYVEMRPVSTSSDSFFKQD-LDKEFSRPLE 749
 Qy 776 BEEDNLVLTFFEDLJCFQAVQAKMEFLFKSCVHRDLAARNVLTGHGKVKICDFGLARD 835
 Db 750 -----LWDLHFSQVAGMAFLASKNCIHRDVAARNVLTSGHVAKTGDGFLARD 800
 Qy 836 IMSDSNVYVRGNARLPVKWMAPESEFEGIYTKSDVMSYGILLWEIFSLGVNYPYGPV 895
 Db 801 IMSDSNVYVRGNARLPVKWMAPESEFEGIYTKSDVMSYGILLWEIFSLGVNYPYGPV 860
 Qy 896 ANFYKLIQNGKMDQPFYATIEIYIMOSCWAFDSRKRPSFNLTSFLGCQLADAEAEAMY 955
 Db 861 NKFYKLVQGVQMAQVPAPKNIYSIMOSCWDLPTTRPTTQOICFLL-----QEQLRL 914
 Qy 956 QNVDRGVSECP 966
 Db 915 ERRDQYANLP 925

RESULT 15
 TVMSND
 N:Contains: colony-stimulating factor 1 receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000
 C:Accession: S01880
 R:Rothwell, V.M.; Rohrschneider, L.R.
 Oncogene Res. 1, 311-324, 1987
 A:Title: Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.
 A:Reference number: S01880; MUID:88217329; PMID:2966922
 A:Accession: S01880
 A:Molecule type: mRNA
 A:Residues: 1-976 <ROT>
 A:Cross-references: EMBL:X06368
 C:Genetics:
 A:Gene: fms
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
 C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
 fic protein kinase
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-976/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT>
 F:20-515/Domain: extracellular #status predicted <EXT>
 F:35-86/Domain: immunoglobulin homology <IMM1>
 F:120-179/Domain: immunoglobulin homology <IMM2>
 F:217-280/Domain: immunoglobulin homology <IMM3>
 F:316-381/Domain: immunoglobulin homology <IMM4>
 F:410-485/Domain: immunoglobulin homology <IMM5>
 F:516-535/Domain: transmembrane #status predicted <TM>
 F:536-976/Domain: intracellular #status predicted <INT>
 F:578-914/Domain: protein kinase homology <KIN>
 F:586-594/Region: protein kinase ATP-binding motif
 F:42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted

F:45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #stat:
 F:614,631,776/Active site: Lys, Glu, Asp #status predicted
 F:781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 22.48; Score 1183.5; DB 1; Length 976;
 Best Local Similarity 33.2%; Pred. No. 2.6e-50;
 Matches 318; Conservative 154; Mismatches 347; Indels 139; Gaps 30;

Qy 83 VDSASITLQVL----VDAGNISCLWVF---KHSSLNCQPHFDLQNRGVVSMVILKMTPE 135
 Db 32 VEPGETVTLRCVNSGVEMDGPISPIWTLDPESPSTLTTSNATFKNTGTGYRCTELEDP 91
 Qy 136 TOAGEYLFIOSEATNYTIL---FTVSTRNTLLYTLRPYFRKMNQDALVCISSEVPEP 192
 Db 92 AGSTTHLYVKDPAHSMNLLAQEVTV-----VEQEAIV-----LPCIL 128
 Qy 193 IVEWVLCDSQESCKEESPAVVKKEKVLHELPGTDIR-----CCARNELGRECT 242
 Db 129 ITDPALKDSV-SLMREGGRQVLRKTVYFSPWRGSIIRAKVLDNSTYVCKTWMVNGREST 187
 Qy 243 RL-FTIDLN---QTPQTTL-PQLFLKV-GEPLMTRCAVHVNHGFLTWELNKALE-- 293
 Db 198 STGIWLKVRVHPEPPQIKLEPSKLVIRGEAAQIVCSATNAEVEGFNVILKRGDTKLEIP 247
 Qy 294 -----EGNYFEMSYSTNRTMIRILFAFVSSVARNDTGYTC-SSSKHPSQSALVT--IV 345
 Db 248 LNSDFQDNYK-----KVRALSINAVDFQDAGIYSCVASNDVTRTATMNFQVV 296
 Qy 346 KGKFINATN-SEDEYIDQYEEFCFSVRPKAYQJR-CTWTFSRKSPFCEQKGLD----- 398
 Db 297 ESAYNLNLSBOSLQEVSGDSLTLTVHADAYPSIOHYNWTLVGPFFE-DORKLEFITOR 355
 Qy 399 --NGYSISKFCNH--KHOPGEYIHAENDDAQFTKMTLNIRKPKOVLAESAQAS-- 451
 Db 356 AIYRTYFKLFLNRKVASAGQYFLMAQNKACWNNLTFLTLYPPEVSVTWMPVNGSDVL 415
 Qy 452 -CFSDGYPLPSWTWKCKSDKSPNCTEETEEGVN-----RKANRKVFGQVWSSTLMSSEA 506
 Db 416 FCDVSGYQPSQVPMWECRGHTDRCDCAQAQLHWNTHPEVLSQKPFQKVIQSKLPGL 475
 Qy 507 IKGFLVKCCAYNSLGTSCETILLNSGPPFFIOONISFYATIGVC---LLFIIVLTLIC 563
 Db 476 KHNMTYFCKTHNSGVNSQYFRAVLSGQSKQLEDLSFTPVVACHMSVMSLLVLLLL 535
 Qy 564 HKYKKQFRYESQLOMVQVGTSSDNEYFYVDREYEDLKWEFPRENLEFGKVLGSAFGK 623
 Db 536 YAYKQPKYQVRWKIIE--RYEGNSYTFIDPTQLPYNEKWEFPNNLQFGLTGAGAFK 593
 Qy 624 VNNATAYGSKTGVSIQAVAKMEKADSSEREAALMSSELKIMSHLGQHENIVNLLGACTL 683
 Db 594 VVEATAFGLGKEDAVLKVAVMLKSTAHADKEALMSSELKIMSHLGQHENIVNLLGACTH 653
 Qy 684 SQPIYLIFECYCGDILLNLSRKRKFHTWTETIPEHNFSPYPTFQSHNSMP----- 738
 Db 654 GGPVLVYTEYCCYGDILLNLSRKRKFHTWTETIPEHNFSPYPTFQSHNSMP----- 703
 Qy 739 -----GSRVQIHPDSDQISGLHGNSPHSDEIEYENQKREEEDNLVLTFFEDL 788
 Db 704 KYVVRDSGFSQGVDTYVEMRPVSTSSDSFFKQD-LDKEHSRPLE-----LWDL 753
 Qy 789 LCFAYQVAKMEFLFKSCVHRDLAARNVLTGHGKVKICDFGLARDIMSDSNVYVRGNA 848
 Db 754 LHFSSQVAGMAFLASKNCIHRDVAARNVLTSGHVAKTGDGFLARDIMSDSNVYVRGNA 813
 Qy 849 RLPVKWMAPESEFEGIYTKSDVMSYGILLWEIFSLGVNYPYGPVVDANFYKLIQNGFKM 908
 Db 814 -LPVKWMAPESEFDCVITVQSDVMSYGILLWEIFSLGVNYPYGPVVDANFYKLIQNGFKM 872
 Qy 909 DQPFVATEEIIYIMOSCWAFDSRKRPSFNLTSFLGCQLADAEAEAMYQNVDRGVSECP 966
 Db 873 AQPVFAPKNIYSIMOSCWDLPTTRPTTQOICFLL-----QEQLRERDDQYANLP 924

Search completed: May 24, 2003, 17:00:37
Job time : 39.5174 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:38:45 ; Search time 18.0091 Seconds
(without alignments)
2286.959 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVLLVWFSAM.....PFSREMDLGLLSPOAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5274	100.0	993	1 FLT3_HUMAN	P36888 homo sapien
2	4429.5	84.0	992	1 FLT3_MOUSE	Q00342 mus musculus
3	1295.5	24.6	978	1 KIT_CAPHI	Q28317 capra hircu
4	1286	24.4	977	1 KIT_BOVIN	P43481 bos taurus
5	1266	24.0	975	1 KIT_MOUSE	P05532 mus musculus
6	1251	23.7	976	1 KIT_HUMAN	P10721 homo sapien
7	1247.5	23.7	975	1 KIT_CANFA	O97799 canis fami
8	1225.5	23.2	980	1 KEMS_FELCA	P13369 felis silve
9	1224.5	23.2	978	1 KIT_FELCA	Q28889 felis silve
10	1224	23.2	978	1 KEMS_FSVMD	P00545 feline sarc
11	1216.5	23.1	972	1 KEMS_HUMAN	P07333 homo sapien
12	1215	22.8	960	1 KIT_CHICK	Q08156 gallus gall
13	1204	22.0	977	1 KEMS_MOUSE	P09581 mus musculus
14	1194	22.6	978	1 KEMS_RAT	Q00495 rattus norv
15	1176	22.3	1088	1 PGDS_RAT	P20786 rattus norv
16	1169	22.2	1089	1 PGDS_MOUSE	P26618 mus musculus
17	1166	22.1	1089	1 PGDS_HUMAN	P16234 homo sapien
18	1128	21.4	1087	1 PGDS_XENLA	P26619 xenopus lae
19	1105.5	21.0	1098	1 PGDR_MOUSE	P05622 mus musculus
20	1086.5	20.6	1106	1 PGDR_HUMAN	P09619 homo sapien
21	990	18.8	1338	1 VGR1_HUMAN	P17948 h vascular
22	989.5	18.8	370	1 KIT_FSVHZ	P04048 feline sarc
23	959.5	18.2	1333	1 VGR1_MOUSE	P35969 mus musculus
24	956	18.1	1336	1 VGR1_RAT	P53767 rattus norv
25	951.5	18.0	1356	1 VGR2_HUMAN	P35968 homo sapien
26	935	17.7	1348	1 VGR2_COTUA	P52583 coturnix co
27	923	17.5	1367	1 VGR2_MOUSE	P35918 mus musculus
28	917.5	17.4	1343	1 VGR2_RAT	O08775 rattus norv
29	907.5	17.2	1363	1 VGR3_MOUSE	P35917 mus musculus
30	904.5	17.2	1298	1 VGR3_HUMAN	P35916 homo sapien
31	874.5	16.6	823	1 CEK3_CHICK	P18461 gallus gall
32	849	16.1	821	1 FGR2_HUMAN	P21802 homo sapien
33	845	16.0	813	1 FGR2_XENLA	Q03364 xenopus lae

ALIGNMENTS

RESULT 1

ID	FLT3_HUMAN	STANDARD;	PRT;	993 AA.
DT	P36888; Q13414;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	FL cytokine receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor FLT3) (Stem cell tyrosine kinase 1) (STK-1) (CD135 antigen).			
DE	receptor FLT3			
GN	FLT3 OR STK1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94119906; PubMed=7507245;			
RA	Small D., Levenstein M., Kim E., Carow C., Amin S., Rockwell P., Witte L., Burrow C., Ratajczak M.Z., Gewirtz A.M., Civin C.I.;			
RA	"STK-1, the human homolog of Flk-2/Flt-3, is selectively expressed in CD34+ human bone marrow cells and is involved in the proliferation of early progenitor/stem cells."			
RT	Proc. Natl. Acad. Sci. U.S.A. 91:459-463(1994).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=93357464; PubMed=8394751;			
RA	Rosnet O., Schiff C., Pebusque M.J., Marchetto S., Tonnelie C., Toiron Y., Birg F., Birnbaum D.;			
RA	"Human FLT3/FLK2 gene: cDNA cloning and expression in hematopoietic cells."			
RT	Blood 82:1110-1119(1993).			
RL	[3]			
RN	SEQUENCE OF 783-942 FROM N.A.			
RP	TISSUE=Testis;			
RC	MEDLINE=91169547; PubMed=2004790;			
RX	Rosnet O., Mattei M.-G., Marchetto S., Birnbaum D.;			
RA	"Isolation and chromosomal localization of a novel FMS-like tyrosine kinase gene."			
RT	Genomics 9:380-385(1991).			
RL	Genomics 9:380-385(1991).			
CC	!- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.			
CC	!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.			
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	!- TISSUE SPECIFICITY: BONE MARROW CELLS.			
CC	!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.			
CC	!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	!- DATABASE: NAME=PROW; NOTE=CD guide CD135 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd135.htm".			
CC	!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;			
CC	WWW="http://www.infobiogen.fr/services/chronocancer/Genes/FLT3ID144.html".			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its			

P21803 mus musculus
P18460 gallus gall
P1804 gallus gall
Q01742 homo sapien
P22182 xenopus lae
P11362 homo sapien
P16092 mus musculus
P22607 homo sapien
Q04589 rattus norv
Q61851 mus musculus
Q09147 drosophila
P35546 mus musculus

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CC EMBL; U02687; AAA18947.1; -
CC EMBL; Z26652; CAA81393.1; -
CC EMBL; L36162; AAA35487.1; -
CC HSSP; P11362; IFGK.
CC Genew; HGNC:3765; FLT3.
DR MIM; 136351; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR001824; RtkinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR Signal; Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 993 FL CYTOKINE RECEPTOR.
FT DOMAIN 27 543 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 544 563 POTENTIAL.
FT DOMAIN 564 993 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 610 943 PROTEIN KINASE.
FT NP_BIND 616 624 ATP (BY SIMILARITY).
FT BINDING 644 644 ATP (BY SIMILARITY).
FT ACT_SITE 811 811 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 473 473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 502 502 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 541 541 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 8 8 A -> G (IN REF. 2).
FT CONFLICT 10 11 TV -> QL (IN REF. 2).
FT CONFLICT 78 78 A -> R (IN REF. 2).
FT CONFLICT 227 227 T -> M (IN REF. 2).
FT CONFLICT 346 346 G -> E (IN REF. 2).
FT CONFLICT 940 940 T -> H (IN REF. 3).
SQ SEQUENCE 993 AA; 112804 MW; 16790124B02F6BBF CRC64;

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVVFSAAMIFGTITNQDLPVVKVILNHNKNDSSVGKSSYPMVVSESP 60
Db 1 MPALARDAGTVLLVVFSAAMIFGTITNQDLPVVKVILNHNKNDSSVGKSSYPMVVSESP 60
Qy 61 EDLGCALRQSSGTYYAAAVDVDSASITLQVLDVDPAGNISCLWVFKHSSLNCPHFDP 120
Db 61 EDLGCALRQSSGTYYAAAVDVDSASITLQVLDVDPAGNISCLWVFKHSSLNCPHFDP 120
Qy 121 QNRGVSVVILKMTQAGEYLLFFQSEATNTYILFTVSRINTLYTLRRPYFRKWNQD 180
Db 121 QNRGVSVVILKMTQAGEYLLFFQSEATNTYILFTVSRINTLYTLRRPYFRKWNQD 180
Qy 181 ALVCISVPEPIVEMVLCDSGESCKEESPAVVKKEKVLHFTGDIRCCARNELGRE 240
Db 181 ALVCISVPEPIVEMVLCDSGESCKEESPAVVKKEKVLHFTGDIRCCARNELGRE 240

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Qy 241 CTRLFTIDLNOTPOTTLPOLFLKVGEPWIRCKAVVNHGFLGTWELENKALEEGNYFEM 300
Db 241 CTRLFTIDLNOTPOTTLPOLFLKVGEPWIRCKAVVNHGFLGTWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILPAPFVSVARNDTGYTCSKSPQSALVTIVCKGFINTATNSSEDEYE 360
Db 301 STYSTNRTMIRILPAPFVSVARNDTGYTCSKSPQSALVTIVCKGFINTATNSSEDEYE 360
Qy 361 IDOYEFCFSVRPKAYPOIRCTWTFSRKSFPCEQGLDNGYSISKFCNKHOPGEVIFHA 420
Db 361 IDOYEFCFSVRPKAYPOIRCTWTFSRKSFPCEQGLDNGYSISKFCNKHOPGEVIFHA 420
Qy 421 ENDDAQFTKMTFLNIRRKPOVLAEASASQSCFSDGYPPLSPMTWKCKSDKSPNCTEITE 480
Db 421 ENDDAQFTKMTFLNIRRKPOVLAEASASQSCFSDGYPPLSPMTWKCKSDKSPNCTEITE 480
Qy 481 GVMNRKANRKVFQGVSSSTLNNSBAIKGLVKCAVNSLGTSCETILLNSPGPPFIQD 540
Db 481 GVMNRKANRKVFQGVSSSTLNNSBAIKGLVKCAVNSLGTSCETILLNSPGPPFIQD 540
Qy 541 NISFYATTIGVCLLFIWLTLLIICHKYKKOPRYESQLOMVOVTGSSDNEYFYVDFREYEYD 600
Db 541 NISFYATTIGVCLLFIWLTLLIICHKYKKOPRYESQLOMVOVTGSSDNEYFYVDFREYEYD 600
Qy 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGSKTGVSIQVAVKMLKEKADSSEREAALMS 660
Db 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGSKTGVSIQVAVKMLKEKADSSEREAALMS 660
Qy 661 ELKMTQLGSHENIVNLLGACTLSGPYILIPYCCYGDLLNLYLRSKREKPHRTWTIFKE 720
Db 661 ELKMTQLGSHENIVNLLGACTLSGPYILIPYCCYGDLLNLYLRSKREKPHRTWTIFKE 720
Qy 721 HNFSPYPTFQSHPNSSMPGSRVQIHPSDQISGLHGNFSHSEDEIEYENQKLESEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPGSRVQIHPSDQISGLHGNFSHSEDEIEYENQKLESEEDL 780
Qy 781 NVLTEDILLCPAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVKVLCDFGLARDIMSDS 840
Db 781 NVLTEDILLCPAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVKVLCDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWMAPELPGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPELPGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Qy 901 LIQNGFKMDQPFYATEEYIINQSWAFDSRKRPSFPNLTSLGCOLADAEAEAMYQNDG 960
Db 901 LIQNGFKMDQPFYATEEYIINQSWAFDSRKRPSFPNLTSLGCOLADAEAEAMYQNDG 960
Qy 961 RVSECPHTYQNRPRPFSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPRPFSREMDLGLLSPQAQVEDS 993

RESULT 2
FLT3 MOUSE
ID FLT3 MOUSE STANDARD; PRT; 992 AA.
AC Q00342;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FL cytokine receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase
GN receptor flk-2) (Fetal liver kinase 2) (Tyrosine-protein kinase FLT3).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91292518; PubMed=1648448;
RA Matthews W., Jordan C.T., Wiegand G.W., Pardoll D., Lemischka I.R.;

```

RT "A receptor tyrosine kinase specific to hematopoietic stem and
 RT progenitor cell-enriched populations.";
 RL Cell 65:1143-1152(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92019834; PubMed=1656368;
 RA Rosnet O., Marchetto S., Delapeyriere O., Birnbaum D.;
 RT "Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the
 RT PDGFR/CSF1R family.";
 RL Oncogene 6:1641-1650(1991).
 RN [3]
 RP CHARACTERIZATION
 RX MEDLINE=93205405; PubMed=8384358;
 RA Maron N., Rotapel R., Rosnet O., Marchetto S., Lavezzi C.,
 RA Mannoni P., Birnbaum D., Dubreuil P.;
 RT "Biochemical characterization and analysis of the transforming
 RT potential of the FLT3/FLK2 receptor tyrosine kinase.";
 RL Oncogene 8:909-918(1993).
 CC -1- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN
 CC KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HEMATOPOIETIC STEM AND PROGENITOR CELL-
 CC ENRICHED POPULATIONS. FOUND IN BRAIN, PLACENTA AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC -----
 DR EMBL; M64689; AAA37634.1; -;
 DR EMBL; X59398; CAA42041.1; -;
 DR PIR; A39931; A39931.
 DR HSSP; P11362; 1FGK.
 DR MGD; MGI:95559; Flt3.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
 DR Signal; Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
 FT SIGNAL 1 27
 FT CHAIN 28 992
 FT DOMAIN 28 544
 FT TRANSMEM 545 564
 FT DOMAIN 565 992
 FT DOMAIN 611 946
 FT NP_BIND 617 625
 FT BINDING 645 645
 FT ACT_SITE 814 814
 FT CARBOHYD 44 44
 FT CARBOHYD 133 133
 FT CARBOHYD 152 152
 FT CARBOHYD 307 307
 FT CARBOHYD 324 324
 FT CARBOHYD 352 352

FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 503 503 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 150 150 R -> A (IN REF. 2).
 FT CONFLICT 242 242 C -> S (IN REF. 2).
 FT CONFLICT 726 726 S -> F (IN REF. 2).
 FT CONFLICT 957 979 CIRTSIHLPKQAAPQOQGLRAQ -> MYQNNMGVNPHEPS
 FT IYQNRPLRSRAGSEPP (IN REF. 2).
 FT CONFLICT 983 983 R -> A (IN REF. 2).
 FT SEQUENCE 992 AA; 113639 MW; 407A067853372100 CRC64;
 Query Match 84.0%; Score 4429.5; DB 1; Length 992;
 Best Local Similarity 84.1%; Pred. No. 3.7e-289;
 Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;
 QY 1 MPALA-RDAGTVPLLVFSAAMIFGTITNODLPVICKVLINHKNDSSVSKSSSPYAVSES 59
 DB 1 MPALAQSRDRRLLLVLSVMILETVTNODLPVICKVLISHENNGSSAGKPSRYMRVGS 60
 QY 60 PEDLGALRQSSGTWYEAADVDVSASITLQVLVDAPGNISCLWVFKHSSLNCOPHFD 119
 DB 61 PEDLQCTPRQSEGTVEAATVEAEGSITLQVQLATFGDLSCLWVFKHSSLGCOPHFD 120
 QY 120 LQNRGVSMVLKMTQAGEYLLFIQSEATNTYLTFTVIRNTLLYTLRRPYFRKMEQ 179
 DB 121 LQNRGIVSMALLNVTQAGEYLLHIQSERANTYTLFTVNRDTQLYLRRPYFRKMEQ 180
 QY 180 DALVICISSVPEPIVWVLCDQSGESKEEPAVVKKEKVLHELPGTDIRCCARNELGR 239
 DB 181 DALLCISGVPETVWVLCSSHRESCKEGBPAVVRKEEVLHELPGTDIRCCARNALGR 240
 QY 240 ECTRLFTDLNQTPTLLPQLFKVGEPLWIRCKAVVNHGFLTWELNKALEEGNYPE 299
 DB 241 ECTKLFTDLNQAPOSTLPQLFKVGEPLWIRCKAIVNHGFLTWELNKALEEGNYPE 300
 QY 300 MSTYSTNTRMIRILFAFVSSVARNDTGYTSSSRKPSQSALVTIVGKGFINATNSSEY 359
 DB 301 MSTYSTNTRMIRILFAFVSSVGRNDTGYTSSSRKPSQSALVTILEKGFINATSSQEEY 360
 QY 360 EIDQYEEFCFSVRKAYQIRCTWTFSRKSFPCEQKGLDNGYSISKFCNHKQPGYIFH 419
 DB 361 EIDPYEKFCFSVRKAYPRIRCTWTFQSAFPCEQGLEDDGYSISKFCDHKPKGEYIF 420
 QY 420 AENDDAQFTKFTLNRKPKQVLAASASQASCFSDGYPLPSMTWKCKSDKSPNCTEIT 479
 DB 421 AENDDAQFTKFTLNRKPKQVLAASASQASCFSDGYPLPSMTWKCKSDKSPNCTEIP 480
 QY 480 EGVNKRANRRVFGQWSSSTLNMSEAIKGLVKVCCAYNSLGTSCETILLNSPGPPFIQ 539
 DB 481 EGVNKRANRRVFGQWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETILLNSPGPPFIQ 540
 QY 540 DNISFYATIGVCLLPIVVLTLIICHYKQKRYESQOLQMVQVGTSSDNEYFYVDFREY 599
 DB 541 DNISFYATIGLCLPIVVLTLIICHYKQKRYESQOLQMVQVGTSSDNEYFYVDFREY 600
 QY 600 DLKWEFPRENLEFGVLGSGAFGKVMNATYGIKTGYISOAVKMLKEKADSSREALM 659
 DB 601 DLKWEFPRENLEFGVLGSGAFGRVMNATYGIKTGYISOAVKMLKEKADSSREALM 660
 QY 660 SELKMTQLGSHENIVNLLGACTLSGPYILPEYCCYGDLLNLSRKPKFRTWTETIFK 719
 DB 661 SELKMTQLGSHENIVNLLGACTLSGPYILPEYCCYGDLLNLSRKPKFRTWTETIFK 720
 QY 720 EHNFSYPTFOHNSNMPGSGREVQIHPSDQISGLHNGSFHSEDEIEYENQKRL--EEE 777
 DB 721 EHNFSYPTFOHNSNMPGSGREVQIHPSDQISGLHNGSFHSEDEIEYENQKRL--EEE 780
 QY 778 EDLNVLTEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLTHGKVKICDFGLARDIM 837
 DB 781 EDLNVLTEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLTHGKVKICDFGLARDIL 840
 QY 838 SDSNYVVRGNARLPVKWMAPESLFEGITIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897

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Db 841 SDSSVVRGNARLPVKWAPSLFEGIVTIKSDVWSYGILLWEIFSLGWNYPGIPVDAN 900
QY 898 FYKLIQNGFMDOPFYATEEYIIWQSCWAFDSKRSPFNLTSLFCQLADAEAMYQN 957
Db 901 FYKLIQSGFKNQEPFYATEGYFYWQSCWAFDSKRSPFNLTSLFCQLADAEAEAC--- 957
QY 958 VDGVRSECPHYQNRPFREMDLGLLSPOAQVE 991
Db 958 ---IRTSIHLPKQAAPQORG-GLRAQSPQRQVK 986

RESULT 3
KIT_CAPHI STANDARD; PRT; 978 AA.
AC Q28317;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Shiba; TISSUE=Cerebellum;
RX MEDLINE=97342548; PubMed=9199245;
RA Tanaka S., Yanagisawa N., Tojo H., Kim Y.-J., Tsujimura T.,
RA Kitamura Y., Sawasaki T., Tachi C.;
RT "Molecular cloning of cDNA encoding the c-kit receptor of Shiba goats
RT and a novel alanine insertion specific to goats and sheep in the
RT Kitashimizu region.";
RL Biochim. Biophys. Acta 1352:151-155(1997).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC -----
CC EMBL; D45168; BAA08116.1; -.
CC HSSP; P11362; IFGK.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003598; Ig_c2.
CC InterPro; IPR003600; Ig_like.
CC InterPro; IPR001824; RfkinaseIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 2.
CC SMART; SM00410; Ig_like; 2.
CC SMART; SM00408; IGC2; 1.
CC SMART; SM00219; Tyfkc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

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DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein_kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 22
FT CHAIN 23 978
FT DOMAIN 23 521
FT TRANSMEM 522 544
FT DOMAIN 545 978
FT DOMAIN 590 939
FT NP_BIND 596 604
FT BINDING 624 624
FT ACT_SITE 794 794
FT MOD_RES 825 825
FT CARBOHYD 94 94
FT CARBOHYD 130 130
FT CARBOHYD 145 145
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FT CARBOHYD 401 401
FT CARBOHYD 464 464
FT CARBOHYD 487 487
SQ SEQUENCE 978 AA; 109722 MW; CA4D63F98205CA9 CRC64;

Query Match 24.6%; Score 1295.5; DB 1; Length 978;
Best Local Similarity 33.3%; Pred. No. 3.9e-79;
Matches 335; Conservative 169; Mismatches 339; Indels 163; Gaps 35;

QY 47 VGKSSSPMSESEPEDLGC-ALRPQSSGTYVAAAIVEDVSASITLQVLVDAPGNISCLW 105
Db 20 VQTGSSQPSV--SPGELSLPSIHPAKS-----ELIVSVGDEIRLLCTDPGFVK--W 66
QY 106 VFHSSSLNCQPHFDLQNRGVSVMLKMTQACGYLLFIQSEAT---NYTILFTVSI RN 162
Db 67 TFE-----ILQLSEKTNPEWIT-EKAEATNGTNGTCTNKGUSS 105
QY 163 TL-----LYTLRRPYFRKMENQDALVCISVPPEPIVEWVLCDQSGESKEESP AV 213
Db 106 SIYVVRDPEKFLIDJLPLYKKEEN-DTLVRCPLTDPB-VTNYSLTGCEGKPLKDLT FV 163
QY 214 -----VKKEKVLHELFTGDIRC--CARNELGRE-CTRLFTID----LNQTPQT LTP 258
Db 164 ADPRAGITIRNVKREYHRL-----CLHCSANQKGKMSKKFTLKVRAAIKAVP VSVS 217
QY 259 Q--LFLKVGPELWIRCKAVHVNHGFLTWELNKALEEGNVFEMSTYSTNRTMIRL PAF 316
Db 218 KTSYLLREGGEFAVTCILIKDVSSSDVMKIENSSQQAQTKKNSWHQGDFFSYLQ ERLT 277
QY 317 VSSVARNDTGYTTCSSSKHPQSALVT---IVGKGFINA-----TNSSEDEYD OY 364
Db 278 ISSARVNDSGVFMCYANNTFGSANVTTLLEVVDKGFINIFPMNTTVFVNDG EVDL---- 334
QY 365 EBFCSVRPKAYPO-----IRCTWTFSRKSPCEQKGLDNGYSISKFNH K H----- 411
Db 335 -----VVEYEAYPKPEHRQWIMYMRNSTDKWDVDPKSE-----NESNIRYV N EHLTRLK 384
QY 412 --QPGEYIEHAENDDAQFTKMTINIRKPKQVLAESA--SQASCFSQGYPLPSP WTKKC 467
Db 385 GTEGGTYTFHVSNDVNSDVSFTFNVNNTKPEILLTHRLVNGMLQCVAA GFPEPTIDWYFC 444
QY 468 SDKSPNCTEEI-TEGVNMRKANRVFGQWSSSTLNMSSEAIKGFVKVCAYNS LGSCTBT 526
Db 445 PGTQRCSVPVGPVDVQIQNSVSPFGKLVVYSIIDDFTFKHNGTVCERAYND VCKSSAS 504
QY 527 ILLNSPGFPFFIQDN-----ISFYATIGVCLLFIIVVLTLLICHYKQ PFRY 572
Db 505 F-----NFAFGKNKEQIHAHTLFTPLLIIGFVIAAGLMCIFVMILT---Y KQLQKPMY 554

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QY 573 ESQLOMV-OVTGSSDNEYFYVDREYEDLKWEFFPRENLEFGKVLGSGAGKUMNATAYG 631
 Db 555 EVQWKVEEING---NNYVIIDPTQPDYHKWEFFPRNRUSFGKTLGAGAGKVEATAYG 611
 QY 632 ISKTGVSIOAVKMLKEKADSSREALMSKMTOLGSHENIVNLLGACTLSGPIYLIF 691
 Db 612 LKSDAAMTAVKMLKPSAHLTEREALMSKLVSLVGNHMINVLLGACTIGGPLVIT 671
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 Db 672 EYCCYGDLLNLYRSKREKPHRTWTE-----IPKEHNFSPYPTFQSHPNSSM---PGSRE 742
 QY 743 VQIHDPDSQISGLHNGSPHSEDEIEVENQKRLSEEDLVNLFEDLLCAYQVAKMEPL 802
 Db 732 VVPTKAADKRRSARGISY-----IERDVTVAIMDEDEL-ALDELDLSFSYQVAKGMAL 785
 QY 803 EFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDSNVYVGNARLPVKWAPESLFE 862
 Db 786 ASKNCIHRDLAARNVLVTHGKVKICDFGLARDIMSDSNVYVGNARLPVKWAPESLFE 862
 QY 863 GIYTIKSDVMSYGILLWEIFSGVNPYPGIPVDANFYKLIQNGKMDQPPYATEEYIIM 922
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 QY 923 QSCWAFDSKRSFNLISFLCQLADAEAEANYQVDRVSEC-PH 967
 Db 906 KTCWDADPLKRFQIVQVLEIKQISESTNHTYSN-----LANCSPH 947
 RESULT 4
 KIT_BOVIN STANDARD; PRT; 977 AA.
 ID KIT_BOVIN STANDARD; PRT; 977 AA.
 AC P43481;
 RA Kubota T., Hikono H., Sasaki E., Sakurai M.;
 OC "Sequence of a bovine c-kit proto-oncogene cDNA."
 OC Gene 141:305-306(1994).
 RL GENE-1: FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D16680; BAA04084.1; -;
 DR HSPG; P11362; IFGK.
 DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR001824; RTKkinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; Ig_like; 2.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferrase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain.
 FT SIGNAL 1 22
 FT CHAIN 23 977
 FT DOMAIN 23 521
 FT TRANSMEM 522 544
 FT DOMAIN 545 977
 FT DOMAIN 590 938
 FT NP_BIND 596 604
 FT BINDING 624 624
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 FT CARBOHYD 401 401
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 FT CARBOHYD 487 487
 SQ SEQUENCE 977 AA; 109685 MW; 4B2719050893B7EF CRC64;
 Query Match 24.4%; Score 1286; DB 1; Length 977;
 Best Local Similarity 33.2%; Pred. No. 1.7e-78;
 Matches 332; Conservative 172; Mismatches 344; Indels 152; Gaps 36;
 QY 47 VCKSSSYPMWSESPEDLGC-ALRPOSSGTVYERAAAEVVDVASITLQVLVADPAGNISCLW 105
 Db 20 VQTGSSQPSV--SPGELSIPSIHPAKS-----ELIVSVGDEIRLLCTDPGFVK--W 66
 QY 106 VFKHSSSLNCPHFQDLQNRGVSMVILKMTETQAGEVLLFIOSEAT---NYTILFTVSIRN 162
 Db 67 TFE-----ILGQSEKTNPEWIT-EKAEATNTGNYTCTNKGGLSS 105
 QY 163 TL-----LYTLRRPYFRKMNQDALVCISESVPEPIVEWVLCDGSGESCKESPASV 213
 Db 106 SIYVVRDPEKFLDLDPLYGKEEN-DTLVRCPLTDPE-VTNYSLTGCCEGKPLPKDLTFV 163
 QY 214 -----VKKEEKLVELHFGTDIRC--CARNELGRE-CTRLFTID----LNQTPPTLTP 258
 Db 164 ADPKAGITIRNVKREYHRL-----CLHCSANQRGKSMLSKFKTLKVAIRAIAKAVPVSVS 217
 QY 259 Q--LFLKVEPLWIRCKAVHNVHGFGLTWELNKALEEGNYEMSTYSTNRTWIRLILFAF 316
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 QY 317 VSSVARNDTGYTCTSSSKHPSQSALVT---IVGKGFINA-----TNSSEDEYIDQY 364
 Db 278 ISSARVNSGVFMCVANNITFGSANVTTLLEVVDKGFINIFPMNNTVTVFNDGENVDL--- 334
 QY 365 BEFCFSVRFKAYPQ-IRCTWTFSRKS-----PFCEQKGLDNGYSISKFCNHKH----- 411
 Db 335 -----VVEYAYPKPVHROWIYMNRTSTDKWDYDPKSE-----NESNIYVNLHLTRUK 384

QY 412 --OPGEYIFHAENDAOFTKMTLNIRKPOVLAESA--SQACFPDGYPLPSWTWKCC 467
 Db 385 GTEGTYTFHVSNDVSVTFNVYVTKBEILTHDLVNGMLQCVAAAGPEPTIDHYFC 444
 QY 468 SDKSPNCTEEI--TEGVNMRKANRVFGQVSSSTIANSEAIKFLVKCCAYNSIGTSCET 526
 Db 445 PGTQRCSVPVGPVDQIQNSVSPFGKLVVYSTIDBSTFKHNGTVECRAYNDVKGSSAS 504
 QY 527 ILLNSPGPPF-----FIQDTSFVATIGVCLLFIIVLTLLCHIKYKQFRYESQLQM 578
 Db 505 FNFAPKGNKEQIHAHTLFTLLIGFVIAAGLMCFIVMLT-----YKLOKPMYEVQWKV 560
 QY 579 V-QVTGSSDNEFYVDREYEDYDLKWPENLEBFGVLGSGAFGKVMNATAYGISKTGV 637
 Db 561 VEEING---NNVYIDPTQLPYDHKNWPPNRLSFGKTLGAGAFKGVVEATAYGLIKSDA 617
 QY 638 SIOVAVKMLKADSSREALMSKLMQTLGSHENIVNLGACTLSGPIYLIFEYCCYG 697
 Db 618 AMTAVKMLKPSAHLTEREALMSKLVLSYLGHNHNVNLGACTIGGPTLVITEYCCYG 677
 QY 698 DLLNVLRSKRKRKPHRTWTE-----IFKEHNFSPYFPQSHPNISM-----PGSREVQIHPD 748
 Db 678 DLLNVLRSKRKRKPHRTWTE-----IFKEHNFSPYFPQSHPNISM-----PGSREVQIHPD 748
 QY 749 SDQISGLHGNFSHSEDETEYENQKLEEDLNLVLTREDLLCFAYQVAKMGMEFLFKSCV 808
 Db 737 ADKRSARIGSY-----IERDVTAPMEDEL-ALDLELLSFSYQVAKMGMAFLASKNCI 790
 QY 809 HRDLAARNVLVTHGKVKVICDFGLARDIMSDSNVYVGNARLPVKWMAPESLFEGIYTIK 868
 Db 791 HRDLAARNVLVTHGKVKVICDFGLARDIMSDSNVYVGNARLPVKWMAPESLFEGIYTIK 868
 QY 869 SDVWSYGILLWEIFSLGNVPYGPVDANFYKLIONGFMQDPFVATEIYIIQSWAF 928
 Db 851 SDVWSYGIFLWELFSLGSPYGPVDMVDFKLIKEGFRMLSPHAPAEYDINKTCMDA 910
 QY 929 DSRKRSPNLTSLFGCOLADAEAEYVQVNDGRVSEC-PH 967
 Db 911 DPKRPTFKQVQLIEKQISESTNHIYSN-----LANCSPH 946

RESULT 5
 KIT_MOUSE
 ID_KIT_MOUSE STANDARD; PRT; 975 AA.
 AC P0532; Q61415; Q61416; Q61417;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT OR SL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c;
 RA MEDLINE=89296403; PubMed=2456920;
 RA Qiu F., Ray P., Brown K., Barker P.E., Jhanwar S., Ruddle F.H.,
 RA Besmer P.;
 RT "Primary structure of c-kit: relationship with the CSF-1/PDGF
 RT receptor kinase family -- oncogenic activation of v-kit involves
 RT deletion of extracellular domain and C terminus.";
 RL EMBO J. 7:1003-1011(1988).
 RN [2]
 RP SEQUENCE FROM N.A. (TRUNCATED FORM).
 RC STRAIN=ICR;
 RX MEDLINE=92331813; PubMed=1378413;
 RA Rossi P., Marziani G., Albanesi C., Charlesworth A., Geremia R.,
 RA Sorrentino V.;
 RT "A novel c-kit transcript, potentially encoding a truncated receptor,

RT originates within a kit gene intron in mouse spermatids.";
 RL Dev. Biol. 152:203-207(1992).
 RN [3]
 RP LIGAND.
 RX MEDLINE=91006023; PubMed=1698611;
 RA Tan J.C., Buck J., Levi E., Besmer P.;
 RT "Candidate ligand for the c-kit transmembrane kinase receptor: KL, a
 RT fibroblast derived growth factor stimulates mast cells and erythroid
 RT progenitors.";
 RL EMBO J. 9:3287-3294(1990).
 RN [4]
 RP VARIANT W42 ASN-790.
 RX MEDLINE=90100577; PubMed=1688471;
 RA Tan J.C., Nocka K., Ray P., Traktman P., Besmer P.;
 RT "The dominant W42 spotting phenotype results from a missense mutation
 RT in the c-kit receptor kinase.";
 RL Science 247:209-212(1990).
 RN [5]
 RP VARIANT W37 LYS-582; WV MET-660 AND W41 MET-831.
 RX MEDLINE=90269214; PubMed=1693331;
 RA Nocka K., Tan J.C., Chiu E., Chu T.Y., Ray P., Traktman P.,
 RA Besmer P.;
 RT "Molecular bases of dominant negative and loss of function mutations
 RT at the murine c-kit/white spotting locus: W37, W41 and W.";
 RL EMBO J. 9:1805-1813(1990).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: WHITE-SPOTTING VARIANT INDUCES SEVERE EFFECTS ON
 CC PIGMENTATION, GAMETOGENESIS AND HEMATOPOIESIS. MICE HOMOZYGOUS
 CC FOR W42 DIE PERINATALLY OF MACROCYTIC ANEMIA.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC EMBL; Y00864; CAA68772.1; -;
 CC EMBL; X65997; CAA46798.1; -;
 CC EMBL; X65998; CAA46799.1; ALT_SEQ.
 CC EMBL; X65998; CAA46800.1; -;
 CC PIR; S00474; TVMSKT.
 CC HSSP; P11362; IFGK.
 CC MGD; MGI:96677; Kit.
 CC InterPro; IPR00719; Euk_pkinase.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003598; Ig_c2.
 CC InterPro; IPR003600; Ig_like.
 CC InterPro; IPR001824; RTKinaseIII.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC ProDom; PD000001; Euk_pkinase; 2.
 CC SMART; SM00410; IG-like; 3.
 CC SMART; SM00408; IGC2; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 CC PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 CC PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
 CC Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 CC Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW

Immunoglobulin domain; Disease mutation.

KW SIGNAL 1 22
 FT CHAIN 23 975
 FT DOMAIN 23 519
 FT TRANSMEM 520 542
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 FT NP BIND 594 602
 FT BINDING 622 622
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 FT VARIANT 831 831
 SQ SEQUENCE 975 AA; 109001 MW; BAB5CA4D9AF9CD2A CRC64;

Query Match 24.0%; Score 1266; DB 1; Length 975;
 Best Local Similarity 33.2%; Pred. No. 3.7e-77;
 Matches 336; Conservative 173; Mismatches 330; Indels 172; Gaps 41;

QY 35 CVLHKNNDSSVSSYPMVSPEDLGLCARPQSGTGYVEAAAEVDVVSASITLQVL 94
 DB 12 CVLVLRLGQTATSPQASGPSPFP-----SHPAOS-----SLIVEAGDTL--- 54
 QY 95 VDPAGNISCL-----NVFKHSLNCPHFQDLQNRGVVSMVLKMTQAGEYLLFTQSE 148
 DB 55 -----SLTCDPDPFVRWTFK-----TYFN-----EMVENKKNWIIQ-EKAE 89
 QY 149 ATNYTLFTVSIKNTL-----LYTLRPPFRKMNODALVCISEPPEIVE 195
 DB 90 ATR-TGYTCSNSNGLTSSIIYFVRDPAKFLVGLPLFGK-EDSDALVRCLTDPQ-VSN 146
 QY 196 WVLCDGSGESCKESPAP-----VKKEKVLHFGTDIRCCARNELGRECTRL--- 244
 DB 147 YSLIECDGKSLPTDLTFVPKPKAGITIKVRAVRLC-----VRCAAQ-----RDGTWLHSD 199
 QY 245 -FTIDLNOT-----POTTLPOL--FLKVGEPILWIRCKAVHNVHGFGLTW-----E 286
 DB 200 KFTLKVREAIKAI PVSVSPETSHLLKGGDTFTVCTTKIDVSTSVSMWLMKMPQPHIAQ 259
 QY 287 LENKALEEGNYFENSTVSTRTMIRILPAFVSSVARNDTGYTTCSSKHPSQSALVT--- 343
 DB 260 VKHNSWHRGDF-----NYERQETLT-----ISSARVDSDGVFMFYANNITFGSANVTTLK 309
 QY 344 IVKGGFINATN--SSEDEIDQYBEFCFSVRKAYPO-IRCTWTFPSRKSFPCEQKGLD--- 398
 DB 310 VVEKGFNISPVKNTVFTVDGENVDLVVEYEAIPKEHQOQWYNNRT--SANKGKDYVK 367
 QY 399 -NGYSISKFCNKHK-----QPGEYIFHAENDDAQFTKFTLNIKRPQVLA--EASAS 448
 DB 368 SDNKSNIYVNLRLTRLKGTEGGTYFLVNSDASASVTENVVNTKPEILTYDRLING 427
 QY 449 QASCFSDGYPLSPWTKKSDKSNCTEITE-GVMKANKRVKFGQWSSSTLNMSAI 507
 DB 428 MLQCVAREGPEPTIDWYFCTGAEOQRTTPSPVDVQVQNVSVSPFGKLVVOSSIDSVFR 487
 QY 508 KGFVLKCAVNSLQTSCTILLNSPFPFPF---TODN-----ISFVATIGVCLLFIVV 557
 DB 488 HNGTVEKASNDVGKS--SAFFN-----FAFKEIQIAHTLTPPLIGFVAAAGAIIVMV 541
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 Db 655 LLGACTVGGPTLVITEYCCYGDLLNLYRSKREKSFIFSQBEQAALYKNLLHSTEPSCD 714
 QY 731 SHPSSM---PGSREVQIHPSDQISGLHGNSFHSEDIENYQKRLEBEEDLNVLTTED 787
 Db 715 S-SNEYMDMKPGSVY-VPTKTDKRRSARIDSY-----IERDVTPIAMEDDEL-ALDLD 766
 QY 788 LLCFAYOVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNVYVRGN 847
 Db 767 LLSFSYQVAKAMAFASKNCIHRDLAARNILITGRITKICDFGLARDIRNSNVVVRGN 826
 QY 848 ARLPVKWMAPELSEFEGYITIKSDVMSYGLLWEIFSLGNVPYGPVDFANFYKLIQNGFK 907
 Db 827 ARLPVKWMAPELSEFEGYITIKSDVMSYGLLWEIFSLGNVPYGPVDFANFYKLIQNGFK 886
 QY 908 MDQPFYATEEYIIWQSCWAFDSRKRPSFPNLTSFLGCOLADAEAMYNQV 958
 Db 887 MVSPEHAPAEYMDVWKTCDADPLKPTFKQVQVQLIEKQISDSTKHYSNL 937

RESULT 6
 KIT HUMAN
 ID KIT HUMAN STANDARD; PRT; 976 AA.
 AC P10721;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR).
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen).
 GN KIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Term placenta, and Fetal brain;
 RX MEDLINE=88111521; PubMed=2448137;
 RA Yarden Y., Kuang W.-J., Yang-Feng T., Coussens L., Munemitsu S.,
 RA Dull T.J., Chen E., Schlessinger J., Francke U., Ullrich A.;
 RT "Human proto-oncogene c-kit: a new cell surface receptor tyrosine
 RT kinase for an unidentified ligand.";
 RL EMBO J. 6:3341-3351(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93064697; PubMed=1279499;
 RA Giebel L.B., Strunk K.M., Holmes S.A., Spritz R.A.;
 RT "Organization and nucleotide sequence of the human KIT (mast/stem
 RT cell growth factor receptor) proto-oncogene.";
 RL Oncogene 7:2207-2217(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97179223; PubMed=9027509;
 RA Andre C., Hampe A., Lachaume P., Martin E., Wang X.P., Manus V.,
 RA Hu W.X., Galibert F.;
 RT "Sequence analysis of two genomic regions containing the KIT and the
 RT FMS receptor tyrosine kinase genes.";
 RL Genomics 39:216-226(1997).
 RN [4]
 RP VARIANT LYS-583.
 RX MEDLINE=92291284; PubMed=1376329;
 RA Fleischman R.A.;
 RT "Human piebald trait resulting from a dominant negative mutant allele
 RT of the c-kit membrane receptor gene.";
 RL J. Clin. Invest. 89:1713-1717(1992).

RN [5] VARIANTS LEU-584.
 RX MEDLINE=92133600; PubMed=1370874;
 RA Spritz R.A., Giebel L.B., Holmes S.A.;
 RT "Dominant negative and loss of function mutations of the c-kit
 RT (mast/stem cell growth factor receptor) proto-oncogene in human
 RT piebaldism.";
 RL Am. J. Hum. Genet. 50:261-269(1992).
 RN [6] VARIANTS ARG-664.
 RX MEDLINE=92020918; PubMed=1717985;
 RA Giebel L.B., Spritz R.A.;
 RT "Mutation of the KIT (mast/stem cell growth factor receptor)
 RT protooncogene in human piebaldism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8696-8699(1991).
 RN [7] VARIANTS VAL-816.
 RX MEDLINE=94013473; PubMed=7691885;
 RA Furutsu T., Tsujimura T., Tono T., Ikeda H., Kitayama H.,
 RA Koshimizu U., Sugahara H., Butterfield J.H., Ashman L.K.,
 RA Kanayama Y., Matsuzawa Y., Kitamura Y., Kanakura Y.;
 RT "Identification of mutations in the coding sequence of the proto-
 RT oncogene c-kit in a human mast cell leukemia cell line causing
 RT ligand-independent activation of c-kit product.";
 RL J. Clin. Invest. 92:1736-1744(1993).
 RN [8] VARIANTS PIEBALDISM GLY-791 AND VAL-812.
 RX MEDLINE=93322624; PubMed=7687267;
 RA Spritz R.A., Holmes S.A., Itin P., Kuester W.;
 RT "Novel mutations of the KIT (mast/stem cell growth factor receptor)
 RT proto-oncogene in human piebaldism.";
 RL J. Invest. Dermatol. 101:22-25(1993).
 RN [9] VARIANTS PIEBALDISM 893-GLU-PRO-896 DEL.
 RX MEDLINE=96287384; PubMed=8680409;
 RA Riva P., Milani N., Gandolfi P., Larizza L.;
 RA "A 12-bp deletion (7818del112) in the c-kit protooncogene in a large
 RT Italian kindred with piebaldism.";
 RL Hum. Mutat. 6:343-345(1995).
 RN [10] VARIANTS GIST VAL-559 DEL.
 RX MEDLINE=98361155; PubMed=9697690;
 RA Nishida T., Hirota S., Taniguchi M., Hashimoto K., Iozaki K.,
 RA Kanakura H., Kanakura Y., Tanaka T., Takabayashi A., Matsuda H.,
 RA Kitamura Y.;
 RT "Familial gastrointestinal stromal tumours with germline mutation of
 RT the KIT gene.";
 RL Nat. Genet. 19:323-324(1998).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A DEVELOPMENTAL
 CC ABNORMALITY KNOWN AS PIEBALDISM. AN AUTOSOMAL DOMINANT GENETIC
 CC DISORDER OF PIGMENTATION CHARACTERIZED BY CONGENITAL PATCHES OF
 CC WHITE SKIN AND HAIR THAT LACK MELANOCYTES.
 CC -1- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A GASTROINTESTINAL
 CC STROMAL TUMOR (GIST).
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD117 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd117.htm".
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/KITD127.html".
 CC -----
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 CC -----
 DR EMBL; X06182; CAA29548.1; -.
 DR EMBL; X69301; CAA49159.1; -.
 DR EMBL; X69302; CAA49159.1; JOINED.
 DR EMBL; X69303; CAA49159.1; JOINED.
 DR EMBL; X69304; CAA49159.1; JOINED.
 DR EMBL; X69305; CAA49159.1; JOINED.
 DR EMBL; X69306; CAA49159.1; JOINED.
 DR EMBL; X69307; CAA49159.1; JOINED.
 DR EMBL; X69308; CAA49159.1; JOINED.
 DR EMBL; X69309; CAA49159.1; JOINED.
 DR EMBL; X69310; CAA49159.1; JOINED.
 DR EMBL; X69311; CAA49159.1; JOINED.
 DR EMBL; X69312; CAA49159.1; JOINED.
 DR EMBL; X69313; CAA49159.1; JOINED.
 DR EMBL; X69314; CAA49159.1; JOINED.
 DR EMBL; X69315; CAA49159.1; JOINED.
 DR EMBL; X69316; CAA49159.1; JOINED.
 DR EMBL; U63834; AAC50968.1; -.
 DR PIR; S01426; TVHUKT.
 DR HSSP; P11362; IFGK.
 DR Genew; HGNC:6342; KIT.
 DR MIM; 164920; -.
 DR MIM; 172800; -.
 DR MIM; 606764; -.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; TyPKG; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR_KIN_III; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Disease mutation.
 FT SIGNAL 1 22
 FT CHAIN 23 976 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
 FT DOMAIN 23 520 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 521 543 POTENTIAL.
 FT DOMAIN 544 976 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 589 937 PROTEIN KINASE.
 FT NP BIND 595 603 ATP (BY SIMILARITY).
 FT BINDING 623 623 ATP (BY SIMILARITY).
 FT ACT SITE 792 792 BY SIMILARITY.
 FT MOD_RES 823 823 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 559 559 MISSING (IN GIST).
 FT VARIANT 583 583 /FTID=VAR_007965.
 FT VARIANT 584 584 E -> K (IN PIEBALDISM).
 FT VARIANT 584 584 F -> L (IN PIEBALDISM).
 FT VARIANT 664 664 /FTID=VAR_004105.
 FT VARIANT 664 664 G -> R (IN PIEBALDISM).

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FT VARIANT 791 791 /FTid=VAR_004106.
FT R -> G (IN PIEBALDISM).
FT /FTid=VAR_004107.
FT VARIANT 812 812 G -> V (IN PIEBALDISM).
FT /FTid=VAR_004108.
FT VARIANT 816 816 D -> V (IN MAST CELL LEUKEMIA;
FT CONSTITUTIVELY ACTIVATED).
FT /FTid=VAR_004109.
FT VARIANT 893 896 MISSING (IN SEVERE PIEBALDISM).
FT /FTid=VAR_004110.
SQ SEQUENCE 976 AA; 109864 MW; 81BCD76817F3454 CRC64;

Query Match 23.7%; Score 1251; DB 1; Length 976;
Best Local Similarity 32.7%; Pred. No. 3.8e-76;
Matches 324; Conservative 166; Mismatches 352; Indels 148; Gaps 34;

QY 47 VGRSSSPMVSESPEDLGCALRPOSSGTVEAAAVEVDVSASITLQVLVADAPGNISCLWV 106
DB 20 VQTGSSQPSVSPG-EPSPPSIHFGKSLDI-----VRVGDRIILLCTDPGFVK--WT 67
QY 107 FKHSLLNCQPHFDLQNRGVSMVILKMTETQAGEYLLFIQSEATN---YTILFTVSIKNT 163
DB 68 FE-----ILDETENKQEWIT-ERAEATNTGKYCTCNKHGLSNS 106
QY 164 L-----LYTLRRPYFRKMNQDALVCISESVPEPIVEWVLCDQSGESCKEE----- 209
DB 107 IYFVRDPKLFVDRSLYGK-EDNDTLRCPLTDPE-VTNYSLKGCQCKPLPKDLRFIP 164
QY 210 ---SPAVVKEEKLHFLFGDTRICCARNELGRECTLFTIDL---NOTPQTLLPO--L 260
DB 165 DPRAGIMIKSVKRAYHRLC---LHCSVDQEGKSVLSKFLKVRPAKPAVVPVSVKASY 221
QY 261 FLKVGEPILWIRKAVHNVHGFGLTWELN---KALBEGNTPEMSTYSTNTRIMIRILFAFV 317
DB 222 LLREGBEFTVTCTIKOVSSSVYSTKRENSQTKLQKYNMHHGDFNVEROAT---LTI 277
QY 318 SSVARNDTGYTCCSSKHPQSALVT---IVGKGFINA-----TNSSEYDEIYOYE 365
DB 278 SSARVNDGVMFCVYANNTFGSANVTTLLEVVDKGFIFIPMINTVVFVNDGENVDL---- 333
QY 366 EFCFSVFKAQPO-IRCTWTFSRKSP--PCQKGLDNGYSISKFNHKKH-----QPGE 415
DB 334 ----IVYEAFPEHQOIMYMNFTFTDKWEDYKPKSESNIRYVSELHLTRLKGTGEGT 389
QY 416 YIFHAENDDAQTKMFTLNIRRKQVILA--EASASQASCFSDGYPPLPSWTWKGCSDKSPN 473
DB 390 YTLVNSDYNAAAFNVYVNTKEILTYDELVNGMLQCVAAGPBTIDWYFCFGEQR 449
QY 474 CTBEITE-GVWNRKANRKYQGWVSSSTLNMSEAIKGLFKCCAYNSLGTSCETILLNSP 532
DB 450 CSASVLPVDVQTLNSSGPPFKLVQSSIDSSAFKRNGTVECKAYNDVGKT--SAYFN-- 505
QY 533 GPPEFIODN-----ISFYATIGVCLLFIVLTLTLLCHYKVKQFVYESQLQM 578
DB 506 --FAFGKNKEQIHPHTLFTPLLLIGFVIVAGMCCIWMILF----YKLOKPMYEVQMW 559
QY 579 V-QVTGSSDNEYFYVDPREYEDLKWFFRENLEFGVLASGAFGKVMNATAYGISKTGV 637
DB 560 VEEING--NNYVYIDTQLPYDHWKFFPNRLSFGKTLGAGAKGVVEATAYGLIKSDA 616
QY 638 SIQAVKMLKEKADSSREALMSKLMWTLGSHENIVNLGACTLSGPIYLIFEYCCYG 697
DB 617 AMTAVKMLKPSAHLTREALMSKLVSLVGNHNMIVNLGACTIGTGLTIVITEYCCYG 676
QY 698 DLLNLYLSKEKPHRTWTE-----IPEHNFSFYPTFQSHPSNM---PGSRREVOIHPD 748
DB 677 DLLNFLRRKRDSDFCCKQEDHAEALYKNLLHSHKSSCSDSSTNEYMDMKPGVSYV-VPTK 735
QY 749 SDQISGLHGNFSHSEDEIYENQKREEDLNVLTFEDLLCPAYQVAKGMFELEFESCV 808
DB 736 ADKRSVRIGSY-----IERDVTFAIMWDEL-ALDEDLLSFSIQVAKMAFLASKNCI 789
QY 809 HRDLAARNVLVTHGKVKVICDFGLARDIMSDSNYSVVRGNARLPVKMMAPESLFGIYTIK 868
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DB 790 HRDLAARNVLVTHGKVKVICDFGLARDIKDSDSNYSVVRGNARLPVKMMAPESLFCNVITYPE 849
QY 869 SDVMSYGIILLWEIFSLGVNYPYGPVDANFYKLQNGFKMDQPPFYATBEIYIIMOSCNWAF 928
DB 850 SDVMSYGIILLWEIFSLGVNYPYGPVDANFYKLQNGFKMDQPPFYATBEIYIIMOSCNWAF 909
QY 929 DSRKRPSFNLTSFLGCQLADAEAMYNQV 958
DB 910 DPLKRPTFKQIVQLIEKQISESTNHIYSNL 939

RESULT 7
KIT CANPA
ID KIT CANFA STANDARD; PRT; 975 AA.
AC O97799;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (SC 2.7.1.112) (SCPR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE=99142897; PubMed=9989791;
RA Ma Y., Longley B.J., Wang X., Blount J.L., Langley K., Caughey G.H.;
RT "Clustering of activating mutations in c-kit's juxtamembrane coding
RT region in canine mast cell neoplasms.";
RL J. Invest. Dermatol. 112:165-170(1999).
CC -I- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -I- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
CC EMBL; AF044249; AA002327.1; -.
CC HSPG; P11362; IFGK.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003600; Ig_like.
CC InterPro; IPR001824; TKKinaseIII.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00047; Ig; 2.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00409; IG; 2.
CC SMART; SM00410; IG_like; 1.
CC SMART; SM00219; TyKc; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
CC Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
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Immunoglobulin domain.
 KW SIGNAL 1 24
 FT CHAIN 25: 975
 FT DOMAIN 25 519
 FT TRANSMEM 520 542
 FT DOMAIN 543 975
 FT DOMAIN 588 936
 FT NP BIND 594 602
 FT BINDING 622 622
 FT ACT SITE 791 791
 FT MOD_RES 822 822
 FT CARBOHYD 96 96
 FT CARBOHYD 132 132
 FT CARBOHYD 147 147
 FT CARBOHYD 286 286
 FT CARBOHYD 296 296
 FT CARBOHYD 303 303
 FT CARBOHYD 355 355
 FT CARBOHYD 370 370
 FT CARBOHYD 403 403
 FT CARBOHYD 466 466
 FT CARBOHYD 489 489
 SQ SEQUENCE 975 AA; 109335 MW; 8F570BDB9F05B1CB CRC64;

Query Match 23.7%; Score 1247.5; DB 1; Length 975;
 Best Local Similarity 33.7%; Pred. No. 6.5e-76;
 Matches 333; Conservative 161; Mismatches 346; Indels 149; Gaps 39;

QY 47 VKGSSSPMUSEPEDLCALRPOSSGTVYAAAEVDVDSASITLOVLVDAPGNISCLWV 106
 DB 22 VRTGSSQFSPGSPSLP-SIHPAKS-----ELIVSGDELRLSLCTDPGPVK--WT 69
 QY 107 FKX--SSLNCPHFLQNRGVSMVLKMTQACEYLLFIQSEATNYTL-----FT 157
 DB 70 FETGLQNETH-----NEWITE-----KABAG-----HTGNYTCTNRDGLRSIY 110
 QY 158 VSIRN--TLTYLRPYFRKMNODALVCISESPVPEVWVLCDSQGSKEESPAPV--- 213
 DB 111 VFVRDPAKLFLVDLPYLGK--EGNDTLVRCLPTDPE--VTNYSLRGCEGKPLPKDLTFVADP 168
 QY 214 -----VKKEKVLHELFGTDIRC--CARNELGRE--CYRLFTID-----INQPTTLPL 260
 DB 169 KAGITIRNVKREYHRL-----CLHGSADQKGRVLSKFTLKRAAIRAVPVVSVSKTS 222
 QY 261 -FLVKGPLMLTRCKAVHVNHFGLTWELN---KALEEGNVFEMSTYSTVTRTMRILFA 315
 DB 223 SLLKEGAFSVMCFIKDVSSVFDVSMWIKENSQQNTAQTSNWHHGDFFERQEKLI--- 279
 QY 316 FVSSVARNDTGYTCCSSSKHPSQSALVT---IVGKGFINA-----TNSSDEYEDQ 363
 DB 280 -ISSARVNDSGVFCYANNTPGSAVNTTLEVDKGFNIFPMSTMSTTFVNDGQNVDL-- 336
 QY 364 YEECFSVRFKAYIQ--IRCTWTFGRKFPCEQKGL---DNGYSISKFCNHGH-----Q 412
 DB 337 -----IVEYEAYPEKPEHQOQIYNNRTFTDWEDYPKSDNESNI--RYVSELHLTRLK 389
 QY 413 PGEYIHAENDAOFTKMTLINRRKPOVLAEASQA--SCFSDGYPLPSMTWKCKSDK 470
 DB 390 GGTTFQVNSDVSSTVFNVTNPKBILTHESLITNGMLQCVAGFPPEVAVGWTFPCGA 449
 QY 471 SPNCTEEI--TEGVNVRKANRVFQGVSSSTLNMSAIAIKFLVKCAYNLSLGTSCETILL 529
 DB 450 EQRCSVPFGPMDVQMONSSLSPSGKLVVQSSIDYSAPKHNGTVBCRAYNNVGRS--SAFF 507
 QY 530 NSPGPFPIQD-----NISFYATIGVCLLPIVVLTLICHYKKQKPPRYESQLQMV 579
 DB 508 N-----FAFKEQIHETHLFTPLLLIGFVIAAGNMCIIVMLT-----YKYLQKPMYEQWKV 559
 QY 580 -QVTGSSDNEYFYVDREYEDLKWEPRENLKGLVKGAGFGKVMNATAYGISKTVS 638
 DB 560 EEING---NNVYIDPTQLPYDHWKFEFPRNRLSPFKTIGAGFGKGVKVEATYGLIKSDAA 616
 QY 639 IQVAYKMLKEKADSSEREAALMSKLMWTQLGSHENIVNLLGACTLSGPIYLIFFEYCCYGD 698

DB 617 MTVAVKMLKPSAHLTEREALMSLKVLSYLGNNHNNVLLGACTVGGPTLVITEYCCYGD 676
 QY 699 LLNVLSRKREKHEHTWTE-----IFKEHNFSFYPTQSHPNSSM---PGSREVOIHPDS 749
 DB 677 LLNPLRRKRSDFICSQEDHGEVALYKMLLHSSKSSCSDSTNEYMDMKPGVSYV--VPTKA 735
 QY 750 DOISGLHGNSFHSDELEYENQKLEBEEEDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVH 809
 DB 736 DKRRSARISY-----IERDVTTPAIMEDEL-ALDLELLSFSYQVAKGMAFLASKNCIH 789
 QY 810 RDLAARNVLVTHGKWKICDFGLARDIMSDNSYVVRGNARLPVKWMAPESELPFGIYTIKS 869
 DB 790 RDLAARNILLTHGRITKICDFGLARDIKDINSYVYVGNARLPVKWMAPESEIFNCVYTFES 849
 QY 870 DVMSYGLLLWEIFSLGVNYPGIPVDANFYKLIQNGFMDQDFVATEEIIYIMOSCAWFD 929
 DB 850 DVMSYGLFWELFSLGSPFPGMPVDSKPYKWKIEGFRMLSPERHAPAEYIMDKTWDAD 909
 QY 930 SRKPSFPNLTSLFLGCOLADAEEAMYNQV 958
 DB 910 PLKPTFKQIVQLLEKQISDSTNHIYSNL 938

RESULT 8
 KFMS FELCA
 ID_KFMS_FELCA STANDARD; PRT; 980 AA.
 AC P13369;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
 DE (EC 2.7.1.112) (Fms proto-oncogene) (c-fms).
 GN CSF1R OR FMS.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8907753; PubMed=2849512;
 RA Woolford J., McAuliffe A., Rohrschneider L.R.;
 RT "Activation of the feline c-fms proto-oncogene: multiple alterations
 RT are required to generate a fully transformed phenotype.";
 RL Cell 55:965-977(1988).
 CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
 CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J03149; AAA30811.1; --
 DR PIR: A31636; TVCTMD.
 DR HSPS; P11362; IFGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF00069; pkinase; 1.

DR ProDom: PD000001; Euk_pkinase; 2.
 DR SMART: SM00410; IG-like; 4.
 DR SMART: SM00408; IG2; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE: PS00240; RECEPTOR TYR_KIN_III; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 980 MACROPHAGE COLONY STIMULATING FACTOR I
 FT RECEPTOR.
 FT DOMAIN 20 509 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 510 535 POTENTIAL.
 FT DOMAIN 536 980 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 104 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 107 197 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 204 298 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 299 397 IG-LIKE C2-TYPE DOMAIN 4.
 FT DOMAIN 398 502 IG-LIKE C2-TYPE DOMAIN 5.
 FT DOMAIN 579 908 PROTEIN KINASE.
 FT NP_BIND 585 593 ATP (BY SIMILARITY).
 FT BINDING 613 613 ATP (BY SIMILARITY).
 FT ACT_SITE 776 776 BY SIMILARITY.
 FT DISULFID 42 84 POTENTIAL.
 FT DISULFID 127 177 POTENTIAL.
 FT DISULFID 224 278 POTENTIAL.
 FT DISULFID 417 482 POTENTIAL.
 FT MOD_RES 807 807 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 490 490 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 980 AA; 108506 MW; 4E5CF661E97CF0FF CRC64;
 Query Match 23.2%; Score 1225.5; DB 1; Length 980;
 Best Local Similarity 33.5%; Pred. No. 1.9e-74;
 Matches 32; Conservative 168; Mismatches 321; Indels 149; Gaps 34;
 QY 83 VDVSASITLQVLVDAPGNISCLW---VFKHSSLNCP-----HFDLQNRGVVSMVIL 131
 DB 32 VEPGTTVTLRCV-----GNGSVWDGPISPHNWLDLDPSSILTTNNATFQNTGYHCT-- 85
 QY 132 KMTETQAGEYL--LPIQSEATNYIL---FTVSTINTLLYTLRPPYFRKMENQDALV-CI 185
 DB 86 EPGNPQGNATIHLYVDKDPAPKVLQAEVTV-----LEGQDALLPCL 128
 QY 186 SESVPEPIVE--WVLCDSQGESCKEE-----SP---AVVKEEKVLHFLGTDIRCCARN 235
 DB 129 ---LUTDPALEAGVSLVRVRGPRVLRQTNYSFSPWHGFTIHKAKFIENHYV---QCSARV 181
 QY 236 ELGRECTRL-----FTIDLNTQPTLL-PQLFLKV-GEPLMIRKCAVNVHFGGLTWELE 288
 DB 182 D-GRTVSMGIWLKVQKDISGATLTLEPAELVRIQEAQIVCSASNIDVNFV----- 235
 QY 289 NKALEEGN-----YEMSTYTNRTMIRILFAVSSVARNDGYTCSSSK---HPSQAL 341
 DB 236 --SLRHGDTKLITISQSDFDHNRQY-KVLTNLNLDHVSFDQAGNYSCTATNAGNHSASV 292
 QY 342 VTIVGKGFINATN--SSEYDELDQVEECFVRPKAYQIR-C-TWTFSRKSPFCQKGLD- 398
 DB 293 FRVVEAYLNLTSQSLQLEVTVGKVDLQVKVEAYFGLSEFNWTV-LGPFSDYQDKLDF 351
 QY 399 ---NGYSISKFCN-----HKHQPGEYIFHAENDDAQTKMFTLIRKRPQVLAEASASQA 450

DB 352 VTIKDTYRTSTSLPRLKRSEAGYSFLARNAGGQNALTFELTRYPPEVRVTMTLNG 411
 QY 451 S-----CFSDGVPPLSWTKKCDKSPNCTEE---ITEGVNRKANRKKVFGOWSSSTLNM 503
 DB 412 SDTLCEASGVPQPSVTWVQCRSHTRDCDESGVLVDSHSEVLSQVPEHIVHSLLA 471
 QY 504 SEAIKGLVLCAYNSLGTSCETILLNSGPPFFIQDNISFYATIGVC---LLFIVVLT 560
 DB 472 GTLEHNRVTECRAFNSVGNSSQTFWPISIGAHTQLPDELFTPVLLTCSIMALLLLLL 531
 QY 561 LICHYKKQFRIESOLQMVQVGTSSDNEYFYVDREYEDLKWEPRENLEFKQKVLGSGA 620
 DB 532 LLLYKQKPKYQVRWKIIE--SYEGNSYTFIDPTQLPYNEKWEPPRNNLQFGKTLGAGA 589
 QY 621 FGKVMNATAYGISTGVSIOVAVKMLKEKADSSREALMSELKMMTQLGSHENIVNLLGA 680
 DB 590 FGKVVETAFGLGKEDAVLKVAVKMLKSTAHADKEALMSELKMMTQLGSHENIVNLLGA 649
 QY 681 CTLSGPIYLIFEYCCYGDLLNLYRSKRE-----KFHRTWTETIFE 720
 DB 650 CTHGGFVLVITEYCCYGDLLNLYRSKRE-----KFHRTWTETIFE 709
 QY 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNSFHSEDEIEYENQKRLSEEDL 780
 DB 710 SDFS-----SQGVDTYVEMRPVSTSSNDSFSEEDLKGEDGRPLE----- 749
 QY 781 NVLTFEDILLCFAYQVAKGMELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
 DB 750 ----LRDLHSSQVQAQMAFLASKNCIHRDVAARNVLLTSGRVAKIGDFGLARDIMSDS 805
 QY 841 NVVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEISLGVNYPYGPVNDANFYK 900
 DB 806 NYIVKGNARLPVKWMAPESEIFDCVTVQSDVMSYGILLWEISLGLNLPYGPVNDANFYK 855
 QY 901 LIQNGKMDQFPYATEEYIIMQSCWAFDSRRKRPFLNLTSLGCOL-ADAEAMYQNV 958
 DB 866 LVKDGQYMAQAFAPAKNIYSIMQACWALEPTERRPFFQICSLQLQQAQEDRRVPNTNL 924
 RESULT 9
 KIT_FELCA
 ID - KIT_FELCA STANDARD; PRT; 978 AA.
 AC Q28889;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=95140426; PubMed=7530827;
 RA Herbst R., Munemitsu S., Ullrich A.;
 RT "Oncogenic activation of v-kit involves deletion of a putative
 RT tyrosine-substrate interaction site.";
 RL Oncogene 10:369-379(1995).
 CC -/- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -/- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -/- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -/- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -/- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC
CC ENBL; S76596; RAB3207.1; --
DR HSP; P11362; IrgK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Irg.
DR InterPro; IPR003006; Irg_MHC.
DR InterPro; IPR003600; Irg_like.
DR InterPro; IPR001824; RkinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Irg; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; Irg; 2.
DR SMART; SM00410; Irg_like; 1.
DR SMART; SM00219; TyfK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
KW Proto-oncogene; tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 22
FT CHAIN 23 978
FT DOMAIN 23 521
FT TRANSMEM 522 544
FT DOMAIN 545 978
FT DOMAIN 590 938
FT NP BIND 596 604
FT BINDING 624 624
FT ACT SITE 793 793
FT MOD_RES 824 824
FT CARBOHYD 94 94
FT CARBOHYD 145 145
FT CARBOHYD 284 284
FT CARBOHYD 294 294
FT CARBOHYD 301 301
FT CARBOHYD 321 321
FT CARBOHYD 353 353
FT CARBOHYD 368 368
FT CARBOHYD 401 401
FT CARBOHYD 464 464
FT CARBOHYD 487 487
SQ SEQUENCE 978 AA; 109449 MW; 6D45472E0744086B CRC64;

Query Match 23.2%; Score 1224.5; DB 1; Length 978;
Best Local Similarity 32.9%; Pred. No. 2.3e-74;
Matches 325; Conservative 167; Mismatches 352; Indels 145; Gaps 35;

Qy 47 VKGSSYPWSESPDLGC-ALRPOSSGTVYEAAYVVDVVSASITLQVLVDAPGNISCLW 105
Db 20 VQTGSSQP--SASPGWLSPIHPATS-----ELIVSAGDEIRLLCTDPGVK--W 66

Qy 106 VFHSSLLQCQPHFDLQNGVSVMLKWTQAGRYLLFIQSEAT--NYTIL----- 155
Db 67 TFE-----TLGQSSSEITHNEMWIT-EKAEANTGNTCTNGGGUSS 105

Qy 156 -FTVSIRN-TLLYTLRRYFRFMENQDALVCITSEVPPEPIVWVLVCDQSGCKSESPAV 213
Db 106 SIYVFRDPAKFLVDLPYLGK-EDHDTLVRCPLTDPE-VTNYSLRGCEGKPLPKDLTFV 163

Qy 214 -----VKKEKVLHFGFDIRCCA-----RNELGECTRLFTIDLNQPTTLPOL- 260
Db 164 TDPKAGITIRNVKREYHRLC---LHCSADRGKSVLSKKFTLKVRAAIRAVPVVSVSKAS 220

Qy 261 -FLKVGEBPLMIRKAVHVNHGFGTLWELENKALBEGYFEMSTYSTYTRTMRILILFAFVSS 319
Db 221 HLLREGEFSCVCLIKDVSSSDVMWIKENSPQTAQPSNSWHQGFNFVRQERLTISS 280

Qy 320 VARNDTGYTCSSSKHPSQALVT---IVKGFINA-----TNSSEYEDIDYEYF 367
Db 281 ARVNDSGVFWCYANNTFGSANVTTLLEVAKGFNIFPMNTTIFVNDGENVDL----- 334

Qy 368 CFSVRFPKAYPO-----TRCTWTFESRKSPCEQKGLDNGYSISKFNHKKH-----Q 412
Db 335 --IVEYAYPKPEHORVWYVNRTLTDKWDYPKS-----DNESNI-RYVSELHLRLKNE 387

Qy 413 PGEYIFHAENDDAQFTKMTLINIRKQPVLAEAS--ASQSCFSDGYPLPSPWTWKCKSDK 470
Db 388 GGTTFQVNSDVSNSVTLNVVYVNTKPEILLTHESLVSGILQCLVAGPPEPTVDVYFCGA 447

Qy 471 SPNTEBITE-GVWNRKANRKFQGWSSSTLNMSEAIKGLVKCCAYNSLGTSCETILL 529
Db 448 EQRCPVPVGLDVQMNSSVPSGKLVVQSSIDYSAFKHNGTVECRASNNVYKGT--SAFF 505

Qy 530 NSPGPEPFIQDN-----ISFYATIGVCLLFIIVLTLLICHYKKKQPRYESQ 575
Db 506 N----FAFKGNSKEQMPHTLFTPLLIGFVIAAGMCIIVMLT-----YKLOKPMYEVQ 557

Qy 576 LQMV-QVTGSSDNEYFYVDREYEDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISK 634
Db 558 WKVVEEING---NNVVIDPTQLPVDHKWEPFRNLSFGKTLGAGAFKVVVEATAYGLIK 614

Qy 635 TGVSIQAVKMLKEKADSSREALMSLKMOTQLGSHENIVNLLGACTLSGPIYILFEYC 694
Db 615 SDAAMTAVAKMLKPSAHLTEREALMSLKVLSYLGNNHNIIVNLLGACTVGGPTLVITEYC 674

Qy 695 CYGDLNVLRSKRKEHRTWTEIFKEHNFSPYPT-FQSHPNSSMPGSRV-VQIHDPDSQI 752
Db 675 CYGDLNPLRRRDSFICSKOEDHAE--VALYKNLLQSKSSCNDSTNEYMDMKGVSVV 732

Qy 753 SGLHNSFHSF--DEIEYENQKRLEEDLNVLTFEDLLCFAYQVAKGMFLEPKSCVH 809
Db 733 VPTKADKERSARIGSYIERDVTVPALMEDDEL-ALDLELLSFSYQVAKGMFLASKNCIH 791

Qy 810 RDLAARNVLVTHGKVKVICDFGLARDIMSDSNVYVVRGNARLPVKWMADESIFEGITYTKS 869
Db 792 RDLAARNILLTHGRITKICDFGLARDIKDNSYVYVKGARLPVKWMADESIFNCVYTTES 851

Qy 870 DVWSYGLLWEIFSLGVNYPGIPVDANFYKLIQNGFKMDQDPFYATEIYIIMOSCAWPD 929
Db 852 DVWSYGLFWELFSLUGSPYPGMPVDISKYKMKEGFRMLSPHEAPAEWYDIMKTCWDAD 911

Qy 930 SRKRPSPFNLSFLGCOLADAEAEAMYQNV 958
Db 912 PLKRPFTKQIVQLIEKQISDSTNHIYSNL 940

RESULT 10
KFMS FSVM
ID KFMS FSVM STANDARD; PRT; 978 AA.
AC P00545; Q86597;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase transforming protein fms (EC 2.7.1.112).
GN V-FMS.
OS Feline sarcoma virus (strain McDonough).
OC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses.
RX NCBI_TaxID=11778;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=84119469; PubMed=6582485;
RA Hampe A.; Gobet M.; Sherr C.J.; Galibert F.;
RT "Nucleotide sequence of the feline retroviral oncogene v-fms shows
RT unexpected homology with oncogenes encoding tyrosine-specific protein
RT kinases."
RL Proc. Natl. Acad. Sci. U.S.A. 81:85-89(1984).

[2]
 RN REVISIONS, SEQUENCE FROM N.A.
 RX MEDLINE=92015516; PubMed=1833563;
 RA Smola U., Hennig D., Hadwiger-Fangmeier A., Schuetz B., Pfaff E.,
 RA Niemann H., Tamura T.;
 RT "Reassessment of the v-fms sequence: threonine phosphorylation of the
 COOH-terminal domain.";
 RL J. Virol. 65:6181-6187(1991).
 CC -!- FUNCTION: V-FMS IS DERIVED FROM THE RECEPTOR FOR COLONY
 CC STIMULATING FACTOR 1 (CSF-1).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FMS
 CC POLYPEPTIDE.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 DR EMBL; K01643; AAA43045.1; -;
 DR EMBL; S59588; AAB20028.1; -;
 DR PIR; A06544; TWMVD.
 DR HSSP; P11362; IFGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; Ig_Like; 4.
 DR SMART; SM00408; IG2; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Polypeptide; Tyrosine-protein kinase; Oncogene; Transferase; Receptor;
 KW Transmembrane; Glycoprotein; Phosphorylation; ATP-binding;
 KW Immunoglobulin domain; Repeat.
 KW DOMAIN 1 543 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 544 568 POTENTIAL.
 FT DOMAIN 569 978 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 58 138 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 141 231 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 238 332 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 333 431 IG-LIKE C2-TYPE DOMAIN 4.
 FT DOMAIN 432 536 IG-LIKE C2-TYPE DOMAIN 5.
 FT DOMAIN 613 942 PROTEIN KINASE.
 FT NP_BIND 619 627 ATP (BY SIMILARITY).
 FT BINDING 647 647 ATP (BY SIMILARITY).
 FT DISULFID 76 118 POTENTIAL.
 FT DISULFID 161 211 POTENTIAL.
 FT DISULFID 258 312 POTENTIAL.
 FT DISULFID 451 516 POTENTIAL.
 FT MOD_RES 841 841 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 973 973 PHOSPHORYLATION.
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 524 524 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 714 714 L -> P (IN REF. 1).
 FT CONFLICT 971 978 QRTPPVAR -> RGPPL (IN REF. 1).
 SQ SEQUENCE 978 AA; 108491 MW; 4C7CAC4835185EBF CRC64;
 Query Match 23.2%; Score 1224; DB 1; Length 978;
 Best Local Similarity 32.6%; Pred. No. 2.4e-74;
 Matches 334; Conservative 173; Mismatches 326; Indels 192; Gaps 39;
 QY 65 CALRPQSSG-----TYEAAAVE-----VDVASITLQVLVDAPGNISCL 104
 DB 28 CCLPEAMGPRALLVLLMATAHQAQVPIQSPGPELVPEPGTIVTLRCV-----GNGSVE 83
 QY 105 W---VFKISLNCQP-----HFDLQNRGVVSMVLKMTETQAGE-----YLLFIQ 146
 DB 84 WDGPISPHWNLDLPSSILTTNNATFQNTGYHC-----TEPGNPRGNATIHLYVK 136
 QY 147 SEATNYTIL---FTVSIRNTLYTLRRPYFRKWNQDALV-CISESVPEPIVE--WVLC 200
 DB 137 DPARPWKVLAQEVTV-----LEGQDALLPCL---LTDPALEAGVSLVR 176
 QY 201 SQGESCKEE-----SP---AVVKEEKLHELFGTDIRCARNELGRECTRL-----FTI 247
 DB 177 VGRPVLRQTNYSFSPWHGFTTHKAKFTENHYV-----QCSARVD-GRVTSMGIWIKVQK 231
 QY 248 DLNQTFQPTL-PQLFLKV-GEPLMIRCKAVHNVHGLTWELNKALEBGN-----YFEMS 301
 DB 232 DISGPATLTLEPAELVRIQEAQVCSASINDVNPDV-----SLRHGDTKLITISQQS 284
 QY 302 TYSTNRTMIRILFAFVSSVARNDTGYTCSSSK---HPSQSALVTIVGKFINATN-SSE 357
 DB 285 DPHDNRYQ-KVLTNLNDHVSFQDAGNYSCATNAMGNHSASMVFRVVEAYSNTSEQSL 343
 QY 358 DYEIDQYSEFCFSFRKAYPQRC-TWTPSRKSFPCQKGLD-----NGVSIKFCN--- 408
 DB 344 LQEVTVGKVDLQVKVEAYPGLESFNWTV-LGFFSDYQDKLDFVTIKTYRTYRSTLSLR 402
 QY 409 -HKHQGEYIFHAENDDAQFTKMTLNIRRKPOVLAEASASQAS-----CFSDGYPLPSWT 463
 DB 403 LKRSESGRYSLARNAGGQNALTFELTLRYPEVVRTMTLINGSDDLCEASGYQPQSVT 462
 QY 464 WKKCDKSPNCTEE---ITEGVNKRANKRVFGQVWSSSTLNMSEAIFLKVCCAYNSL 520
 DB 463 WQCRSHTRDCDESAGLVLEDSHSEVLSQLVPFYEVIVHSLAIGTLNHRNRYECRAFNSV 522
 QY 521 GTSCEITLLNSPGPPFIQDNISFYATIGVC---LLFIVVLTLILCHYKQKQRYESQLQ 577
 DB 523 GNSSTFWPISIGAHMTPDELFTPVLLTCSIMALLLLLLLLLLLYKQKQRYQVRWK 582
 QY 578 MVQVTSSSDNEYFYVDPREYEDLKWEFPRENLEFGKVLGSAFGKVMNATAYGISKTGV 637
 DB 583 IIE--SYEGNSYTFIDPTQLPYNKWEPRNNLQFGKTLGTGAFGKGVATEAFLGKEDA 640
 QY 638 SIQVAVKMLKEKADSSEREAALMSLKMMTQLGSHENIVNLLGACTLSGIYLIPEYCCYG 697
 DB 641 VLKVAVKMLKSTAHADAKEALMSLKMIMSHLQGHENIVNLLGACTHGGPVLVITEYCCYG 700
 QY 698 DLLNVLRSKRE-----KFRHTWTWEIFKEHNFSEYFTFQSHFNSSM 737
 DB 701 DLLNFRQAEAMLGPSLSVGQDPEAGAKYKNHLEKKYVRDSDGFS----- 747
 QY 738 PGSREVRQIHPSDDQISGLHGNFSHSEDEIEYENQKRLKEEEDLNVLTFDDLLCFAYQVAK 797
 DB 748 --SQGVTVYENRPSYSSNDSDSFEEDLGKEDGRPLE-----LRDLHFFSQVAQ 796
 QY 798 GMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDSNYVVRGNARLPVKWMAP 857
 DB 797 GMAFLASKNCIHRDVAARNVLLTSGRVAKIGDFGLARDIMSDSNYVVRGNARLPVKWMAP 856

QY 858 ESLEPGIYTIKSDVWSYGLILLWEIFSLGVNPPYGPVDFANFYKLIQNGKMDOPFYATEE 917
 DB 857 ESIFDCVYTVQSDVWSYGLILLWEIFSLGVNPPYGPVDFANFYKLIQNGKMDOPFYATEE 916
 QY 918 IYIMQSCWAFDRKRPSPFNLTSLFCQADAEAMYNQVGRV---SBCPHYQNR-- 972
 DB 917 IYISIMQACWALEPTRRPTFOQICSLQKQ---AQE-----DRVPNTNLPSSSSRL 967
 QY 973 RPFSS 977
 DB 968 RPNQR 972

RESULT 11
 XFMS_HUMAN STANDARD; PRT; 972 AA.
 AC P07333;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
 DE (EC 2.7.1.112) (fms proto-oncogene) (c-fms) (CD115 antigen).
 GN CSF1R OR FMS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89239490; PubMed=2524025;
 RA Hampe A., Shamon B.M., Gobet M., Sherr C.J., Galibert P.;
 RT "Nucleotide sequence and structural organization of the human FMS
 RT proto-oncogene.";
 RL Oncogene Res. 4:9-17(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86175013; PubMed=2421165;
 RA Coussens L., van Beveren C., Smith D., Chen E., Mitchell R.L.,
 RA Isacke C.M., Verma I.M., Ullrich A.;
 RT "Structural alteration of viral homologue of receptor proto-oncogene
 RT fms at carboxyl terminus.";
 RL Nature 320:277-280(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97179223; PubMed=9027509;
 RA Andre C., Hampe A., Lacharme P., Martin E., Wang X.P., Manus V.,
 RA Hu W.X., Galibert P.;
 RT "Sequence analysis of two genomic regions containing the KIT and the
 RT FMS receptor tyrosine kinase genes.";
 RL Genomics 39:216-226(1997).
 RN [4]
 RP SEQUENCE OF 1-16 FROM N.A.
 RX MEDLINE=89261741; PubMed=2524648;
 RA Visvader J., Verma I.M.;
 RT "Differential transcription of exon 1 of the human c-fms gene in
 RT placental trophoblasts and monocytes.";
 RL Mol. Cell. Biol. 9:1336-1341(1989).
 RN [5]
 RP SEQUENCE OF 1-16 FROM N.A.
 RX MEDLINE=86281820; PubMed=3525854;
 RA Wheeler E.F., Rousel M.F., Hampe A., Walker M.H., Fried V.A.,
 RA Look A.T., Rettenmier C.W., Sherr C.J.;
 RT "The amino-terminal domain of the v-fms oncogene product includes a
 RT functional signal peptide that directs synthesis of a transforming
 RT glycoprotein in the absence of feline leukemia virus gag sequences.";
 RL J. Virol. 59:224-233(1986).
 CC -1- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
 CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
 CC -1- TYROSINE KINASE ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-

CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 1:13-21(2000);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1999017666_g.htm".
 CC
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 CC
 DR EMBL; M25786; AA58421.1; -;
 DR EMBL; U63963; AA51696.1; -;
 DR EMBL; M14002; AA35849.1; -;
 DR EMBL; X03663; CAA27300.1; -;
 DR PIR; S08123; TVHUMD.
 DR HSSP; P11362; LFQK.
 DR Genew; HGNC:2433; CSF1R.
 DR MIM; 164770; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG_Like; 3.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR_KIN_III; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; Signal;
 KW Immunoglobulin domain; Repeat; Polymorphism.
 FT SIGNAL 1 19
 FT CHAIN 20 972
 FT MACROPHAGE COLONY STIMULATING FACTOR I
 FT RECEPTOR.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE C2-TYPE DOMAIN 1.
 FT IG-LIKE C2-TYPE DOMAIN 2.
 FT IG-LIKE C2-TYPE DOMAIN 3.
 FT IG-LIKE C2-TYPE DOMAIN 4.
 FT IG-LIKE C2-TYPE DOMAIN 5.
 FT PROTEIN KINASE.
 FT ATP (BY SIMILARITY).
 FT ATP (BY SIMILARITY).
 FT BY SIMILARITY.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT PHOSPHORYLATION (AUTO-) (IN VITRO) (BY
 FT SIMILARITY).
 FT PHOSPHORYLATION (AUTO-) (IN VIVO) (BY
 FT SIMILARITY).
 FT PHOSPHORYLATION (AUTO-) (IN VITRO) (BY
 FT SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 45 45
 FT CARBOHYD 73 73
 FT CARBOHYD 153 153
 FT CARBOHYD 240 240
 FT CARBOHYD 275 275
 FT CARBOHYD 302 302
 FT CARBOHYD 335 335
 FT CARBOHYD 353 353

FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 960 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT DOMAIN 25 505 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 506 530 POTENTIAL.
FT DOMAIN 531 960 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 575 913 PROTEIN KINASE.
FT NP BIND 581 589 ATP (BY SIMILARITY).
FT BINDING 609 609 ATP (BY SIMILARITY).
FT ACT SITE 777 777 BY SIMILARITY.
FT MOD_RES 808 808 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 960 AA; 107311 MW; 0893850527AB68F6 CRC64;
Query Match 23.0%; Score 1215; DB 1; Length 960;
Best Local Similarity 32.3%; Pred. No. 9.6e-74;
Matches 314; Conservative 165; Mismatches 370; Indels 124; Gaps 34;
QY 66 ALRQSGTVEAAAEVDVDSASTLQVLVDAPGNISCLWFKUSSI-----LNCQPHFD 119
DB 18 SLIPAGSGVPHEESLVNKGEEELRLKNERGP-----VTWNFQNSDPSAKTRISNEKEWH 73
QY 120 LQNRGV--VSMVLKMTQAGEVLLTQSEATNVTILFTVSIINTLLYTLRRPVRKWE 177
DB 74 TKNATIRDIGYECKSGKSVNSFVFKOP-----NVLFV-----DSLII-----GKED 119
QY 178 NQDALVCISEVPBP-IVEWLVCDSQGSCKEESPAVVKKEE-----KVLHFLFGTDIRCC 232
DB 120 SDILLVC---PLTDPDLNFTLRKCDGKPLPKNTFTIPNPKQGIILKNVQSFQCYQCL 176
QY 233 AR-NELGRECTRLFTIDLNTQPT-OTTLPOL-----FLKVGELPLWTRKAVHNVHGL 283
DB 177 AKHNGVEKISEHIF---LNVRFVHKALPVITLSKSYELLKEGEFEVFTCIITDVSYSVA 233
QY 284 TWELNKALBEGNFEMSTYSTNRTMIRILPAFVSSVARNDTGYVTCSSSKHP--SQSAL 341
DB 234 SWISYKAIVTSKRNUGDYGERK-----LTLNRSVGNDSGEFTC-QAENPFQKTNAT 288
QY 342 VTI--VGKGFIN---ATNSSEDIYDQYEEFCFSVRKAYPQIR-CTWTFSRKSPPCBQK 395
DB 289 VTLKALAKGFVRLPATMNTTIDINAGONGN--LTVEYEAYPKPEEVWVYNNETL--QN 343
QY 396 GLDNGYSISKFCNKHK-----OPEYIFHAENDDAQFTKMTLNRKPKQVLA 443
DB 344 SSDHVYFKTVGNNSYTSSELHLTRLKGTGEGTYTFVSNDSASSSVTFNVVYTKPEILT 403
QY 444 BASASQ--ASCFSDGYPLSPWTKKCDKSPNCTEETEGVWNRKANRKFQWVSSSTL 501
DB 404 LDMGLNDILQCVATGFPAFTIYWFPCGTORCLDSPTISPMVDKVS-----YTNSSVP 457
QY 502 NMSBAIKGFLVCCAYNSLGTSCETILNLSGPPFPF-----IQDNISFYA-----TIGV 550
DB 458 SFERILVESTVNASMFKSTGTICCEASSNGDKSSVFPFPAIKEQIRTHLTPPLIAGV 517
QY 551 CLLFIVLTLICHKKYKQFYESQLQW-QVTGSSDNEYFYVDPREYDYLKWEFFREN 609
DB 518 AAGLMCIIVMLVLYLKPKYEQVMQVVEING---NNYVYIDPTQLPYDHKWEFFRNR 574
QY 610 LEFGVLGSGAGFKMNTATYGISKTGVSIVQAVKMLKEKADSSREALMSKLKMTOLG 669
DB 575 LSFQKTLGAGAFKGVVEATYAGLFLKSDAAMTVAVKMLKPSAHLTEREALMSKLKLYLG 634
QY 670 SHENIVNLGACTLSGPIYLIFFEYCCYGDLLNLYLSKREKE----HRTWTEIFFKEHNFSF 725

DB 635 NHINIVNLLGACTIGGPTLVITTEYCCYGDGLNPLNRRKEDSFICPKHBAHAAVYENL-- 692
QY 726 YPTQSHPS-----SMFGSREVQIHPDSDQISGLHGNFSFHEDETEYENQKLEBEE 778
DB 693 --LHQAEPTADAVNEMDMKPGVYAVPPKADKKRPVKSGSYTQDD-----VTLNMLEDE 746
QY 779 DLNVLTFEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVKVICDFGLARDIMS 838
DB 747 --LALDVEDLLSFSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIRN 804
QY 839 DSNVTVGNARLPVKWNAPELPGIYTIKSDVMSYGILLWEIFSLGVNPPGIPVDANF 898
DB 805 DSNVTVGNARLPVKWNAPELPGIYTIKSDVMSYGILLWEIFSLGVNPPGIPVDANF 864
QY 899 YKLQNGFKMDQPPYATTEIIVIMOSCWAPDSRKRPSNPNTLSFLGCOLADAEEAMYNV 958
DB 865 YKMIKEGRMFSPECSPPEMIDIMKSCWDADLPORPTFKQIVOLIEQOULSDNAPRYAN- 923
QY 959 DGRVSECPHTYQN 971
DB 924 ---FSTPSTOEN 933
RESULT 13
KFMS MOUSE
ID KFMS MOUSE STANDARD; PRT; 977 AA.
AC P09581; Q9DBH9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor 1 receptor precursor (CSF-1-R)
DE (EC 2.7.1.112) (Fms proto-oncogene) (c-fms).
GN CSF1R OR CSFMR OR FMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8217329; PubMed=2966922;
RA Rothwell V.M., Rohrschneider L.R.;
RT "Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.";
RL Oncogene Res. 1:311-324 (1987).
RN [2]
RP REVISIONS.
RA Rothwell V.M.;
RL Submitted (SEP-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RX MEDLINE=93181280; PubMed=8441691;
RA de Parseval N., Boredeaux D., Gisselbrecht S., Sola B.;
RT "Reassessment of the murine c-fms proto-oncogene sequence.";
RL Nucleic Acids Res. 21:750-750 (1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli P., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE OF 1-16 FROM N.A.
 RX MEDLINE=93268269; PubMed=8497248;
 RA Yue X., Favot P., Dunn T.L., Cassady A.I., Hume D.A.;
 RT "Expression of mRNA encoding the macrophage colony-stimulating factor
 RT receptor (c-fms) is controlled by a constitutive promoter and tissue-
 RT specific transcription elongation";
 RL Mol. Cell. Biol. 13:3191-3201(1993).
 RN [6]
 RP AUTOPHOSPHORYLATION SITES.
 RX MEDLINE=90258890; PubMed=2160591;
 RA van der Geer P., Hunter T.;
 RT "Identification of tyrosine 706 in the kinase insert as the major
 RT colony-stimulating factor 1 (CSF-1)-stimulated autophosphorylation
 RT site in the CSF-1 receptor in a murine macrophage cell line";
 RL Mol. Cell. Biol. 10:2991-3002(1990).
 CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
 CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 DR EMBL; X06368; CAA29666.1; ALT SEQ.
 DR EMBL; AK004947; BAB23691.1; -
 DR EMBL; S62219; -; NOT_ANNOTATED_CDS.
 DR PIR; S01880; TVMSMD.
 DR HSP; P11362; IFGK.
 DR MGD; MG1:1339758; Csf1r.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; Ig_Like; 3.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 977
 FT DOMAIN 20 511
 FT TRANSMEM 512 536
 FT DOMAIN 537 977
 FT DOMAIN 24 104
 FT DOMAIN 107 197
 FT DOMAIN 204 298

FT DOMAIN 299 397
 FT DOMAIN 398 503
 FT NP_BIND 580 913
 FT BINDING 586 594
 FT ACT_SITE 614 614
 FT ACT_SITE 776 776
 FT DISULFID 42 84
 FT DISULFID 127 177
 FT DISULFID 224 278
 FT DISULFID 417 483
 FT MOD_RES 697 697
 FT MOD_RES 706 706
 FT MOD_RES 807 807
 FT CARBOHYD 45 45
 FT CARBOHYD 73 73
 FT CARBOHYD 302 302
 FT CARBOHYD 335 335
 FT CARBOHYD 389 389
 FT CARBOHYD 410 410
 FT CARBOHYD 449 449
 FT CARBOHYD 478 478
 FT CARBOHYD 491 491
 FT CONFLICT 446 446
 FT CONFLICT 553 553
 FT CONFLICT 616 616
 FT CONFLICT 744 744
 FT CONFLICT 814 814
 SQ SEQUENCE 977 AA; 109178 MW; 7EDF8310CCF98906 CRC64;
 Query Match 22.8%; Score 1204; DB 1; Length 977;
 Best Local Similarity 33.2%; Pred. No. 5.3e-73;
 Matches 322; Conservative 155; Mismatches 330; Indels 164; Gaps 32;
 QY 83 VDVSASITLQVL---VDAPGNISCLWFKHSLNCQPHFDLQNGVV-----SMWLK 133
 DB 32 VPGTIVTLKCVSGSVEWDGPISPYWTLDPS-----PGSTLTTRNATFNKTYRTEL 87
 QY 134 TETQAGEYL--LFIQSEATNYTIL---FTVSIRNTLLTYLRPPYFRKMNQDALVCISES 188
 DB 88 EDPMAGSTTHLYVKDPAHSMNLLAQEVTV-----VEQEA----- 124
 QY 189 VPEPIVEWVLCDSQGESCKEESPAVVK-----EKKVHELFGTDIRCCAR 234
 DB 125 LPLCLITDPAKDSV-SLMREGGRQVLRKTVYFFSPWRGFIIRKAKVL-----DSNTYVCKT 179
 QY 235 NELGRECTRL-FTIDLN---OTPOTTL-PQLFLKV-GEPLATRCCKAVHNHGFGLTWEL 287
 DB 180 MVNGRESTSTGIWLKVNVRVHPPEPQIKUEPSKLVIRGEAAQIVCSATNABVGFNVILKR 239
 QY 288 ENKALE-----EGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTC-SSSKHPSQS 339
 DB 240 GDTKLEIPLNSDPQDNYK-----KVRALSLNAVDFQDAGIYSCVASNDVGTRT 288
 QY 340 ALVT--IVKGFFINATN-SSEDIYDIQVEEFCFSVRFKAYPOIR-CTWTFSRKSPFCEQK 395
 DB 289 ATMPQVVEASAYLNLTSQSLIQEVSVDLSLITLVHADAPYSIQHYNWTYLGPFPE-DQR 347
 QY 396 GLD-----NGYSISKFCNH--KHQPGEYIHAENDDAQFTKMTFLNRRKPOVLAEAS 446
 DB 348 KLEFITORAIRVYTPKFLNLRVKASEAQYFLMAQNKAGMNNLTPELTLYRYPPEVSVTWM 407
 QY 447 ASQAS-----CFSDGYPLPSWTWKCKSDKSPNCTEITEGVN-----RKANRKFVGOMVSS 498
 DB 408 PVNGSDVLFCDSVGYPSQPSVTWMECRGHTDRCDCAQLQVWNDTHPEVLSQKPFDKVIQ 467
 QY 499 STLNMSEAIGFLVCKCAYNSLGTSCETILLNSPGPFPIQDNISFYATIGVC---LLFI 555
 DB 468 SOLPIGLKHNMTYFCKTHNSVGNSSQYFRAVLSGSKQLPDESLETPVVVACMSVMSLL 527
 QY 556 VVLTLLICHKKQPRYESQLQMVQVTGSSDNEYVYVDFPREYEDLKWFEPRENLEFGKV 615
 DB 528 VLLLLLLLYKKQPKYQVRWKIIE--RYEGNSYTFIDPTQLPYNEKEWFEPRNLLQFGKT 585

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Qy 616 LGSGAFGKVMNATAYGISKTGVSIOAVKMLKEKADSSEREAALMSELKMTQOLGSHENIV 675
Dy 586 LGAGAFGKVVETATFLGKEDAVLKVAVKMLKSTAHADEKALMSELKIMSHLGQHENIV 645
Qy 676 NLGACTLSGPIYLFYCCYCDLLNLYRSKRE-----KPHRTWT 715
Dy 646 NLGACTHGGPVLVITEYCCYCDLLNLYRSKRE-----KPHRTWT 715
Qy 716 ELFKHNFSFYFTFQSHPNSSMPGSRVQIHPDSQISGLHNSPHSDELEYENQKLE 775
Dy 706 YVRDSGFS-----SGVDYVEMRPVTSSTSSDSFFKQD-LDKESARLE 749
Qy 776 EREDNLVTLFEDLLCFAYQVAKMGFLFKSCVHRDLAARNVLTGHVKVICKDFGLARD 835
Dy 750 -----LWLLHFSSQVAGMAFLAKSKNCIHRDVAARNVLTGHVAKIGDFGLARD 800
Qy 836 IMSDSNVVRGNARLPVKWMAPESEFEGIIYTKSDVWSYGILLWEIFSLGVNPPYGPVVD 895
Dy 801 IMSDSNVVRGNARLPVKWMAPESEFEGIIYTKSDVWSYGILLWEIFSLGVNPPYGPVVD 895
Qy 896 ANFYKLQNGKMDOPFYATEEIIYIMOSWAFDSCRKPSFNLTSFLGCQLADAEAMY 955
Dy 861 NKFYKLVDGYQMAQVPFAPKNIYIMOSWAFDSCRKPSFNLTSFLGCQLADAEAMY 955
Qy 956 QNVGRVSECP 966
Dy 915 EREDQYANLP 925

RESULT 14
ID_KFMS RAT STANDARD; PRT; 978 AA.
AC Q00495;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
DE (EC 2.7.1.112) (Fms proto-oncogene) (c-fms).
GN CSF1R OR CSFMR OR FMS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Wistar; TISSUE=Skeletal muscle;
RX MEDLINE=93001225; PubMed=1389227;
RA Borycki A.G., Guillier M., Leibovitch M.P., Leibovitch S.A.;
RT "Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence
RT analysis and regulation during myogenesis.";
RL Growth Factors 6:209-218(1992)
CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
CC -!- TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC -!- tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC -!- PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
Dy EMBL; X61479; CAA43706.1; --
Dy PIR; S16385; S16385.
Dy HSSP; P11362; 1FGK.
Dy InterPro; IPR000719; Euk_pkinase.
Dy InterPro; IPR003006; Ig_pkinase.
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DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG_Like; 3.
DR SMART; SM00408; IGS2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferrase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 978 MACROPHAGE COLONY STIMULATING FACTOR I
FT RECEPTOR.
FT DOMAIN 20 511 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 512 536 POTENTIAL.
FT DOMAIN 537 978 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 104 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 107 197 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 204 298 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 299 397 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 398 503 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 580 914 PROTEIN KINASE.
FT NP_BIND 586 594 ATP (BY SIMILARITY).
FT BINDING 614 614 ATP (BY SIMILARITY).
FT ACT_SITE 776 776 POTENTIAL.
FT DISULFID 42 84 POTENTIAL.
FT DISULFID 224 278 POTENTIAL.
FT DISULFID 417 483 POTENTIAL.
FT MOD_RES 697 697 PHOSPHORYLATION (AUTO-) (IN VITRO)
FT MOD_RES 706 706 PHOSPHORYLATION (AUTO-) (IN VIVO)
FT MOD_RES 807 807 PHOSPHORYLATION (AUTO-) (IN VITRO)
FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 978 AA; 109264 MW; 0A684568F56BC7E3 CRC64;
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Query Match 22.6%; Score 1194; DB 1; Length 978;

Best Local Similarity 33.1%; Pred. No. 2.5e-72;

Matches 321; Conservative 154; Mismatches 332; Indels 164; Gaps 32;

Qy 83 VDVSASITLQVL-----VDAPGNISCLWVFKHSLNCQPHFDLQNRGV-----SWILKM 133

Dy 32 VFPGFTVTLRCVNSGVWDGPISPYWTLDPS-----PGSTLTTRNATPKNTGYRCTEL 87

Qy 134 TETQAGEYL--LFIOSEANNTYL---FTVSIRNTLLTLRRPYFRKMENQDALVCISES 188

Dy 88 EDPMAGSTTHLYVKDPAHNSWLLAQEVTV-----VSGQEA-----VSGQEA----- 124

Qy 189 VPEPIVWVLCDSQGESCKEESPAVVK-----EKKVHELFGFDIRCCAR 234

Dy 125 LPCLITDPALKDSV-SLMREGGRQVLRKTVFFSAWRGIIRKAKVL-----DSNTVCKT 179

Qy 235 NELGRECTEL-FTIDLN-----QTPQTTL-PQLFLKV-GEPLMIRCAVHVHGFGLTWEL 287

Dy 180 MVNGRESTGTGIWLKYNRVHVPPEPKLEFSLVIRGEAAQIVCSATNAEVGNVILKR 239

Sat May 24 16:50:26 2003

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Query Match      22.3%; Score 1176; DB 1; Length 1088;
Best Local Similarity 35.6%; Pred. No. 4.6e-71;
Matches 294; Conservative 128; Mismatches 288; Indels 115; Gaps 24;

Qy 246 TIDLNOTPTTLPOLFLKVGPELMIRCAVHNHGFGLTW----ELENKA---LEEGNYF 298
Db 210 TSELNLEMDTR--QTVYKAGETIVVTC-AVFENNEVDLQWTYPGEVRNKGITMLEE---- 262

Qy 299 EMSTYSTNRWIRILFAP-VSSVARNDRGYTCS---SSKHPQSALVTIV--GKGFIN- 351
Db 263 -----IKLPSIKLVYTLTVPKATVKGSDGYECAARQATKEVKEMKTVTISVHEKGFVQI 316

Qy 352 --ATNSSDYEDIDVVEEFCFSVRKAPQIRCTWTFSRKSF-----PCEQKGLDNGY 401
Db 317 RPTGHLTVNLHVRETV--VEQAYTTPRISWLKNDLNTLIENLTTEITTDVQRSQETRY 374

Qy 402 -SISKFCNHHQO-PGEYIFHAENDDAQFTKMTLNIRKPOVL-----AEASASQASC 452
Db 375 QSKLKLIRAKEEDSGHYTIIQNDDDMKSYTFELSTLVPASILELVDHGHSGGGQTVRC 434

Qy 453 FSDGYPLPSWTW-----KKCSDK-----SPNCTEEITEGVWNRKANRKYFGQWVSST 500
Db 435 TAEGTPLENIEMWICKDKCNNDTSWTVLASNVSNIITE--FHGRSTVEGR----- 486

Qy 501 LNMSEAIKGLVKCCAYNSLGTSCETILLNSPGPPPIQDNISFYATIGVCILFIWVLT 560
Db 487 VSPAKVEETIAVRCLAKNDLGLGNRELKLVAPS-----LRSELTVAADVLLVIVISLI 542

Qy 561 LICHKYKQPRYESQLOQVQVTGSSDNEYFYVDPREYDYLKWEPPRENLEFGKVLGSGA 620
Db 543 VLVVWIKQKPRYIEIRWVIESIPDGHEYIYVPMQLPYDSRWEPFRDGLVLRILGSGA 602

Qy 621 FGKVNATAYGLSKTGVSIQAVAKMLKSKADSSEREALMSLKMKTOLGSHENIUNLGA 680
Db 603 FGKVVVEGTAYGLSRQPVNKMVAKMLKPTARSSEKQALMSLKIIMTHLGPLHNIUNLGA 662

Qy 681 CTLSGPIYLIPEYCCVGDLLNLYLRGKREKF-----HRTWTEI 717
Db 663 CTKSGPIYIITEYCFYGDLLVNYLHKNRDSFMSRHPKPKKDLDFGLNPADESTSYVIL 722

Qy 718 FKEHNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGN--SFHSEDEIEYENQKRL 775
Db 723 SPENNGDYVDMKQADTTQYVPMLEKREKSVKSDIQRSLYDRPASYKKKSMLDSE-AKNLL 781

Qy 776 EEDLNVLTFEDLLCFAYQVAKMBLEPKSCVHRDLAARNVLTGHGVKVICDFGLARD 835
Db 782 SDDSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARD 841

Qy 836 IMSDSNYVVRGNARLPVKWMAPESLFEGYITIKSDVWSYGILLWEIFSLGVNPPGIPVD 895
Db 842 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGVLLWEIFSLGGTFYFGMVD 901

Qy 896 ANFYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDPSKRPSPNLTSLFCQCLADAEAMY 955
Db 902 STFYKNIKSGYRMAKPDHATSEVYEIMVQCNSEPEKRPSPFYHLSIEVENLLPGQYKSY 961

Qy 956 QNV--DGRVSECPH-----TYQNRPPFSREMDLGL 983
Db 962 EKIHLDPLKSDHPAVARMVRVDSNAYIGVITYKNEEDKLEWEGGL 1006
```

Search completed: May 24, 2003, 16:56:54
Job time : 23.0091 secs

GenCore version 5.1.4_p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:51:00 ; Search time 71.0358 Seconds
(without alignments)
2880.307 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVPLLVFSAM.....PFSREMDLGLLSPOAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1271.5	24.1	976	13 Q9W755	Q9W755 brachydanio
2	1265.5	24.0	974	11 Q63702	Q63702 rattus ratt
3	1263.5	24.0	978	11 Q63116	Q63116 rattus norv
4	1262.5	23.9	964	6 Q97744	Q97744 sus scrofa
5	1261.5	23.9	964	6 Q9TQ01	Q9TQ01 sus scrofa
6	1261.5	23.9	964	6 Q9TQ00	Q9TQ00 sus scrofa
7	1250.5	23.7	979	6 Q8W23	Q8W23 canis famil
8	1247	23.6	972	4 Q9S662	Q9S662 homo sapien
9	1244	23.6	978	6 Q9XS93	Q9XS93 canis famil
10	1230.5	23.3	945	13 Q98SU1	Q98SU1 danio nigro
11	1229	23.3	945	6 Q77589	Q77589 equus cabal
12	1228	23.3	974	13 Q98SU3	Q98SU3 danio dangi
13	1226	23.2	954	13 Q91909	Q91909 xenopus lae
14	1223.5	23.2	977	13 Q918N6	Q918N6 brachydanio
15	1221	23.2	948	6 Q9TDT7	Q9TDT7 trichosurus
16	1219	23.1	724	6 Q9MYN0	Q9MYN0 bos taurus

17	1214	23.0	977	13 Q98SU2	Q98SU2 danio kerri
18	1213	23.0	975	13 P79750	P79750 fugu rubrip
19	1211	23.0	977	13 Q98SU4	Q98SU4 danio albol
20	1141.5	21.6	1059	13 Q9DE49	Q9DE49 brachydanio
21	1126	21.4	1087	13 Q9PUF6	Q9PUF6 gallus gall
22	1111.5	21.1	1097	11 Q8R406	Q8R406 rattus norv
23	1080	20.5	1048	13 P79749	P79749 fugu rubrip
24	1079	20.5	1019	13 Q8UVR8	Q8UVR8 fugu rubrip
25	1046	19.8	923	6 Q97745	Q97745 sus scrofa
26	1038	19.7	986	13 Q8UVR9	Q8UVR9 fugu rubrip
27	965.5	18.3	563	11 Q925F7	Q925F7 rattus norv
28	952.5	18.1	1173	13 Q9PTL0	Q9PTL0 brachydanio
29	950.5	18.0	1301	13 Q8UW9	Q8UW9 brachydanio
30	948.5	18.0	1327	13 Q8QHL3	Q8QHL3 gallus gall
31	934	17.7	1345	11 Q8VCD0	Q8VCD0 mus musculu
32	932	17.7	1379	13 P79701	P79701 coturnix co
33	916.5	17.4	323	11 Q9EQ22	Q9EQ22 rattus norv
34	909.5	17.2	1363	11 Q91ZT1	Q91ZT1 rattus norv
35	892.5	16.9	323	11 Q9EQ24	Q9EQ24 rattus norv
36	850	16.1	819	4 Q96KM0	Q96KM0 homo sapien
37	842	16.0	766	4 Q96KM2	Q96KM2 homo sapien
38	842	16.0	785	4 Q96KM1	Q96KM1 homo sapien
39	841	15.9	824	13 Q90749	Q90749 gallus gall
40	837.5	15.9	820	4 Q96KL9	Q96KL9 homo sapien
41	836	15.9	782	6 Q9TTZ3	Q9TTZ3 oryctolagus
42	835	15.8	350	13 Q91416	Q91416 xenopus lae
43	832.5	15.8	824	13 Q91286	Q91286 pleurodeles
44	828.5	15.7	822	4 Q14672	Q14672 homo sapien
45	827	15.7	796	13 Q91287	Q91287 pleurodeles

ALIGNMENTS

RESULT 1

Q9W755 PRELIMINARY; PRT; 976 AA.
 ID Q9W755;
 AC Q9W755;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Kit receptor tyrosine kinase.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99196707; PubMed=10393121;
 RA Parichy D.M., Rawls J.F., Pratt S.J., Whitfield T.T., Johnson S.L.;
 RT "Zebrafish sparse corresponds to an orthologue of c-kit and is
 RT required for the morphogenesis of a subpopulation of melanocytes, but
 RT is not essential for hematopoiesis or primordial germ cell
 RT development."
 RL Development 126:3425-3436(1999).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 DR EMBL; AF153446; AAD41890.1; -.
 DR HSSP; P11362; 1FGK.
 DR ZFIN; ZDB-GENE-980526-464; kit.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; ig; 3.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00408; IGC2; 1.

Db 930 GTYTLVNSDVSAVTFDVTYVNTKPEILTYDRLMNGRLQCVAAAGPEPTIDWYFCTGAE 449
 Qy 472 PNCTEEITE-GYNNRKANKRVFGQWVSSSTLNMSEBAIKGFLVKCCAYNSLGTSCETILLN 530
 Db 450 QRCCTVPVPVVDVQIQNASVSPFGKLVQSSIDSSVFRHNGTVECKASNAVGKS--SAFFN 507
 Qy 531 SPGPPPP---IQDN-----ISFYATIGVCLLFIIVLTLCHIKYKKQFRYESQLQWV- 579
 Db 508 ----FAFKGSKQEQPHLFTPLLLIGFVVVTA--LMGIIVMVL--AYKYLQKPMYEVQWKVVE 559
 Qy 580 QVTSSDNEYFVVDPREYEDYDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVS 639
 Db 560 EING---NNYVIIDTQLPYDHKWEFPNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAM 616
 Qy 640 QVAVKMLKEKADSSREALMSELKMTOLGSHENIVNLLGACTLSGPIYLIFFEYCCYGLD 699
 Db 617 TVAVKMLKPSAHLTEREALMSELKVLVSLGNHNMIVNLLGACTVGGPTLVITEYCCYGLD 676
 Qy 700 LNYLRSKREKHFRTWTEIFKEHNFSPYTFQSHPNSSMPGSR--VOIHPDSDQISGLHGN 758
 Db 677 LNFLRRKRDSE--IFSKEQEQADAALYKNLLHKSKESSCDSSNEYMDKPGVSVVPTKTD 734
 Qy 759 SFHS---EDEIYENQKREBEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAAR 815
 Db 735 KRSARIDSYIERDVTPTAIMEDEL-ALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAAR 793
 Qy 816 NVLTHGVKWKICDGLARDIMSDSNVYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYG 875
 Db 794 NILTHGRIKICDGLARDIRDSNVYVKGARLPVKWMAPESLFNCVYTFESDVWSYG 853
 Qy 876 ILLWEIFSLGNPNYPIGVANFYKLIQNGFQMDOPFVATEBIYIMOSCAWAFDSEKRP 935
 Db 854 IFLWELFSLGSPYPCMPVDSKFKYKMEKGFRLMSPEHAPAAANYEVMKTCWADPLKRP 913
 Qy 936 FPNLTSLFGCLADAEAEAMYQNV 958
 Db 914 FKQVQLIEKQISDSSKHIYSNL 936

RESULT 3
 Q63116 PRELIMINARY; PRT; 978 AA.
 ID Q63116
 AC Q63116;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE C-kit receptor tyrosine kinase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=92003944; PubMed=1912577;
 RA Tsujimura T., Hirota S., Nomura S., Niwa Y., Yamazaki M., Tono T.,
 RA Morii E., Kim H., Kondo K., Nishimune Y., Kitamura Y.
 RT "Characterization of Ws mutant allele of rats: A 12-base deletion in
 RT tyrosine kinase domain of c-kit gene."
 RL Blood 78:1942-1946(1991).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 DR EMBL; D12524; BAA02094.1; -;
 DR HSSP; P11362; IFGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Euk_pkinase; 2.
 SMART; SM00408; IGC2; 1.
 SMART; SM00410; IG_like; 3.
 SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
 KW Phosphorylation; Receptor; Transferase; Transmembrane;
 KW Tyrosine-protein kinase.
 SQ SEQUENCE 978 AA; 109341 MW; 0958C33F19889051 CRC64;
 Query Match 24.0%; Score 1263.5; DB 11; Length 978;
 Best Local Similarity 33.8%; Pred. No. 1.6e-95;
 Matches 334; Conservative 171; Mismatches 361; Indels 121; Gaps 37;
 Qy 35 CVLIHNKNDSSVSGSSSPMVSESPEDLGCAIRPOSSGTVTVEAAAVEVDVSATLQVL 94
 Db 12 CVLLVLLRGQTGTSQFSASPGFSP-----SIQPAQS-----ELIVEAGDTIRLT 57
 Qy 95 VDAPGNISCLVWFKHSSLNCQPHFQDQNRGVVSMVLKMTQ--TQAGEYLLFIQSEATNYT 153
 Db 58 CTDPAFVK--WTFE-----ILDVRIENKQSEWIREKAEATHTKYTCVSSSGLRSSI 107
 Qy 154 ILFTVSIRN--TLTYLRRPYFRKMNQDALVCISESVPEPIVEMVLCDSQGESCKEESPA 212
 Db 108 YVF---VRDPAVLFLVGLPLFGK--EDNDALVRCPLTDPO--VSNSYLIECDKSLPTDLKF 162
 Qy 213 V-----VKEEKVLHELFGTDIRCCARNELGRCTRLLFTID----LNQTFQTLPLQL 260
 Db 163 VENPKAGITIKNVKAYHRLC---IRCAAQREGKWMRSKDTLKVRAAIIKAIPIVWSVPET 219
 Qy 261 --FLKVGEPWLRKAVHVNHGFLTW-----ELENKALEEGNYFEMS--TYSNTRMTIR 311
 Db 220 SHLLKEGDTFTVICIKOVSTSVDSVMWIKLNFPQSKAQVKRNSWHQGDNYERQETLT- 278
 Qy 312 ILFAFVSSVARNDGYTCTSSSKHPSQSALVT---IVGKGFN---ATNSISKFCNHKH- 365
 Db 279 ----ISSARVNDSGVFMCYANNTFGSANVTTLTKVVEKGFNIFPVQNTT--VFVTDGE 331
 Qy 366 EFCFSVRKAYPO--TRCTWTFSRKSPPCQKGLD-----NGYSISKFCNHKH-----QP 413
 Db 332 NVDLVVEFEAYPKPEHQQIYNNRT--PTNRGEDIYKSDNQSNIRYVNELELRLTKGTEG 389
 Qy 414 GEYIFHAENDDAQFTKMFNLNIRKPOVLA--EASASQASCFSDGYPLPSMTWKCKSDKS 471
 Db 390 GYITFLVNSDVSAVTFDVTYVNTKPEILTYDRLMNGRLQCVAAAGPEPTIDWYFCTGAE 449
 Qy 472 PNCTEEITE-GYNNRKANKRVFGQWVSSSTLNMSEBAIKGFLVKCCAYNSLGTSCETILLN 530
 Db 450 QRCCTVPVPVVDVQIQNASVSPFGKLVQSSIDSSVFRHNGTVECKASNAVGKS--SAFFN 507
 Qy 531 SPGPPPP-----IQDN-----ISFYATIGVCLLFIIVLTLCHIKYKKQFRYESQL 576
 Db 508 ----FAFKGSKQEQPHLFTPLLLIGFVVVTA--LMGIIVMVL--AYKYLQKPMYEVQW 559
 Qy 577 QMV-QVTSSDNEYFVVDPREYEDYDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKT 635
 Db 560 KVEEBING---NNYVIIDTQLPYDHKWEFPNRLSFGKTLGAGAFGKVVEATAYGLIKS 616
 Qy 636 GVSIOVAVKMLKEKADSSREALMSELKMTOLGSHENIVNLLGACTLSGPIYLIFFEYCC 695
 Db 617 DAAMTVAVKMLKPSAHLTEREALMSELKVLVSLGNHNMIVNLLGACTVGGPTLVITEYCC 676
 Qy 696 YGDLNLNLRKREKHFRTWTEIFKEHNFSPYTFQSHPNSSMPGSR--VOIHPDSDQISG 754
 Db 677 YGDLNLNLRKREKDSF--IFSKEQEQADAALYKNLLHKSKESSCDSSNEYMDKPGVSVVVP 734
 Qy 755 LHGNSFHS---EDEIYENQKREBEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRD 811
 Db 735 TKTDKRSARIDSYIERDVTPTAIMEDEL-ALDLEDLLSFSYQVAKGMAFLASKNCIHRD 793

RA Marklund S., Kijas J., Rodriguez-Martinez H., Roenstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.,
RT "Molecular evolution of the dominant white phenotype in the domestic
RL pig.",
RL Genome Res. 8:826-833(1998).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AJ223230; CAAL1198.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PS00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON TER 964 964
SQ SEQUENCE 964 AA; 108287 MW; 1B21292A962E9191 CRC64;

Query Match 23.9%; Score 1261.5; DB 6; Length 964;
Best Local Similarity 33.4%; Pred. No. 2.2e-95;
Matches 332; Conservative 169; Mismatches 349; Indels 143; Gaps 38;

QY 47 VKGSSYPWVESPEDLCALRPOSSGTVYEAFAAEEVDVSAISITLQVLVDAPGNISCLWV 106
DB 20 VOTGSSQPSV--SPEEL-----SPSIHPAKS-ELIVSAGDEIRLCTDPGSKV--WT 67
QY 107 PKHSLNCQPHFDLQNRGVSMWILKMTETQAGEVLLFIQSEATNYTLFTVSTRN-TLL 165
DB 68 PETLGL-----QLSENTHAEWIKAEAMNTGNYTCTNEGGLSSIIYVF---VRDPEKL 117
QY 166 YTLRRPYRKMENODALVCISEPPEIVVWLCDSQSCKEESPAV-----VKKE 217
DB 118 FLVDPPLVYK-EDNDALVRCPLDPE-VTNYSLTGCEGKPLDKLTFFVADPKAGITIRNV 175
QY 218 EKVLHFLGTDIRC--CARNELGRE-CTRLFTID----LNQTPOTLPQ--LFLKVGSEPL 268
DB 176 KREYHRL-----CLHCSANQGGKSVLSKFTLVKRAAIRAVPVAVSVKSYLLREGSEF 229
QY 269 WIRKAVHNVHFGTLWELEN---KALEBEGNFEMSTYSTNRTMIRILPAFVSSVARNDT 325
DB 230 AVMCCLKIDVSSVSDVMSWIRENSQTKAQVKNRSHWQGFN----FLRQEKLTSSARVND 285
QY 326 GYITCSSSKHPSQALVT---IVGKGFTNA-----TNSSDEYEDIQVEEFCFSYRF 373
DB 286 GVFWCYANNFTGSANVTTLLEVVDKGFNIFPMNTTVFVNDGEDVDL-----IVEY 337
QY 374 KAYPQ-----IRCTWTFGRKSPPCQKQGLDNGYSISKFNHKK-----QPGEYIF 418
DB 338 EAYPKPEHRQWYNNRTATDKWEDPKSE-----NESNIRYVSELHLTLKTEGTYTF 392
QY 419 HAENDDAQFTKMTLNIRKQVOLA--BASASQACSFSDGVLPLPSWTKKCDKSPNCTE 476
DB 393 LVSNADVNSSVTFNVYVNTKPEILLTHRLMNGMLQCVAAGPEPTIDWYFCPGTEQRCSV 452
QY 477 EI-TEGVNRKANKRVQGVSSSTLANSEALKGLVKKCAYNLSGTCEITLLNSPPFF 535
DB 453 PVGPVDVQIQNSVSPFGKLVHSSIDYSFAFKHNGTVECRAYNDVGKS--SAFFN----F 506
QY 536 PFIQD-----NISFYATIGVCLLFIIVLITLICHYKKQPRYESQLQMV-QVTGS 584

DB 507 AFKEQIHAHTLFTPLLLIGFVIAAGMCIIVMLT-----YKLOKPMYEQWVKVBEING- 561
QY 585 SDNEFYVDYDFEYEDLKWEPRENLEFGKVLGSGAGFKVMNATAYGISTGVSIOVAVK 644
DB 562 --NNYVYIDPTQLPVDHKKWEPNRNLSFGKTLGAGAFKVVEATAYGLIKSDAAMTAVK 619
QY 645 MLKEKASSEREALMSSELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYCGDLLNLYR 704
DB 620 MLKPSAHLTEREALMSSELKVLVSLGNHNNIVNLLGACTIGGPTLVITEYCCYCGDLLNFLR 679
QY 705 SKREKPHRTWTE-----IFKEHNFSPYPTQSHPNSSM---PGSREVOIHPDSOISGL 755
DB 680 RKDSFICSKQEDHAEALYKNLLHSKSSCSDSNTEYMDMKPGVSIV-VPTKADKRSR 738
QY 756 HGNSFHSDELEYENQKLEBEEDLNVLTFEDLLCFAYQVAKGMEFLFKPSCVHRDLAAR 815
DB 739 RIGSY-----IERDVTPAIMEDDEL-ALDLELLSFSYQVAKGMAPLASKNCIHRDLAAR 792
QY 816 NVLVTHGKVKICDPGLARDIMSDSNVYVRGNARLPVKWMAPESEFEGITYTIKSDVWSYG 875
DB 793 NILITHGRIITKICDPGLARDIKNDSNVYVKGARLPVKWMAPESEFNCVYTFESDVWSYG 852
QY 876 ILLWEIFSLGVNPPGIPVDANFYKLIQNGFMDOPFFVATEIYIIMOSCAWAFDSRKRPS 935
DB 853 IFLWELFSLGSPYGPMDVDSKFKYKMIKEGFRMLSPERHAPVEMYDIMKTCWDADPLKRPT 912
QY 936 FPNLTSLFGCLADAEAEAMYQNVDRVSEC-PH 967
DB 913 FKQIVQLIEKOISESTNNHIYSN----LANCSPH 941

RESULT 7
Q8WN23 ID Q8WN23 PRELIMINARY; PRT; 979 AA.
AC Q8WN23;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Zemke D., Yuzbasiyan-Gurkan V.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448148; AAL40833.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig like.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00410; IG like; 2.
DR SMART; SM00220; S TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN_1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; UNKNOWN_1.
SQ SEQUENCE 979 AA; 109753 MW; 46C30D5DEB8E33D3 CRC64;

Query Match 23.7%; Score 1250.5; DB 6; Length 979;
Best Local Similarity 33.6%; Pred. No. 1.9e-94;
Matches 334; Conservative 161; Mismatches 345; Indels 153; Gaps 39;


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Db 278 SSARVNDGVMFCVANNVTFGSANVTTLTLEVVVDKGFNIFPMINTVTFVNDGENVDL----- 333
Qy 366 EFCFSVRFKAYPO-IRCTWTFSRKSF--PCEQKGLDNGYSISKFCNKH-----OPGE 415
Db 334 ----IVEYEAPKPEHQWIYMNRTFTDKWEDYPKSENENIRVYSELHLTRLKGTGEGT 389
Qy 416 YIFHAENDDAQTKMFTLNIRRKPOVLA--BASASQACSFSDGYPPLPSWTKKCDKSPN 473
Db 390 YTELVSNSDVNAALAFNVYNTKPEILTYDRLVNGMLQCQAAGPEPTIDYFPCFGEQR 449
Qy 474 CTEBEITE-GVMNRKANRKFVGQWSSSTLAMSBAIKFLVKCCAYNSLGTSCETILLNSP 532
Db 450 CSASVLPVDVQTLNSGPPPEKLVQSISSAFKNGTVECKAYNDVGKT--SAYFN-- 505
Qy 533 GPPFFIOD-----NISFYATIGVCLLFIIVLLTLLCHKYKFOFRYBSQWV--QV 581
Db 506 --FAFKEQIHPHTLFTPLLIGFVIVAGMCIIVMLT-----YKYLQPMYEVQMKVVEI 559
Qy 582 TGSDDNBYFVDPREYEDYDLKWEPPRENLEFGKVLGSGAGFKVNNATAYGLSKTGVSIQV 641
Db 560 NG---NNYVYIDPTQLPYDHKWEPPRNRLSFGKTLGAGAFGVVEATAYGLIKSDAAMTV 616
Qy 642 AVKMLKEKADSSERREALMSELKMTOLGSHENIVNLLGACTLSGPVILIPYCCVGDLLN 701
Db 617 AVKMLKPSAHLTEREALMSELKUSLYLGNHNIIVNLLGACTIGGTLVITYCYGDLLN 676
Qy 702 YLRSKREKFRHTWTE-----IFKEHNFSPYPTPQSHPNSSM---PGSREYQIHPDSQI 752
Db 677 FLKRKDSFCSKQEDHAEALYKNLLHSKSSCSDSTNEYMDMKPGVSYV-VPTKADKR 735
Qy 753 SGLHNSFHSEDEIYENQKRLBEEDNLVLTFFDLCPAQVAKGMEFLBFKSCVHRDL 812
Db 736 RSVRIGSY-----IERDVTPEIMDEDEL-ALDLEDLLSFSYQVAKGNAFLASKNCIHRDL 789
Qy 813 AARNVLTGHGVKVICDPLGLARDTMSDYSNVVRCNARLPVKWMAPESLFEGYTIKSDVW 872
Db 790 AARNILTHGRITKICDPLGLARDTMSDYSNVVRCNARLPVKWMAPESLFNCVITYFESDVW 849
Qy 873 SYGILLWEIFSLGNPNYPGIPVDANFYKLIQNGFMKQOPFYATBEIYIMOSCAWAFDSRK 932
Db 850 SYGIFLWELFSLGSPYFGNVPDVSFKYMKIEGFRMLSPHAPAEYMDIMKTCWDADPLK 909
Qy 933 RPSPNLITFLGQCLADAEAMYNQV 958
Db 910 RPTPKQIVOLIEKQISESTNHIYSNL 935

RESULT 9
Q9XS93 ID Q9XS93 PRELIMINARY; PRT; 978 AA.
AC Q9XS93;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE KIT.
GN C-KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RA London C.A., Galli S.J., Yuuki T., Hu Z.-Q., Helfand S.C.,
RA Geisler E.N.;
RT "Spontaneous canine mast cell tumors express tandem duplications in
the proto-oncogene c-kit.";
RL Exp. Hematol. 0:0-0(1999).
CC -[- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -[- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES.
DR EMBL; AF099030; AAD28369.1; -.
DR HSPG; P11362; IFGK.

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DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS0109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 978 AA; 109651 MW; 5AC31ESAC4E9910F CRC64;

Query Match 23.6%; Score 1244; DB 6; Length 978;
Best Local Similarity 33.2%; Pred. No. 6.4e-94;
Matches 330; Conservative 161; Mismatches 346; Indels 158; Gaps 38;

Qy 47 VKSSSPMWSESEDLGCLARPOSSGTVYEAAVEVDVSASITLOVLVDAPGNISCLWV 106
Db 22 VQTGSQSPSVSPGPEPLP-SIHPAKS-----ELIVSVGDELRLSCTDPGVK--WT 69
Qy 107 PKH--SSLNCQPHDLQNRGVVSWILKMTQTOAGEVLLFIOSEATNYTIL-----FT 157
Db 70 FETLGQNLNETH----NEWITE-----KABAG-----HTGNYTCNRDGLSRSIY 110
Qy 158 VSIRN-TLLYTLRLRPYFRKMENQDALVCISBPVPPVVEWVLCDSQSGSKCESPAV--- 213
Db 111 VFVRDPAKFLVDLPYLYGK-EGNDTLVRCPLTDPV-VTNSYLRGCEGKPLKDLTFVADP 168
Qy 214 -----VKEEKVLHELFTDTRC--CARNELGRE-CTRLFTID-----LNQTPQTLPLQ- 260
Db 169 KAGITIRINKEVYHRL-----CLHCSADQKGRTVLSKKFTLKVRAAIRAVPVWSVKTS 222
Qy 261 -FLKVGPELWLRCKAVHVNHGFLTWELN---KALESGNYFEMSTYSTNRTMIRLPFAF 316
Db 223 SLLKEGEAFSVMCFIKDVSSFVDSMWIKENSQTNATQTSNWHHGDNFEREKL---- 278
Qy 317 VSSVARNDTYTCTSSSKHPSQSALVT---IVGKGFINA-----TNSSEDEYIDQY 364
Db 279 ISSARVNDGVMFCVANNVTFGSANVTTLTLEVVVDKGFNIFPMWSTTIFVNDGENVDL--- 335
Qy 365 EFCFSVRFKAYPO-IRCTWTFSRKSFCEQKGL---DNGYSISKFCNKH-----QP 413
Db 336 ----IVEYEAPKPEHQWIYMNRTFTDKWEDYPKSDNESNI-RYVSELHLTRLKGNEG 389
Qy 414 GEYIFHAENDDAQTKMFTLNIRRKPOVLAESAQA--SCFSDGVPPLPSWTKKCDKSKS 471
Db 390 GTYTFQVNSDVNSVTFNVYNTKPEILTHESLTNGMLQCVVAGFPPEPAVDWYFCPGA 449
Qy 472 PNCTEEI-TEGVNRKANRKFVGQWSSSTLAMSBAIKGFLVKCCAYNSLGTSCETILLN 530
Db 450 QRCSPVIGPMDVQMNSSLSPGKLVQSSIDYSAFKNGTVECRAYNNVGRS--SAFNP 507
Qy 531 SPGPPFPFTQDN-----ISFYATIGVCLLFIIVLLTLLCHKYKFOFRYBSQ- 576
Db 508 ----FAFKGSKEQIHPHTLFTPLLIGFVIVAGMCIIVMLT-----YKYLQPMYEVQW 559
Qy 577 QMW-QVTGSSDNEYFYVDREYEDYDLKWEPPRENLEFGKVLGSGAGFKVNNATAYGISKT 635
Db 560 KVVBEING---NNYVYIDPTQLPYDHKWEPPRNRLSFGKTLGAGAFGVVEATAYGLIKS 616
Qy 636 GVSQTQAVKMLKEKADSSERREALMSELKMTOLGSHENIVNLLGACTLSGPVILIPYCC 695
Db 617 DAAMTVAVKMLKPSAHLTEREALMSELKUSLYLGNHNIIVNLLGACTVGGTFLVITYEYCC 676
Qy 696 YGDLNLYLRSKREKFRHTWTEIFKEH-NFSFYPTFQSHPNSSMPGSRVQIHPDSQISG 754

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Db 677 YGDLNLFRRKDSFICKQKQ---DHGEVALYKNNLHSSKSSCSDS-----THEYMDM 726
Qy 755 LHGNSFHSEDEIEYENQKRLSE-----EEDLNVLTFFEDLLCFAYQVAKGMFEPLF 803
Db 727 KPGDSYVVPTRADKRRSRIGSYIERDVTPAIMEDELALDLELLSFSYQVAKGMFLA 786
Qy 804 PKSCVHRDLAARNVLVTHGVKVKICDFGLARDIMSDSNVYVTCGNARLPVKWNAPELFE 863
Db 787 SKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSNVVVKGNARLPVKWNAPESEI 846
Qy 864 IYTKSDVWSYGILLWEIFSLGVNVPYGPVDANFYKLIQNGFKMDQPPYATEEIIYIMQ 923
Db 847 VITESDVWSYGIFLWEIFSLGSSYPGVPDSKFKYKMKKEGFRMLSPBEHAEYDINK 906
Qy 924 SCWAFDSKRFRSPFNLTSLFGLQCLADAPEAMYQNV 958
Db 907 TCWDADLPKRPTSKQIVQLIEKQISDSNTHIYSNL 941

RESULT 10
Q98SUI
ID Q98SUI PRELIMINARY; PRT; 977 AA.
AC Q98SUI
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase Fms.
OS Danio nigrofasciatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=144739;
RN [1]
RX MEDLINE=21359118; PubMed=11466528;
RA Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
RT diversification in Danio.";
RL Dev. Genes Evol. 211:319-328(2001).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF324481; AAK15303.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig_c2.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig_4.
DR Pfam; PF00069; pkinase_1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane.
FT VARIANT 60 V -> L.
FT VARIANT 103 103 A -> S.
FT VARIANT 742 742 P -> S.
FT VARIANT 899 899 E -> D.
FT SEQUENCE 977 AA; 109881 MW; CF54E129FAB10E3E CRC64;

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Query Match 23.3%; Score 1230.5; DB 13; Length 977;
Best local Similarity 32.8%; Pred. No. 8.4e-93;
Matches 326; Conservative 174; Mismatches 367; Indels 127; Gaps 34;

Qy 71 SSGTVYEAADVEVDYSASITLQVLVDAPGNISCL-WVFKHSSLNCOPHFLQNRGVVSMV 129
Db 27 NSGAL---AGTDVILDSGSPQLVCEGDPTVFPVAXH-----KRYISKEVGRSPR 78
Qy 130 ILKMTETQAGEY-LFIQSEATNYTILFTVSIRNT-LLY-----TLRPPYFRKMEMQDAL 182
Db 79 VEKATVDFGTGKVCVINGSNLSASSVHFVRDSRVLFVSPSSLR--VYRK-EGEDLL 135
Qy 183 V-CISESPEP-IVEWLDCSQGESCKEESPAVKEEKL-----HELFTDIRCCARNE 236
Db 136 LPCL---LTPDPTDFTFRMDNGSAAPYGMNATFDRPKGVLIERNVHPGNADYICSA 192
Qy 237 LGRECTRLFTIDLNQTPQTLPLFLK-----VGEPLWIRCKAVHNVHFGTLWELEN 289
Db 193 GAEKVSKIPFINVIOQLRFP-PYVILKRNEYVKLUGERLOISCTTNPNFYNNVTHSS 251
Qy 290 KALBEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPSQSALVT---IVG 346
Db 252 KRLPKPE--EKSTMEGDLAIESILT-ISSVOLSDTGNITCTGQNEAGANSITQLLV 308
Qy 347 KGF-----NATNSDEYIDQVEEFCFSVRKAYQIIRC-TW---TFSRKSPPCEQ 394
Db 309 EPIYIRLSPKLKSLTHRGLSIEVSEGEDVDLGLVLI EAYPPLTSHWTETPTSHNASLP--- 365
Qy 395 KGLDNGYSISKFCNHK-----HQPGEVIFHAENDDAQFTKMTLINRRKQP 440
Db 366 -----ENRFYNDRYEAALLFLKRLNFEIGQVTLNVKNMSKASITFDIKMTYKP 417
Qy 441 VLAE-ASASQASCFSDGYPLPSWTWKCKDKSPNCTEEITE-----GVNRRKANRKFVG 495
Db 418 ARVKENVTTLSCRSYGVPAISLWVQCTGIRTCENTDLOPIQOTQVFOKESGAV 477
Qy 496 VSSSTLNMSKALKGLVKCCAYNSLGTSCETILLNSPGPPFIQDINSFYATTG-VCLL 553
Db 478 GVESVLTVGPN-RRMTVVCVAFNLVQGGSDTFSMD-----VSDQIFTSAMCGSTVAM 529
Qy 554 FTVLTLTILCHYKKQFRVESQLQWQVVTGSSDNEYFYVDFREYEDLKWEFFRENLEFG 613
Db 530 VGLGLLIIFMYKKQPRYERIKWII EAT--NGNNVTFFIDTQLPYNEKWEFFPRDLKLG 587
Qy 614 KVLGSGAFGKVMNATAYGISKTGVSTQVAVKMLKERADSSEREALMSLKMMTQLGSHEN 673
Db 588 KTLGAGAGKVVETATYGLGKEDNITRVAVKMLKASHPDEREALMSLKLHLGQHK 647
Qy 674 IVNLGACTLSGPIYLIFCYCYGDLNLYLRSKREKFRHTWTEIFKEHNFSFYPTQSH 733
Db 648 IVNLGACTHGGFVLVITEYCCGDLNLFRLSKAENF-----LNFVMTI---P 692
Qy 734 NSSMP-----GSREVQIHPDSQISGLHNSFHSDEIEYENQKRLSE-----EEDLN 782
Db 693 NPPEPVTDYKVNSTERMFVRSDSGISSTCSHDYLDNRPVTSRPTNSALDPSSDCQDS 752
Qy 783 LTFEDLLCFAYQVAKGMFEPLFKSCVHRDLAARNVLVTHGVKVKICDFGLARDIMSD 842
Db 753 LMDDDLRFSSQVACGLDPLAANKCIHRDVAARNVLLTNSRVAKICDFGLARDIMSD 812
Qy 843 VYRGNARLPVKWNAPESEIFEGYITIKSDVWSYGILLWEIFSLGVNVPYGPVDANFY 902
Db 813 VYKGNARLPVKWNAPESEIFECVYTVQSDVWSYGIMLWEIFSLGKSPYNILVDSKFY 872
Qy 903 QNGFKMDQPPYATEEIIYIMQSCWAFDSKRFRSPFNLTSLFGLQCLADAPEAM-----YQNV 958
Db 873 KGYQMSRPDPFAPPENYTIMKMCNLEAERPTFSKISQMIQRMILGETSEQDQTYKNI 932
Qy 959 DGRVSECPHYQNRPRPFRSMDLGLLSPQAQVED 992
Db 933 PSE-AEVEQPLESCDPVKHDESFETSCEPEEED 965

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[illegible]


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Db 254 LPKAE--EKSTWEGDRLAIESILT-IPVSQLSHTGNICTGONEAGANSSTQLLVVEEP 310
Qy 349 FI-----NATNSEDYEIDQYEEFCFSVRFPKAYQIIRC-----TWTFSRKSFCEQKG 396
Db 311 YIRLSPKLSKLTHRLGSIIEVSGDDVLGVLEIAYPLTSHKWTPTSHNASLP-----365
Qy 397 LONGYSISKFNHK-----HQPGEYIFHAENDDAQAQTKMFTLNIRKRPQVL 442
Db 366 -----ENRFFHNDRYEALLKLKLNFEIEGQYTLNKNMKSASITFDIKMYTKPVAR 419
Qy 443 AE-ASASQSCFSDGYPPLPSWTWKCDKSPNCTEITE-----GVNWKANKKVFQGWVS 497
Db 420 VKWENVTLSCRSYGPAPSILWYCTGIRTPCPTNTDLOPIQTQTFQKESFGAVCV 479
Qy 498 SSTLNMSAIGFLVKCCAYNSLGTSCETILNSPGPPFFQDNISFYATIC--VCLLFI 555
Db 480 ESVLTGVGN-RRMTVVCVAFNLVGGSDTFSE-----VSDQIFTSAMCGSTVAMVVL 531
Qy 556 VVLTLILCHYKKQFRYSQLOMVQVGTSSDNEYVYDFREYEDLKWEFFPRENLEFGKV 615
Db 532 GLLLIFMYIKYKQPRYBIRWKIIEAT--NGNNYTFIDPTQLPYNEKWEFFPRDKLGLGT 589
Qy 616 LGSGAFGVKNATAGISKTGVSIVQAVKMLKEKADSSERELMSLKMOTOLGSHENIV 675
Db 590 LGAGAFGVKEATAYGLGKEDNITKVAVMKLSAHPDEREALMSLKLHLGQHKNIIV 649
Qy 676 NLLGACTLSGPIYLFYCCYGDLLNLYLRSKREK-----HRT 713
Db 650 NLLGACTGGPVLTVEYCCGGDLNLFNRSKAENFLNFWTIPNPEPMTDYKNVSTERM 709
Qy 714 W-----TEIFKEHNFYPTFQSHPNSSMPGSRVQIHPDSDQIISGLHGNSFHSDEI 766
Db 710 FVRSDGISSTCSHDYDMRPVTPRPTNSALDSSECO-----747
Qy 767 EYENQKLEBEDLNLVTFEDLLCFAYOVAKGMELEKSCVHRDLAARNVLVTHGVVK 826
Db 748 -----EDSWPLDMDDLRFSSQVAGGLDLFAAKNCIHRDVAARNVLLTNSRAK 796
Qy 827 ICDPLGARDIMSDSNVYVRGNARLPVKWAPESLPPEGIYTIKSDVWSYGILLWEIFSLGV 886
Db 797 ICDPLGARDIMSDSNVYVRGNARLPVKWAPESIEFVYTVQSDVWSYGIMLWEIFSLGK 856
Qy 887 NPYGIPVDANFYKLIQNGKQDPFYATEIYIMQSCWAPDSRSPNLPNLFGLQ 946
Db 857 SPYENILVDSKPYKMKICGYQMSRDPFAPPENYTIMKCNWLDAAERPTFSKISQIMQ 916
Qy 947 LADAEAM-----YQNV-----DGRVSCPHYQNRPP-----SREMDLGLSP 986
Db 917 LGSETSEQDQTOEYKNIPTAEABEQLESQDPVKHDESFETSQDEEDQPLMKP 971

RESULT 15
Q9TDD7 PRELIMINARY; PRT: 948 AA.
AC Q9TDD7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Stem cell factor receptor (Fragment).
GN C-KIT.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawrence S.B., Greenwood P., Tisdall D.J., McNatty K.P., Fidler A.E.;
RT "Partial cDNA sequence of the c-kit homologue of brushtail possum
RT (Trichosurus vulpecula).";
RL Submitted (FEB-1999) to the ENBL/GenBank/DBJ databases.
DR EMBL; AF131209; AAF22141.1; -.
DR HSSP; P11362; 1FGK.
```

```
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Immunoglobulin domain; Receptor; Tyrosine-protein kinase.
FT NON TER 948
SQ SEQUENCE 948 AA; 106323 MW; 708E0258FFC4D07D CRC64;

Query Match 23.2%; Score 1221; DB 6; Length 948;
Best Local Similarity 33.2%; Pred. No. 4.9e-92;
Matches 319; Conservative 160; Mismatches 363; Indels 118; Gaps 32;

Qy 67 LRPOSSTGYEAAAEVDVDSASITLQVLVDAPGNISCL-----WVFKHSSSLNCQHPDL 120
Db 24 LQSTSPANYSPST---TPARSQLTNVFSGSEIKLSCDLHFVNWTFENAAHLLE-----75
Qy 121 QNRGVVSMVLKMTQTQAGEYLLFIQSEATNYTLFTVSIRNTLYTLRRPYFRKMNQD 180
Db 76 SSRTTETLWTNAQAQDGRYCTCNKMGSLSSIVFVKDPK--ILFLDLRLLYGN-EGSD 132
Qy 181 ALVCISESVPFIVWV--LCD-----SQGESCKEESPVVVKKEKVLHEL 224
Db 133 ALVNCFTVDPE-VTFNLTLLCDGKPLPKDLTLIPDIQKGITIKN-----VKRSNKIC---184
Qy 225 FGTDIRCCARNELGECTRLFTIDLNOTPQTLTPOL-----FLKVGELWIRKRAVHV 277
Db 185 ----FQCSAYQDQGLKLSDRMTLVKRPAPQ-SVPEVSLIQTNYLLREGETFOATCMKDV 239
Qy 278 NHGFLGTWELENKALEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTCSKSK---334
Db 240 ASSVVSMMIKDNNRI---STHTQSRHSGDYAYERQDILTISPVRVNDSGVFTCFANNTFG 296
Qy 335 HPSQALVTIVCKGGINA-TNSEDYEIDQYEEFCFSVRFPKAYQ-----IRCTWTFSR 387
Db 297 PANVTATLKVEKGFINIPFPKNTTIFINDGENIDLVVEYEAFFKPEHLQWIMYMGTVTD 356
Qy 388 KSFPCEQKGLDNGYISIKFCNHK-----OPGEYIFHAENDDAQFTKMTLNIRKPKQ 440
Db 357 KWDDYTKPGE---STIRYISLHLNRLKGTGGPTTFVSNSDSVSTVTFKYVYTKPE 413
Qy 441 VLAEASASQA--SCFSDGYPPLPSWTWKCDKSPNCTEITEGVNWKANKRKV---FGOW 495
Db 414 ILTSDRLMNLGLQCVAAAGPPEPTIDWYFCPGTEQRCSTSLP--MDVKTNSMLPPFGKI 471
Qy 496 VSSSTLNMSAIGFLVKCCAYNSLGTSCETILNSPGPPFP--IQDNISFYATICVCLL- 553
Db 472 VVESTIDSSAFRYNGTVECKASNDVG-----KSSAFNFKAKEQITSHLTFTLLIG 523
Qy 554 FIV-----VLTLLIICHYKKQFRYSQLOMV-QVTGSSDNEYVYDFREYEDLKWEFP 606
Db 524 FVVAAGLMCVIILTYKYPQPMYEVQWKVVEING---NNYVIDPTQLPVDHKEWFP 580
Qy 607 RENLBFKVLGSGAFGVKNMATAYGISKTGVSIVQAVKMLKEKADSSERELMSLKMNT 666
Db 581 RNRLSFGKTLGAGAFGVKEATAYGLFKSDAAMTAVAKMLKPSAHLTEREALMSLKVLS 640
Qy 667 QLGSHEINVLGACTLSQPIYLIPEYCYGDLLNLYLRSKREKFRHTWTWEIFKEH----N 722
Db 641 YLGNHWNINILGACTIGGTGLVITEYCCYGDLLNLFRRKDSF-----ICSKHEDHAE 694
Qy 723 FSYFTFQSHPNSSMPGSRV-QIHPDSDQIISGLHGNSFHS-----DEIYENOKRLEEE 778
Db 695 AALYKNLQSKSSCDGANEYMDMKPGSVYVPTKAEKRSARVSGYIERDVTTAIMEDD 754
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Qy	779	DLNVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMS	838
Db	755	EL-ALDIEDLLSPSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARIKN	813
Qy	839	DSNYVRCNARLPVKWAPESLFEGIYTIKSDVWSYGILLWEI FSLGVNYPYGPVDANF	898
Db	814	DSNYWVKGARLPVKWAPESIFNCVTFESDVWSYGIFLWELFSLGSSPYGMPVDSKF	873
Qy	899	YKLIQNGFKMDQPFYATEEYIIMQSCWAFDSRKRPSFPNLTSFLGCOLADAEAMYNV	958
Db	874	YKMIKEGFRMLSPCAPPEMYEINKSCWNEDPLQRPFKLIVOLIEQQLDSTNHNYSNI	933

Search completed: May 24, 2003, 16:59:25
Job time : 78.0358 secs

XX 18-JUN-1993; 93US-0080244.
PR 21-JUN-1993; 93US-0081508.
PR 23-NOV-1993; 93US-0157490.
XX (UYPR-) UNIV PRINCETON.
PA Lemischka IR;
PI WPI; 1995-052014/07.
XX N-PSDB; AAQ81013.
DR
XX Ligand for receptor protein tyrosine kinase - useful for the
PT stimulation of primitive haematopoietic stem cells causing
PT proliferation and/or differentiation
XX
PS Disclosure; Fig 1b; 11pp; English.
XX
CC The sequence corresponds to a human Flk2 (fetal liver kinase)
CC receptor protein-tyrosine-kinase, which is expressed in primitive
CC hematopoietic cells but not in mature hematopoietic cells. The
CC protein is useful in isolation of receptor ligands, which have
CC applications in diagnosis of bone marrow disorders, and in
CC stimulating proliferation and/or differentiation of primitive
CC hematopoietic stem cells.
XX
SQ Sequence 993 AA;
Query Match 100.0%; Score 5274; DB 16; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPALARDAGTVPLVVFSGAMIFGTTNODLPVVKVLIHKNNDSSVGKSSSYPMVSESP 60
Db 1 MPALARDAGTVPLVVFSGAMIFGTTNODLPVVKVLIHKNNDSSVGKSSSYPMVSESP 60
Qy 61 EDLGCALPQSSGTVYEAAYVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCPHFDL 120
Db 61 EDLGCALPQSSGTVYEAAYVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCPHFDL 120
Qy 121 QNRGVSMVILKMTQAGEVLLFFIQSBATNYTLFTVSIRNTLLYTLRRPYFRXENQD 180
Db 121 QNRGVSMVILKMTQAGEVLLFFIQSBATNYTLFTVSIRNTLLYTLRRPYFRXENQD 180
Qy 181 ALVCISESVPEIWEVWLCDGSGESKESPAVVKKEKVLHFGTDIRCCARNEGRE 240
Db 181 ALVCISESVPEIWEVWLCDGSGESKESPAVVKKEKVLHFGTDIRCCARNEGRE 240
Qy 241 CTRLEFTIDNTPQTLPLQFLKVGEPWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Db 241 CTRLEFTIDNTPQTLPLQFLKVGEPWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAPVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDE 360
Db 301 STYSTNRTMIRILFAPVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDE 360
Qy 361 IDOYEFCFSVPKAYPQIRCTWTSRSPCEQKGLDNGYSISKFCNHKHPGGEYIFHA 420
Db 361 IDOYEFCFSVPKAYPQIRCTWTSRSPCEQKGLDNGYSISKFCNHKHPGGEYIFHA 420
Qy 421 ENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPPLPSWTWKCKSPNCTEEITE 480
Db 421 ENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPPLPSWTWKCKSPNCTEEITE 480
Qy 481 GVMNKAARKVFGQWSSSTLANSEBAIKGLVKCCAYNSLGTSCETILNSPGPPFIOD 540
Db 481 GVMNKAARKVFGQWSSSTLANSEBAIKGLVKCCAYNSLGTSCETILNSPGPPFIOD 540
Qy 541 NISFYATIGVCLLIYVLLTLLCHKYKKQFRYESQLOMVOVTGSSDNEYVDREYED 600
Db 541 NISFYATIGVCLLIYVLLTLLCHKYKKQFRYESQLOMVOVTGSSDNEYVDREYED 600
Qy 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIQVAVMLKEKADSSREALMS 660

Db 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIQVAVMLKEKADSSREALMS 660
Qy 661 ELKMTQOLGSHENIVNLLGACTLSGPIYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFKE 720
Db 661 ELKMTQOLGSHENIVNLLGACTLSGPIYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFKE 720
Qy 721 HNFSEYPTFQSHPNSSMPGSGREVQIHPDSQIISGLHNSFHSDEIEIYENOKRLEEBEDL 780
Db 721 HNFSEYPTFQSHPNSSMPGSGREVQIHPDSQIISGLHNSFHSDEIEIYENOKRLEEBEDL 780
Qy 781 NVLTFEDLLCFAYQVAKGMBLEFKSCVHRDLAARNVLVTHGKVKICDGLARDIMSDS 840
Db 781 NVLTFEDLLCFAYQVAKGMBLEFKSCVHRDLAARNVLVTHGKVKICDGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVPDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVPDANFYK 900
Qy 901 LIQNGFKMDQPFYATEEIIIMQSCWAFDSKRKPSFNNLTSLFLGCOLADABEAMYQNVVG 960
Db 901 LIQNGFKMDQPFYATEEIIIMQSCWAFDSKRKPSFNNLTSLFLGCOLADABEAMYQNVVG 960
Qy 961 RVSECPHTYQNRPFPSREMDLGLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPFPSREMDLGLSPQAQVEDS 993
RESULT 2
AAR67536
ID AAR67536 standard; Protein; 993 AA.
XX AC AAR67536;
XX AC AAR67536;
DT 04-JUL-1995 (first entry)
XX Human flk-2.
XX Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
KW hematopoiesis; stem cell.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..27
FT Domain 28..543 /label= Sig_peptide
FT Region /label= Extracellular_receptor_domain
FT Domain 544..563 /label= Transmembrane_region
FT Domain 564..993 /label= Intracellular_catalytic_domain
XX USS367057-A.
PN 22-NOV-1994.
PD 02-APR-1991; 91US-0679666.
PF 02-APR-1991; 91US-0679666.
XX 28-JUN-1991; 91US-0728913.
PR 15-NOV-1991; 91US-0793065.
PR 24-DEC-1991; 91US-0813593.
PR 26-JUN-1992; 92US-0906397.
PR 12-NOV-1992; 92US-0975049.
PR 19-NOV-1992; 92US-0977451.
PR 30-APR-1993; 93US-0055269.
XX (UYPR-) UNIV PRINCETON.
PA Lemischka IR;
PI WPI; 1995-005894/01.
DR

DR N-PSDB; AAQ79069.
XX Murine flk-2 receptor protein tyrosine kinase - used to stimulate
PT proliferation and/or stimulation of primitive mammalian
PT haematopoietic stem cells in vitro or in vivo.
XX
XX Disclosure; Fig. 2A-1F; 69pp; English.
XX
CC cDNAs encoding receptor protein tyrosine-kinases, mouse fetal liver
CC kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAQ79068-70,
CC respectively, and the deduced amino acid sequences in AAQ79068-70,
CC respectively.
XX
XX Sequence 993 AA;
SQ

Query Match 100.0%; Score 5274; DB 16; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPLLVVFSAMIFGTTTQDLPVVKVILNHKNKNDSSVGKSSYPMVSESP 60
Db 1 MPALARDAGTVPLLVVFSAMIFGTTTQDLPVVKVILNHKNKNDSSVGKSSYPMVSESP 60
Qy 61 EDLGCALRQSSGTVYEAADVDSASITLQVLVDAPGNI SCLWVFKHSSLNCOPHFDL 120
Db 61 EDLGCALRQSSGTVYEAADVDSASITLQVLVDAPGNI SCLWVFKHSSLNCOPHFDL 120
Qy 121 QNRGVSVVILKWTQAGEYLLFTQSEATNYTILFTVSI RNTLLYLRPPYFRKMNQD 180
Db 121 QNRGVSVVILKWTQAGEYLLFTQSEATNYTILFTVSI RNTLLYLRPPYFRKMNQD 180
Qy 181 ALVCISESVPEPIVEMVLCDSGESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEPIVEMVLCDSGESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLEFDLNOTPOTTLQFLKVGCEPLWIRCKAVVNHGFLTWELNKALEEGNYFEM 300
Db 241 CTRLEFDLNOTPOTTLQFLKVGCEPLWIRCKAVVNHGFLTWELNKALEEGNYFEM 300
Qy 301 STYSNTRMIRILFAFVSSVARNDGYTTCSSSKHPSQSALVTIVGKGFINATNSSEDEY 360
Db 301 STYSNTRMIRILFAFVSSVARNDGYTTCSSSKHPSQSALVTIVGKGFINATNSSEDEY 360
Qy 361 IDQYEEFCFVAFKAYQIRCTWTFSTRKSPFCEQKGLDNGYSISKFCNHHQGFYIFHA 420
Db 361 IDQYEEFCFVAFKAYQIRCTWTFSTRKSPFCEQKGLDNGYSISKFCNHHQGFYIFHA 420
Qy 421 ENDDAQFTKMFTLNIRRKQVLAESAASQSCFSDGYPLPSWTWKCKSDKSPNCTEEITE 480
Db 421 ENDDAQFTKMFTLNIRRKQVLAESAASQSCFSDGYPLPSWTWKCKSDKSPNCTEEITE 480
Qy 481 GWNKRNKRVFGQVSSSTLNSBAIKGFLVKCCAYNSLGTSCETILLNSPGPPFFIQD 540
Db 481 GWNKRNKRVFGQVSSSTLNSBAIKGFLVKCCAYNSLGTSCETILLNSPGPPFFIQD 540
Qy 541 NISFYATIGVCLLFIVLTLCHYKKQFRYESQLQMVQVQTSSDNEYFYVDREYED 600
Db 541 NISFYATIGVCLLFIVLTLCHYKKQFRYESQLQMVQVQTSSDNEYFYVDREYED 600
Qy 601 LKWEFPRENLEFGKVLGSAFGKVNATAYGISKTVGVSQVAVKMLKEKADSSEREALMS 660
Db 601 LKWEFPRENLEFGKVLGSAFGKVNATAYGISKTVGVSQVAVKMLKEKADSSEREALMS 660
Qy 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIPEYCCVGLDNLNLSRKREKPHRTWTWEIFKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIPEYCCVGLDNLNLSRKREKPHRTWTWEIFKE 720
Qy 721 HNFSPYPTQSHPNSSMPGSRVQIHDPDSQISGLHNSFHSDEIETEXENQKLEEBEEDL 780
Db 721 HNFSPYPTQSHPNSSMPGSRVQIHDPDSQISGLHNSFHSDEIETEXENQKLEEBEEDL 780
Qy 781 NVLTPEDDLCPAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
|||||

Db 781 NVLTPEDDLCPAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWNPAPESLPBEGITYTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWNPAPESLPBEGITYTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFYK 900
Qy 901 LIQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPSPPNLTSLGCOLADAEEAMYQNVDG 960
Db 901 LIQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPSPPNLTSLGCOLADAEEAMYQNVDG 960
Qy 961 RVSECPHYQNRPRPESREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHYQNRPRPESREMDLGLLSPQAQVEDS 993

RESULT 3
AAR97419
ID AAR97419 standard; Protein; 993 AA.
XX
AC AAR97419;
XX
DT 11-DEC-1996 - (first entry)
XX
DE Murine foetal liver kinase 2.
XX
KW Murine; foetal liver kinase 2; flk-2; protein tyrosine kinase;
KW monoclonal; antibody; extracellular domain; receptor assay;
KW haematopoietic stem cell; ligand; stimulation; proliferation;
KW differentiation; treatment; anaemia; bone marrow damage;
KW cancer chemotherapy; radiation.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT Peptide /label= sig_peptide
FT Peptide 28..993
FT Peptide /label= mat_peptide
FT Domain 28..544
FT Domain /label= extracellular_domain
FT Domain 545..564
FT Domain /label= transmembrane_domain
FT Domain 565..993
FT Domain /label= intracellular_domain
XX
PN US5548065-A.
XX
PD 20-AUG-1996.
XX
PF 02-APR-1991; 91US-0679666.
XX
PR 19-NOV-1992; 92US-0977451.
PR 02-APR-1991; 91US-0679666.
PR 28-JUN-1991; 91US-0728913.
PR 15-NOV-1991; 91US-0793065.
PR 24-DEC-1991; 91US-0813593.
PR 26-JUN-1992; 92US-0906397.
PR 12-NOV-1992; 92US-0975049.
PR 30-APR-1993; 93US-005269.
PR 31-OCT-1994; 94US-0252517.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Lemischka IR;
XX
XX WPI; 1996-392678/39.
DR N-PSDB; AAT38734.
XX
PT Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,
PT for isolating haematopoietic stem cells expressing receptor and for
PT obtaining ligands
XX
PS Claim 1; Columns 39-48; 50pp; English.

XX The present sequence is murine foetal liver kinase 2 (flk-2),
CC a protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
CC raised against the extracellular portion of flk-2 can be used to
CC assay for flk receptors on the surface of primitive haematopoietic
CC stem cells, and to isolate positive cells. The antibodies can also
CC be used as, or to obtain ligands, which stimulate the proliferation
CC and/or differentiation of stem cells. The ligands can be used, e.g.
CC for treating anaemia, or bone marrow damage resulting from cancer
CC chemotherapy, or radiation.

XX Sequence 993 AA;
SQ

Query Match 100.0%; Score 5274; DB 17; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPVLLVVSAMIFGTITNODLVKICVLINHKQNDSSVGKSSSYPMVSESP 60
Db 1 MPALARDAGTVPVLLVVSAMIFGTITNODLVKICVLINHKQNDSSVGKSSSYPMVSESP 60

Qy 61 EDLGCALRPQSSGTYEAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSINCPHFDL 120
Db 61 EDLGCALRPQSSGTYEAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSINCPHFDL 120

Qy 121 QNRGVSVMLKMTETQAGEYLLFIQSEATNYTLFTVSIRNTLLYTLRRPYFRMENQD 180
Db 121 QNRGVSVMLKMTETQAGEYLLFIQSEATNYTLFTVSIRNTLLYTLRRPYFRMENQD 180

Qy 181 ALVCISESVPEPIVEWVLCDQSGESKEESPAVVKKEKVLHELPGTDIRCARNELGRE 240
Db 181 ALVCISESVPEPIVEWVLCDQSGESKEESPAVVKKEKVLHELPGTDIRCARNELGRE 240

Qy 241 CTRFTIDLNOTPTTLPLQFLKVGEPILWIRCKAVVNHGFLTWELNKALEEGNYFEM 300
Db 241 CTRFTIDLNOTPTTLPLQFLKVGEPILWIRCKAVVNHGFLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSRKPSQSALVTIVGKGFINATNSSEDE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSRKPSQSALVTIVGKGFINATNSSEDE 360

Qy 361 IDQVEEFCFSVRFKAYPOIRCTWTFSRKSPFCEQKGLDNGYSISKFCNHKQPGYIIFHA 420
Db 361 IDQVEEFCFSVRFKAYPOIRCTWTFSRKSPFCEQKGLDNGYSISKFCNHKQPGYIIFHA 420

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Db 421 ENDDAQFTKMTLNRKPOVLAEASQASCFSDGYPLPSWTWKCKSDKSPNCTEEITE 480

Qy 481 GVMNRKANRKFVGQWSSSTLNMSEAIKGLVKKCCAYNSLGTSCETILLNSPGPPFFIQD 540
Db 481 GVMNRKANRKFVGQWSSSTLNMSEAIKGLVKKCCAYNSLGTSCETILLNSPGPPFFIQD 540

Qy 541 NISFYATTGCVLLFTIVLTLI CHYKQKQRYESQLOQVQVGTSSDNEYFYVDPREYED 600
Db 541 NISFYATTGCVLLFTIVLTLI CHYKQKQRYESQLOQVQVGTSSDNEYFYVDPREYED 600

Qy 601 LKWEPPRENLEBFGVLGSGAGFKVNNATAYGISTKGTGVSIOAVKMLKEKADSSEREALMS 660
Db 601 LKWEPPRENLEBFGVLGSGAGFKVNNATAYGISTKGTGVSIOAVKMLKEKADSSEREALMS 660

Qy 661 ELKMMTQLGSHENIVNLLGACTLSGPYLIIFEYCCYGDLNLYRSKREKFRHTWTETFEKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPYLIIFEYCCYGDLNLYRSKREKFRHTWTETFEKE 720

Qy 721 HNFSPYPTFQSHNPSMPSGSRVQIHPSDQISGLHGNFSHSEDEIYENQKRLBEEDL 780
Db 721 HNFSPYPTFQSHNPSMPSGSRVQIHPSDQISGLHGNFSHSEDEIYENQKRLBEEDL 780

Qy 781 NVLTPEDLCLFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTPEDLCLFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840

Qy 841 NYVVRGNARLPVKWAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900

Qy 901 LIQNGFKMDQPFYATEEIIIMQSCWAFDSRKPSFPNLTSLFLGCOLADAEAMYQNVDG 960
Db 901 LIQNGFKMDQPFYATEEIIIMQSCWAFDSRKPSFPNLTSLFLGCOLADAEAMYQNVDG 960

Qy 961 RVSECPHTYQNRPRPFSREMDLGLLSPOQAQVEDS 993
Db 961 RVSECPHTYQNRPRPFSREMDLGLLSPOQAQVEDS 993

RESULT 4
AAW19873
ID AAW19873 standard; Protein; 993 AA.

XX AC AAW19873;
XX DT 19-AUG-1997 (first entry)
XX DB Human flk-2 receptor.

XX Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
KW pTK; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
KW haematopoietic hierarchy; extracellular domain; soluble form; ligand;
KW proliferation; differentiation; mammalian; haematopoietic stem cell;
KW macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Peptide 1..27
FT Protein /note= "Signal peptide"
FT Protein 28..993
FT Protein /note= "Mature flk-2"

XX US5621090-A.
XX FN 15-APR-1997.
XX PD 02-APR-1991; 91US-0679666.
XX PF 26-JUN-1992; 92US-0906397.
XX PR 02-APR-1991; 91US-0679666.
XX PR 28-JUN-1991; 91US-0728913.
XX PR 15-NOV-1991; 91US-0793065.
XX PR 24-DEC-1991; 91US-0813593.

XX (UYPR-) UNIV PRINCETON.
XX PA Lemischka IR;
XX PI WPI; 1997-235228/21.
XX DR N-PSDB; AAT72117.
XX XX Protein containing the extracellular domain of human flk-2 - used
PT for identification of primitive haematopoietic cell proliferation
PT and differentiation stimulatory ligands, e.g. for treating anaemia
XX Claim 1; Fig 1B; 55pp; English.

XX This sequence represents human fetal liver kinase 2 (flk2). flk-2 is
XX a receptor protein tyrosine kinase (pTK) and is important in transducing
XX putative self-renewal signals from the environment. flk-2 is expressed
XX in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
XX and it is thought that flk-2 is expressed in the entire primitive portion
XX of the haematopoietic hierarchy. The invention concerns a recombinant
XX nucleic acid, preferably mRNA, which encodes a protein containing only
XX the extracellular domain of human flk-2 and lacking the flk-2 intra-
XX cellular catalytic domain. The resultant protein represents a soluble
XX form of flk-2 which is used to isolate specific ligands for flk-2. These
XX ligands can be used to stimulate proliferation and/or differentiation of

CC mammalian haematopoietic stem cells, in vivo or in vitro, e.g. for
CC treatment of macrocytic or aplastic anaemia or bone marrow damage caused
CC by cancer treatment or radiation.
XX
SQ Sequence 993 AA;

Query Match	100.0%;	Score 5274;	DB 18;	Length 993;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 993;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MPALARDAGTVPVLLVVFSGAMIFGTTNQDLPVVKVLIHKNKNDSSVGKSSSPYPMVSESP	60	
Db	1	MPALARDAGTVPVLLVVFSGAMIFGTTNQDLPVVKVLIHKNKNDSSVGKSSSPYPMVSESP	60	
Qy	61	EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVWFKHSSLNCPHFDL	120	
Db	61	EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVWFKHSSLNCPHFDL	120	
Qy	121	QNRGVVSVILKWTQAGEYLLFQSEATNTYILFTVIRNTLLYTLRRPYFRKMNQD	180	
Db	121	QNRGVVSVILKWTQAGEYLLFQSEATNTYILFTVIRNTLLYTLRRPYFRKMNQD	180	
Qy	181	ALVCISSEVPEPIVWLVLCDSQGESCKEBSPAVVKKEKVLHELFGTDIRCCARNELGRE	240	
Db	181	ALVCISSEVPEPIVWLVLCDSQGESCKEBSPAVVKKEKVLHELFGTDIRCCARNELGRE	240	
Qy	241	CTRLETFIDNLTOTPTTLQFLKVGLEPLWIRCKAVVNHGFGITWELENKALEEGNYFEM	300	
Db	241	CTRLETFIDNLTOTPTTLQFLKVGLEPLWIRCKAVVNHGFGITWELENKALEEGNYFEM	300	
Qy	301	STYSTNRTMIRILFAFVSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEY	360	
Db	301	STYSTNRTMIRILFAFVSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEY	360	
Qy	361	IDQYEEFCFSVRKAYPOIRCTWTFSRSPCEQKGLDNGYSISKFCNKHQGPGEYIPHA	420	
Db	361	IDQYEEFCFSVRKAYPOIRCTWTFSRSPCEQKGLDNGYSISKFCNKHQGPGEYIPHA	420	
Qy	421	ENDDAQFTKMTFLNRRKPOVLAEASASQSCFSDGYPLPSWTWKCKDKNCTEEITE	480	
Db	421	ENDDAQFTKMTFLNRRKPOVLAEASASQSCFSDGYPLPSWTWKCKDKNCTEEITE	480	
Qy	481	GVNKRKANRKFQGVQWSSSTLNMSEAIKGLVKCAYNLSGTSCTILLNSPGPPFIQD	540	
Db	481	GVNKRKANRKFQGVQWSSSTLNMSEAIKGLVKCAYNLSGTSCTILLNSPGPPFIQD	540	
Qy	541	NISFYATIGVCLLFIVLTLLIHKYKQFRYESQLQWQVGTSSDNEYFYVDREYED	600	
Db	541	NISFYATIGVCLLFIVLTLLIHKYKQFRYESQLQWQVGTSSDNEYFYVDREYED	600	
Qy	601	LKWEPPRENLEFGKVGAGFKVNNATAYGTSKTVGSIQVAVKMLKEKADSSREALMS	660	
Db	601	LKWEPPRENLEFGKVGAGFKVNNATAYGTSKTVGSIQVAVKMLKEKADSSREALMS	660	
Qy	661	ELKMTQLGSHENIIVNLGACTLSGPVILYIPEYCCVGDLLNLRKREKPHRTWTETIPE	720	
Db	661	ELKMTQLGSHENIIVNLGACTLSGPVILYIPEYCCVGDLLNLRKREKPHRTWTETIPE	720	
Qy	721	HNFSFYPTFQSHPNSSMPGSRVQIHPDSQDQISGLHGNFSHSEDEIYEYENQKLEEEED	780	
Db	721	HNFSFYPTFQSHPNSSMPGSRVQIHPDSQDQISGLHGNFSHSEDEIYEYENQKLEEEED	780	
Qy	781	NVLTFEDILCFAYQVAKWMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS	840	
Db	781	NVLTFEDILCFAYQVAKWMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS	840	
Qy	841	NVVRGNARLPVKWMAPSLPEGIYITKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK	900	
Db	841	NVVRGNARLPVKWMAPSLPEGIYITKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK	900	
Qy	901	LIQNGFKMDQFPYATEEYIIMQSCWAFDSRKRFPNLTSLPLGCOLADAEAMTQNVGD	960	
Db	901	LIQNGFKMDQFPYATEEYIIMQSCWAFDSRKRFPNLTSLPLGCOLADAEAMTQNVGD	960	

Qy 961 RVSECHTYQNRPPSRFEMDLGLLSPQAQVEDS 993
Db 961 RVSECHTYQNRPPSRFEMDLGLLSPQAQVEDS 993

RESULT 5

AAV08617
ID AAY08617 standard; Protein; 993 AA.

XX AAY08617;

XX 05-AUG-1999 (first entry)

XX Human flk-2 protein.

XX Human; flk-2; flk-1; cell isolation; fetal liver kinase; receptor;
KW monoclonal; polyclonal; antibody; tyrosine kinase.

XX Homo sapiens.

PN US5912133-A.

XX 15-JUN-1999.

XX 10-FEB-1998; 98US-0021324.

XX 19-NOV-1992; 92US-0977451.

PR 02-APR-1991; 91US-0679666.

PR 28-JUN-1991; 91US-0728913.

PR 15-NOV-1991; 91US-0793065.

PR 24-DEC-1991; 91US-0813593.

PR 26-JUN-1992; 92US-0906397.

PR 12-NOV-1992; 92US-0975049.

PR 30-APR-1993; 93US-0055269.

PR 31-OCT-1994; 94US-0252498.

PR 15-FEB-1996; 96US-0601891.

XX (UYPR-) UNIV PRINCETON.

XX Lemischka IR;

XX WPI; 1999-3571194/30.

XX N-PSDB; AAX77515.

XX Isolating hematopoietic cells expressing fetal liver kinase 1

XX receptors

XX Disclosure; Fig 1b; 59pp; English.

XX This invention describes a novel method of isolating cells expressing

XX fetal liver kinase 1 (flk-1) receptors on their surface and comprises

XX binding the cells to a polyclonal or monoclonal antibody specific to

XX the FLK-1 receptor and isolating the cells that have bound to the

XX antibody. The method can be used to isolate hematopoietic stem cells in

XX any mammal but preferably a rat, mouse, rabbit or human. The proteins of

XX the invention belong to the receptor protein family. This sequence

XX represents the human flk-2 protein which is used in the method of the

XX invention.

XX SQ Sequence 993 AA;

Query Match 100.0%; Score 5274; DB 20; Length 993;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPVLLVVFSGAMIFGTTNQDLPVVKVLIHKNKNDSSVGKSSSPYPMVSESP 60

Db 1 MPALARDAGTVPVLLVVFSGAMIFGTTNQDLPVVKVLIHKNKNDSSVGKSSSPYPMVSESP 60

Qy 61 EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVWFKHSSLNCPHFDL 120

Db 61 EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVWFKHSSLNCPHFDL 120


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Qy 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLTIDLNQTPQTLPLQFLKVGEPWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Db 241 CTRLTIDLNQTPQTLPLQFLKVGEPWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTSCSSKHPQSALVTIIVGKGFINATNSSEDE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTSCSSKHPQSALVTIIVGKGFINATNSSEDE 360
Qy 361 IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEOKGLDNGYSISKFCNHKQPGQYIIFHA 420
Db 361 IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEOKGLDNGYSISKFCNHKQPGQYIIFHA 420
Qy 421 ENDDAQFTMTLIRRRKPOVLASASQASCFSDGYPLPSMTWKCKSDKSPNCTEEITE 480
Db 421 ENDDAQFTMTLIRRRKPOVLASASQASCFSDGYPLPSMTWKCKSDKSPNCTEEITE 480
Qy 481 GWNRKANRKFVGQVSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNRKANRKFVGQVSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Qy 541 NISFYATIGVCLLFIVLTLICHYKQKQRYESQOLQVQVGTGSSDNEYFYVDFREYED 600
Db 541 NISFYATIGVCLLFIVLTLICHYKQKQRYESQOLQVQVGTGSSDNEYFYVDFREYED 600
Qy 601 LKWEFPRENLEFGVLGSGAGKVMNATAYGISTKGTISQVAVKMLKEKADSSEREALMS 660
Db 601 LKWEFPRENLEFGVLGSGAGKVMNATAYGISTKGTISQVAVKMLKEKADSSEREALMS 660
Qy 661 ELKWMQTLGSHENIVNLGACTLSGPIYLIPEYCCYGDLLNVLRSKREKFRHTWTEIFKE 720
Db 661 ELKWMQTLGSHENIVNLGACTLSGPIYLIPEYCCYGDLLNVLRSKREKFRHTWTEIFKE 720
Qy 721 HNFSGYPTFQSHPNSSMPGSRVQIHPSDQISGLHGNSPHSEDEIEYENQKLEEEEDL 780
Db 721 HNFSGYPTFQSHPNSSMPGSRVQIHPSDQISGLHGNSPHSEDEIEYENQKLEEEEDL 780
Qy 781 NVLTFEDLLCFAYQVAKMEPELSEKCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
Db 781 NVLTFEDLLCFAYQVAKMEPELSEKCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWMAPELSEKGVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 900
Db 841 NYVVRGNARLPVKWMAPELSEKGVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 900
Qy 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKPSPNLTSLFLGCOLADAEAMYNQVNDG 960
Db 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKPSPNLTSLFLGCOLADAEAMYNQVNDG 960
Qy 961 RVSECPHTYQNRPFPSREMDLGLLSPQAEVDS 993
Db 961 RVSECPHTYQNRPFPSREMDLGLLSPQAEVDS 993

RESULT 7
AAR44995
ID AAR44995 standard; Protein; 993 AA.
AC
XX
AC AAR44995;
XX
XX
DT 27-JUN-1994 (first entry)
XX
DE Human flk-2 receptor protein tyrosine kinase.
XX
KW Receptor protein tyrosine kinase; pTK family; foetal liver kinase;
KW flk1; primitive; totipotent; haematopoietic cell; stem cell;
KW proliferation; stromal cell.
XX
OS Homo sapiens.

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XX Key Location/Qualifiers
FH 1..27
FT /label= signal sequence
FT /note= "hydrophobic leader"
FT Protein
FT 28..993
FT /label= flk-2
FT /note= "mature protein"
FT 28..544
FT /label= extracellular_domain
FT 545..563
FT /label= transmembrane_region
FT 564..993
FT /label= intracellular_catalytic_domain
XX
XX US5270458-A.
XX
XX 14-DEC-1993.
XX
XX 02-APR-1991; 91US-0679666.
XX
XX 02-APR-1991; 91US-0679666.
XX
XX 28-JUN-1991; 91US-0728913.
XX
XX 15-NOV-1991; 91US-0793065.
XX
XX 24-DEC-1991; 91US-0813593.
XX
XX 26-JUN-1992; 92US-0906397.
XX
XX 12-NOV-1992; 92US-0975049.
XX
XX 19-NOV-1992; 92US-0977451.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI; 1993-405021/50.
XX
XX N-PSDB; AAQ53503.
XX
XX Isolated nucleic acid molecules of hematopoietic stem cell
XX receptor flk-2 - encoding mammalian receptor protein tyrosine
XX kinases expressed in primitive haematopoietic cells
XX
XX Disclosure; Fig 1b; 60pp; English.
XX
XX Nucleic acid sequences coding for murine flk-2 and specified
XX subfragments of it are claimed. The human flk-2 coding sequence
XX (i.e. AAQ53503) is also disclosed. The murine and human flk-2
XX polypeptides represent a new class of receptor protein tyrosine
XX kinases which are expressed only in primitive haematopoietic cells.
XX
XX Sequence 993 AA;
XX
XX Query Match 99.8%; Score 5266; DB 14; Length 993;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 992; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MPALARDAGTVPLLVVFSAMIFGTTNQDLPVICKVLINHKNDSSVGKSSYPMVSESP 60
Db 1 MPALARDAGTVPLLVVFSAMIFGTTNQDLPVICKVLINHKNDSSVGKSSYPMVSESP 60
Qy 61 EDLGCALRPQSSGTVYAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQHPFDL 120
Db 61 EDLGCALRPQSSGTVYAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQHPFDL 120
Qy 121 QNRGVSMVLKMTETQAGEYLLFIQSEATNTYTLFTVSIKNTLLYLRPFRKMNOD 180
Db 121 QNRGVSMVLKMTETQAGEYLLFIQSEATNTYTLFTVSIKNTLLYLRPFRKMNOD 180
Qy 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLTIDLNQTPQTLPLQFLKVGEPWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Db 241 CTRLTIDLNQTPQTLPLQFLKVGEPWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300

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QY 301 STYSTNTRMIRILPAFVSSVARNDGTYYTCSSSKHPQSALVTIVGKGFNATNSSSEDE 360
 DB 301 STYSTNTRMIRILPAFVSSVARNDGTYYTCSSSKHPQSALVTIVGKGFNATNSSSEDE 360
 QY 361 IDQYEEFCFSVRFKAYPOIRCTWTFRSKSPCEOKGLDNGYSISKFCNKHQPOGEYIPHA 420
 DB 361 IDQYEEFCFSVRFKAYPOIRCTWTFRSKSPCEOKGLDNGYSISKFCNKHQPOGEYIPHA 420
 QY 421 ENDDAQTKMFTLIRRKPOVLAASASQSCFSDGYPLPSWTWKCKSDKSPNCTEBITE 480
 DB 421 ENDDAQTKMFTLIRRKPOVLAASASQSCFSDGYPLPSWTWKCKSDKSPNCTEBITE 480
 QY 481 GVMNRKANRVFGQWSSSTLNMSAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
 DB 481 GVMNRKANRVFGQWSSSTLNMSAIGFLVKCCAYNSLGTSCETILLNSAGPPFIQD 540
 QY 541 NISFYATIGVCLLFIIVLTLICHYKKQRYESQLOQVQVQSSDNEYFYVDREYED 600
 DB 541 NISFYATIGVCLLFIIVLTLICHYKKQRYESQLOQVQVQSSDNEYFYVDREYED 600
 QY 601 LKWEFFRENLEFGVLGSGAFKVMNATAYGISKTGYSIQAVVRLKEKADSSEREALMS 660
 DB 601 LKWEFFRENLEFGVLGSGAFKVMNATAYGISKTGYSIQAVVRLKEKADSSEREALMS 660
 QY 661 ELKWMQOLGSHENIVNLGACTLSGPIYLIPEYCCYGDLLNLYRSKREKPHRTWTEIFKE 720
 DB 661 ELKWMQOLGSHENIVNLGACTLSGPIYLIPEYCCYGDLLNLYRSKREKPHRTWTEIFKE 720
 QY 721 HNFSPYFTQSHPNSSMPGSRVQIHDPDSQISGLHNSFSEDEIEYENOKRLEEBEDL 780
 DB 721 HNFSPYFTQSHPNSSMPGSRVQIHDPDSQISGLHNSFSEDEIEYENOKRLEEBEDL 780
 QY 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
 DB 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
 QY 841 NYVVRGNARLPVKWMAPELSEFEGYITIKSDVMSYILLWEIFSLGVNYPGIPVDANFYK 900
 DB 841 NYVVRGNARLPVKWMAPELSEFEGYITIKSDVMSYILLWEIFSLGVNYPGIPVDANFYK 900
 QY 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSKRSFPLNLTSLGCOLADAEAMYQNVVDG 960
 DB 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSKRSFPLNLTSLGCOLADAEAMYQNVVDG 960
 QY 961 RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS 993
 DB 961 RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS 993

RESULT 8
 AAR75961 ID AAR75961 standard; Protein; 993 AA.
 XX AC AAR75961;
 XX AC AAR75961;
 XX DT 29-DEC-1995 (first entry)
 XX DE Human STK-1.
 XX KW STK-1; receptor PTK; protein tyrosine kinase.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal
 FT /note= "unique PTK receptor sequence"
 FT Cleavage-site 25..26
 FT Domain 35..524
 FT /note= "part of extracellular domain contg.
 22 Cys residues marked on Fig. 1"
 FT Modified-site 43..45

FT Modified-site /label= potential N-linked glycosylation site
 FT 100..102
 FT /label= see above
 FT Modified-site 151..153
 FT /label= see above
 FT Modified-site 250..252
 FT /label= see above
 FT Modified-site 306..308
 FT /label= see above
 FT Modified-site 323..325
 FT /label= see above
 FT Modified-site 351..353
 FT /label= see above
 FT Modified-site 354..356
 FT /label= see above
 FT Modified-site 473..475
 FT /label= see above
 FT Modified-site 502..504
 FT /label= see above
 FT Region 542..562
 FT /label= transmembrane spanning region
 FT Region 708..782
 FT /label= Kinase insert region
 FT Domain 617..622
 FT /label= ATP binding domain
 FT Domain 835..840
 FT /label= WMAPES motifs
 FT /note= "cytoplasmic domain"
 FT Peptide 808..813
 FT /note= "used to design PCR oligos"
 FT Peptide 870..875
 FT /note= "used to design PCR oligos"
 FT XX WO9519175-A.
 XX PN.
 XX 20-JUL-1995.
 XX PD
 XX 06-JAN-1995; 95WO-US00176.
 XX PF
 XX 14-JAN-1994; 94US-0183211.
 XX PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX PA
 XX Civin CI, Gewirtz AM, Small D;
 XX WPI; 1995-263709/34.
 XX N-PSDB; AAQ91356.
 XX PS
 XX Disclosure; Fig 1; 66pp; English.
 XX CC The STK-1 gene encodes a receptor PTK which is expressed in
 CC proliferating hematopoietic stem cells but not in quiescent stem
 CC cells. The STK-1 gene is also expressed in certain malignant cells
 CC of non-hematopoietic origin. An antisense oligo specific for STK-1
 CC is an oligo having a sequence (i) capable of forming a stable
 CC triplex with a portion of the STK-1 gene, or (ii) capable of forming
 CC a stable duplex with a portion of an mRNA transcript of the STK-1
 CC gene. Antisense oligos capable of forming a stable duplex with a
 CC portion of a STK-1 mRNA transcript are given in AAQ91536 FT and in
 CC AAQ91537 and AAQ91538. The antisense oligos of the invention are useful
 CC in the treatment of hematologic malignancies characterised by
 CC STK-1 expression. Several of the conserved domains of PTKs
 CC including the ATP binding domain and the WMAPES motifs are
 CC found in the STK-1 protein (see AAR75961 FT).
 XX Sequence 993 AA;
 SQ Query Match 99.8%; Score 5266; DB 16; Length 993;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 992; Conservative 0;

Qy 1 MPALARDAGTVPVLLVFSAMIFGTITNQDLPVVKVILNHKNQDSSVGKSSYPMVSESP 60
Db 1 MPALARDAGTVPVLLVFSAMIFGTITNQDLPVVKVILNHKNQDSSVGKSSYPMVSESP 60

Qy 61 EDLGCALRPOSSGTYEAAAEVDVVSASITLOVLVDAPGNISCLWFKHSLNCQPHFDL 120
Db 61 EDLGCALRPOSSGTYEAAAEVDVVSASITLOVLVDAPGNISCLWFKHSLNCQPHFDL 120

Qy 121 QNRGVSMVILKMTETQAGEYLLFIQSEATNTYTLFTVSRNTLLYTLRRPYFRKMENQD 180
Db 121 QNRGVSMVILKMTETQAGEYLLFIQSEATNTYTLFTVSRNTLLYTLRRPYFRKMENQD 180

Qy 181 ALVCISSEVPPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISSEVPPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

Qy 241 CTRLTIDLNQTPQTTLPOLFLKVGEPWIRCKAVHVNHGFLTWELNKALEEGNYFEM 300
Db 241 CTRLTIDLNQTPQTTLPOLFLKVGEPWIRCKAVHVNHGFLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSDEYE 360

Qy 361 IDOYEFCFSVRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHPQGEYIPHA 420
Db 361 IDOYEFCFSVRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHPQGEYIPHA 420

Qy 421 ENDDAQTKMFTLNIRKPKQVLAASASQASCFSDGYPPLPSWTWKKCSDKSPNCTEITE 480
Db 421 ENDDAQTKMFTLNIRKPKQVLAASASQASCFSDGYPPLPSWTWKKCSDKSPNCTEITE 480

Qy 481 GVNRRKANRVFGQWSSSTLNMSEALKGLVCKCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GVNRRKANRVFGQWSSSTLNMSEALKGLVCKCAYNSLGTSCETILLNSPGPPFIQD 540

Qy 541 NISFYATIGVCLLFIIVLTLIHKYKQFYESQLOVQVVTGSSDNEFYFVDPREYED 600
Db 541 NISFYATIGVCLLFIIVLTLIHKYKQFYESQLOVQVVTGSSDNEFYFVDPREYED 600

Qy 601 LKWEFFRENLEFGKVLGSGAFGKVMNATAYGISTGTGSIQVAVKMLKADSSREALMS 660
Db 601 LKWEFFRENLEFGKVLGSGAFGKVMNATAYGISTGTGSIQVAVKMLKADSSREALMS 660

Qy 661 ELKQMTQLGSHENIVNLGACTLSGPIYLIIEYCCYDGLLNLVLSKREKPHRTWTEIFEK 720
Db 661 ELKQMTQLGSHENIVNLGACTLSGPIYLIIEYCCYDGLLNLVLSKREKPHRTWTEIFEK 720

Qy 721 HNFSEFYPTFQSHPNSSMPGSRREVQIHPDSQITSLHGNFSHSEDEIEYENQKLEEBEDL 780
Db 721 HNFSEFYPTFQSHPNSSMPGSRREVQIHPDSQITSLHGNFSHSEDEIEYENQKLEEBEDL 780

Qy 781 NVLTFEDLLCFAYQVAKGMEFLEPKSCVHRDLARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTFEDLLCFAYQVAKGMEFLEPKSCVHRDLARNVLVTHGKVVKICDFGLARDIMSDS 840

Qy 841 NYVVRGNARLPVKWAPESLPEGIYTIKSDVNSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWAPESLPEGIYTIKSDVNSYGILLWEIFSLGVNYPGIPVDANFYK 900

Qy 901 LIQNGFMDQPFYATEEYIIMQSCWAFDSRKRFPNLTSLFGLCOLADAEAMYQNVDG 960
Db 901 LIQNGFMDQPFYATEEYIIMQSCWAFDSRKRFPNLTSLFGLCOLADAEAMYQNVDG 960

Qy 961 RVSECPHTYQNRPPSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPPSREMDLGLLSPQAQVEDS 993

RESULT 9

AAR81869

ID AAR81869 standard; Protein; 993 AA.

XX

AC AAR81869;

XX

DT 19-MAR-1996 (first entry)

XX

DE Human Flk2/flt3 tyrosine kinase receptor.

XX

KW Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;
KW haematopoiesis; hypoplasia; anaemia; thrombocytopenia; stem cell.

XX

OS Homo sapiens.

XX

PN WO9527062-A1.

XX

PD 12-OCT-1995.

XX

PF 23-MAR-1995; 95WO-US037118.

XX

PR 04-APR-1994; 94US-0222299.

XX

PA (GETH) GENENTECH INC.

XX

PI Bennett BD, Broz SD, Matthews W, Zeigler FC;

XX

DR WPI; 1995-358636/46.

XX

DR N-PSDB; AAT00802.

XX

PT Agonist antibody which binds to flk2-flt3 tyrosine kinase receptor
PT - enhances proliferation of haematopoietic stem cells, in the
PT treatment of hypoplasia, anaemia, etc.

XX

PS Disclosure; Page 44-47; 59pp; English.

XX

CC DNA (AAT00801) coding for murine stem cell tyrosine kinase receptor flk2
CC (also called flt3) (AAR81868) was obtd. by RT-PCR amplification of RNA
CC isolated from mid-gestation mouse foetal livers using primers based
CC on the murine flt3 sequence, and subcloning of the product into pRK5.1.
CC An flk2/flt3 extracellular domain-IgG1 Fc fusion protein was
CC constructed and used to raise agonist antibodies able to bind to, and
CC activate, flk2/flt3. The human flk2/flt3 receptor gene (AAT00802) and
CC amino acid sequence (AAR81869) are also given.

XX

SQ Sequence 993; AA;

Query Match 99.8%; Score 5265; DB 16; Length 993;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 992; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPVLLVFSAMIFGTITNQDLPVVKVILNHKNQDSSVGKSSYPMVSESP 60

Db 1 MPALARDAGTVPVLLVFSAMIFGTITNQDLPVVKVILNHKNQDSSVGKSSYPMVSESP 60

Qy 61 EDLGCALRPOSSGTYEAAAEVDVVSASITLOVLVDAPGNISCLWFKHSLNCQPHFDL 120

Db 61 EDLGCALRPOSSGTYEAAAEVDVVSASITLOVLVDAPGNISCLWFKHSLNCQPHFDL 120

Qy 121 QNRGVSMVILKMTETQAGEYLLFIQSEATNTYTLFTVSRNTLLYTLRRPYFRKMENQD 180

Db 121 QNRGVSMVILKMTETQAGEYLLFIQSEATNTYTLFTVSRNTLLYTLRRPYFRKMENQD 180

Qy 181 ALVCISSEVPPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

Db 181 ALVCISSEVPPIVEWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

Qy 241 CTRLTIDLNQTPQTTLPOLFLKVGEPWIRCKAVHVNHGFLTWELNKALEEGNYFEM 300

Db 241 CTRLTIDLNQTPQTTLPOLFLKVGEPWIRCKAVHVNHGFLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSDEYE 360

Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSDEYE 360


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Db 380 IDQVEEFCFSVRKAYQPIRCTWTSRSPCEQKGLDNGYSISKFCNKHQEPGEYIFHA 439
Qy 421 ENDDAQFTQKFTLNIRRKPOVLAEASQASQCFSDGYPLPSWTWKCKSDKSPNCTEEITE 480
Db 440 ENDDAQFTQKFTLNIRRKPOVLAEASQASQCFSDGYPLPSWTWKCKSDKSPNCTEEITE 499
Qy 481 GWNRKANRKFVQGVSSSTLNSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 500 GWNRKANRKFVQGVSSSTLNSEAIKGLVKCCAYNSLGTSCETILLNSAGPPFIQD 559
Qy 541 NISFYATIGVCLLFIIVLTLICHYKKQFYESQLOQVQVTSQSDNEFYFVDPREYED 600
Db 560 NISFYATIGVCLLFIIVLTLICHYKKQFYESQLOQVQVTSQSDNEFYFVDPREYED 619
Qy 601 LKWEPPRENLEFGKVLGSGAFKGMVNATAYGISKTGVSQVAVKMLKEKADSSREALMS 660
Db 620 LKWEPPRENLEFGKVLGSGAFKGMVNATAYGISKTGVSQVAVKMLKEKADSSREALMS 679
Qy 661 ELKQMTQLGSHENTVNLGACTLSGPYLIIFCYCCYGDLLNLYLSKREKPHRTWTEIFKE 720
Db 680 ELKQMTQLGSHENTVNLGACTLSGPYLIIFCYCCYGDLLNLYLSKREKPHRTWTEIFKE 739
Qy 721 HNPSEYPTFQSHPNSSPGSREVQIHDPDSQISGLHGNSPHSEDEIEYENOKRLEEBEDL 780
Db 740 HNPSEYPTFQSHPNSSPGSREVQIHDPDSQISGLHGNSPHSEDEIEYENOKRLEEBEDL 799
Qy 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTHTGKVVKICDFGLARDIMSDS 840
Db 800 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTHTGKVVKICDFGLARDIMSDS 859
Qy 841 NYVVRGNARLPVKWMAPESLPEGIYITIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 860 NYVVRGNARLPVKWMAPESLPEGIYITIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 919
Qy 901 LIQNGFKMDQPFYATEEYIIMQSCWAFDSRKRPSFNNLTSLFLGCOLADAEAMYQNVDG 960
Db 920 LIQNGFKMDQPFYATEEYIIMQSCWAFDSRKRPSFNNLTSLFLGCOLADAEAMYQNVDG 979
Qy 961 RVSECPHTYQNRPRPSREMDLGLLSPOQAQVEDS 993
Db 980 RVSECPHTYQNRPRPSREMDLGLLSPOQAQVEDS 1012

RESULT 11
AAW63588
ID AAW63588 standard; Protein; 983 AA.
XX
AC AAW63588;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human receptor type protein kinase FLT3 protein SEQ ID NO:19.
XX
KW Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
KW membrane-vicinal region; tyrosine kinase; juxtamembrane region.
XX
OS Homo sapiens.
XX
PN WO9817808-A1.
XX
PD 30-APR-1998.
XX
PF 13-OCT-1997; 97WO-JP03667.
XX
PR 18-OCT-1996; 96JP-0297329.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
PI Yokota S;
XX
WP1; 1998-362333/31.
DR N-PSDB; AAV39041.
DR
```

```
XX Nucleic acid sequences encoding receptor type protein kinase -
PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes
PT M2
XX
PS Claim 6; Page 45-50; 80pp; Japanese.
XX
CC New nucleic acid sequences have been isolated which encode receptor type
CC protein kinases (especially a tyrosine kinases) having tandem repeats in
CC the juxtamembrane region. Also described in the present invention are:
CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
CC representing FLT3 juxtamembrane receptor type protein kinases found in
CC leukaemia patients of FAB subclass M2, M4 or M5 (nucleic acid sequences
CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
CC recognising the kinases or their portions including the tandem repeat
CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
CC (4) a method for detecting the nucleic acid sequences in human tissue
CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
CC gene, and (iii) determining the size of the gene for comparing the size
CC of the normal gene not containing tandem repeats, and (5) kits for
CC carrying out the detection. The products and methods may be used for
CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.
XX
SQ Sequence 983 AA;

Query Match 97.8%; Score 5159; DB 19; Length 983;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 973; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 1 MPALARDAGTVPLLVFSAMIFGTITNODLPVICKVLINHKNDSSVGKSSSPVWVSESP 60
Db 1 MPALARDAGTVPLLVFSAMIFGTITNODLPVICKVLINHKNDSSVGKSSSPVWVSESP 60
Qy 61 EDLGCALRQSSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLVFKHSSLNCQHPDPL 120
Db 61 EDLGCALRQSSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLVFKHSSLNCQHPDPL 120
Qy 121 QNRGVSVVILKMTETQAGEYLLFFIQSEATNTYTLFTVSRITLTYLRRPFRKMNOD 180
Db 121 QNRGVSVVILKMTETQAGEYLLFFIQSEATNTYTLFTVSRITLTYLRRPFRKMNOD 180
Qy 181 ALVCISESVPEPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLFTIDLNTQPTTLPLQLFKVGEPLWIRCKAVVNHGFGTLWELENKALEEGNYFEM 300
Db 241 CTRLFTIDLNTQPTTLPLQLFKVGEPLWIRCKAVVNHGFGTLWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTTCSSSKHPSQSALVTIVGKGFINATNSSEDE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTTCSSSKHPSQSALVTIVGKGFINATNSSEDE 360
Qy 361 IDQVEEFCFSVRKAYQPIRCTWTSRSPCEQKGLDNGYSISKFCNKHQEPGEYIFHA 420
Db 361 IDQVEEFCFSVRKAYQPIRCTWTSRSPCEQKGLDNGYSISKFCNKHQEPGEYIFHA 420
Qy 421 ENDDAQFTQKFTLNIRRKPOVLAEASQASQCFSDGYPLPSWTWKCKSDKSPNCTEEITE 480
Db 421 ENDDAQFTQKFTLNIRRKPOVLAEASQASQCFSDGYPLPSWTWKCKSDKSPNCTEEITE 480
Qy 481 GWNRKANRKFVQGVSSSTLNSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNRKANRKFVQGVSSSTLNSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Qy 541 NISFYATIGVCLLFIIVLTLICHYKKQFYESQLOQVQVTSQSDNEFYFVDPREYED 600
Db 541 NISFYATIGVCLLFIIVLTLICHYKKQFYESQLOQVQVTSQSDNEFYFVDPREYED 600
Qy 601 L-----KWEPRENLEFGKVLGSGAFKGMVNATAYGISKTGVSQVAVKMLKEKA 650
Db 601 LKWEPRENWHKWEPPRENLEFGKVLGSGAFKGMVNATAYGISKTGVSQVAVKMLKEKA 660
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QY 651 DSSERREALMSELKQMTQLGSHENIVNLLGACTLSGPIYLIIFYECCYCGDLLNLYLSRKEKF 710
 D 661 DSSERREALMSELKQMTQLGSHENIVNLLGACTLSGPIYLIIFYECCYCGDLLNLYLSRKEKF 720
 QY 711 HRTWTETIFKEHNFSFYPTFQSHNSNMPGSRREVOIHPDSDQISGLHNSPHSDEIEYEN 770
 D 721 HRTWTETIFKEHNFSFYPTFQSHNSNMPGSRREVOIHPDSDQISGLHNSPHSDEIEYEN 780
 QY 771 QKLEEEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDF 830
 D 781 QKLEEEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDF 840
 QY 831 GLARDIMSDSNVYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGNPYP 890
 D 841 GLARDIMSDSNVYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGNPYP 900
 QY 891 GIPVDANFYKLIQNGFKMDQFPFYATEBEIYIMOSWAFDSRKRPSPNLTSLFLGCQLADA 950
 D 901 GIPVDANFYKLIQNGFKMDQFPFYATEBEIYIMOSWAFDSRKRPSPNLTSLFLGCQLADA 960
 QY 951 EAMYNQVNDGRVSECPHTYQNR 973
 D 961 EAMYNQVNDGRVSECPHTYQNR 983

RESULT 12
 ID AAW63587
 AC AAW63587 standard; Protein; 986 AA.
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Human receptor type protein kinase FLT3 protein SEQ ID NO:18.
 XX
 KW Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
 XX membrane-vicinal region; tyrosine kinase; juxtamembrane region.
 OS Homo sapiens.
 XX
 PN WO9817808-A1.
 XX
 PD 30-APR-1998.
 XX
 PF 13-OCT-1997; 97WO-JP03667.
 XX
 PR 18-OCT-1996; 96JP-0297329.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Yokota S;
 XX
 DR WPI; 1998-362333/31.
 DR N-PSDB; AAV39040.
 XX
 PT Nucleic acid sequences encoding receptor type protein kinase -
 PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes
 PT M2
 XX
 PS Claim 6; Page 40-45; 80pp; Japanese.
 XX
 CC New nucleic acid sequences have been isolated which encode receptor type
 CC protein kinases (especially a tyrosine kinases) having tandem repeats in
 CC the juxtamembrane region. Also described in the present invention are:
 CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
 CC representing FLT3 juxtamembrane receptor type protein kinases found in
 CC leukaemia patients of FAB subclass M2, M4 or M5 (nucleic acid sequences
 CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
 CC recognising the kinases or their portions including the tandem repeat
 CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
 CC (4) a method for detecting the nucleic acid sequences in human tissue
 CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
 CC gene, and (iii) determining the size of the gene for comparing the size

CC of the normal gene not containing tandem repeats, and (5) kits for
 CC carrying out the detection. The products and methods may be used for
 CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.
 XX
 SQ Sequence 986 AA;
 Query Match 97.8%; Score 5157.5; DB 19; Length 986;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 973; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKVLINHNKNDSSVGKSSSYPMVSESP 60
 D 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKVLINHNKNDSSVGKSSSYPMVSESP 60
 QY 61 EDLGCALRPOSSGTGYEAAAEEVDVVSASITLQVLVDPAGNISCLVWPKHSLNQCQPHDL 120
 D 61 EDLGCALRPOSSGTGYEAAAEEVDVVSASITLQVLVDPAGNISCLVWPKHSLNQCQPHDL 120
 QY 121 QNRGVVSMVILKMTETQAGEYLLFIQSEATNYTLFTVSRINTLLYTLRRPYFRKMNOD 180
 D 121 QNRGVVSMVILKMTETQAGEYLLFIQSEATNYTLFTVSRINTLLYTLRRPYFRKMNOD 180
 QY 181 ALVCISSEVPEPIVEWVLCDSQGESCKEESPAVVVKEEVLHELFGTDIRCCARNELGRE 240
 D 181 ALVCISSEVPEPIVEWVLCDSQGESCKEESPAVVVKEEVLHELFGTDIRCCARNELGRE 240
 QY 241 CTRLFTIDLNQTPQTLQPLFLKVGEPWIRKAVVHNGFGLTWELNKALEBGNVPEM 300
 D 241 CTRLFTIDLNQTPQTLQPLFLKVGEPWIRKAVVHNGFGLTWELNKALEBGNVPEM 300
 QY 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPQSALVTIVGKFINATNSSEDE 360
 D 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPQSALVTIVGKFINATNSSEDE 360
 QY 361 IDQEEFCFVSVRKAYPOIRCTWTFSRKSPCEQGLDNGYSISKFNHKKHPOGEYIEHA 420
 D 361 IDQEEFCFVSVRKAYPOIRCTWTFSRKSPCEQGLDNGYSISKFNHKKHPOGEYIEHA 420
 QY 421 ENDDAQFTKMTLNIIRKPOVLAESAQSCFSDGYPLPSWTWKKCDKSPNCTEITE 480
 D 421 ENDDAQFTKMTLNIIRKPOVLAESAQSCFSDGYPLPSWTWKKCDKSPNCTEITE 480
 QY 481 GWNRKANRKFVGQWSSSTLNMSEAIKGLVKCCAYNSLGTSCETILLNSPGPFPTQD 540
 D 481 GWNRKANRKFVGQWSSSTLNMSEAIKGLVKCCAYNSLGTSCETILLNSPGPFPTQD 540
 QY 541 NISFYATIGVCLLFIVLTLIICHYKKOPRYESQLOQWQVTGSSDNEYFYV- 592
 D 541 NISFYATIGVCLLFIVLTLIICHYKKOPRYESQLOQWQVTGSSDNEYFYVDFREYBD 600
 QY 593 -----DFREYEDLKWEFPFRENLEFGVLGSGAFGKVMNATAYGISKTGVSIOAVKMLK 647
 D 601 LKWEFDREYEDLKWEFPFRENLEFGVLGSGAFGKVMNATAYGISKTGVSIOAVKMLK 660
 QY 648 EKASSRREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIIFYECCYCGDLLNLYLSRKR 707
 D 661 EKASSRREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIIFYECCYCGDLLNLYLSRKR 720
 QY 708 EKFHRTWTEIFKEHNFSFYPTFQSHNSNMPGSRREVOIHPDSDQISGLHNSPHSDEIE 767
 D 721 EKFHRTWTEIFKEHNFSFYPTFQSHNSNMPGSRREVOIHPDSDQISGLHNSPHSDEIE 780
 QY 768 YENQKLEEEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKI 827
 D 781 YENQKLEEEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKI 840
 QY 828 CDFGLARDIMSDSNVYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGN 887
 D 841 CDFGLARDIMSDSNVYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGN 900
 QY 888 PYPGIPVDANFYKLIQNGFKMDQFPFYATEBEIYIMOSWAFDSRKRPSPNLTSLFLGCOL 947
 D 901 PYPGIPVDANFYKLIQNGFKMDQFPFYATEBEIYIMOSWAFDSRKRPSPNLTSLFLGCOL 960

Qy 948 ADABEAMYQNDGRVSECPHTYQNR 973
 Db 961 ADABEAMYQNDGRVSECPHTYQNR 986

RESULT 13

AAW63589
 ID AAW63589 standard; Protein; 986 AA.

XX AC AAW63589;

XX DT 12-OCT-1998 (first entry)

XX DE Human receptor type protein kinase FLT3 protein SEQ ID NO:20.

XX KW Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
 KW membrane-vicinal region; tyrosine kinase; juxtamembrane region.

XX OS Homo sapiens.

XX PN WO9817808-A1.

XX PD 30-APR-1998.

XX PF 13-OCT-1997; 97WO-JP03667.

XX PR 18-OCT-1996; 96JP-0297329.

XX PA (TAKI) TAKARA SHUZO CO LTD.

XX PI Yokota S;

XX DR WPI; 1998-362333/31.

XX DR N-PSDB; AAV39042.

XX PT Nucleic acid sequences encoding receptor type protein kinase -

XX PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes

XX PT M2

XX PS Claim 6; Page 50-55; 80pp; Japanese.

XX CC New nucleic acid sequences have been isolated which encode receptor type
 CC protein kinases (especially a tyrosine kinases) having tandem repeats in
 CC the juxtamembrane region. Also described in the present invention are:
 CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
 CC representing FLT3 juxtamembrane receptor type protein kinases found in
 CC leukemia patients of FAB subclass M2, M4 or M5 (nucleic acid sequences
 CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
 CC recognising the kinases or their portions including the tandem repeat
 CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
 CC (4) a method for detecting the nucleic acid sequences in human tissue
 CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
 CC gene, and (iii) determining the size of the gene for comparing the size
 CC of the normal gene not containing tandem repeats, and (5) kits for
 CC carrying out the detection. The products and methods may be used for
 CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.

XX SQ Sequence 986 AA;

Query Match 97.8%; Score 5157.5; DB 19; Length 986;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 973; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 MPALARDAGTVPLLVVFSAAMIFGITNODLPVVKVNLNKNKNDSSVGKSSSYPMVSESP 60

Db 1 MPALARDAGTVPLLVVFSAAMIFGITNODLPVVKVNLNKNKNDSSVGKSSSYPMVSESP 60

Qy 61 EDLGCALPQSSGTVEAAAEVDVDSASITLQVLVDAPGNTSCLVFKHSSLNCPHFDL 120

Db 61 EDLGCALPQSSGTVEAAAEVDVDSASITLQVLVDAPGNTSCLVFKHSSLNCPHFDL 120

Qy 121 QNRGVSVMLKMTETQAGEYLLFIQSEATNTYTLFTVSIRNTLLYTLRRPYFRKMNQD 180

Db 121 QNRGVSVMLKMTETQAGEYLLFIQSEATNTYTLFTVSIRNTLLYTLRRPYFRKMNQD 180
 Qy 181 ALVCISESVPEPIVEWVLCDSSQESCKEESPAVVKKEKVLHELFTDTRCCARNELGRE 240
 Db 181 ALVCISESVPEPIVEWVLCDSSQESCKEESPAVVKKEKVLHELFTDTRCCARNELGRE 240
 Qy 241 CTRLFITIDNQTPTTLQFLKVGEPILWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
 Db 241 CTRLFITIDNQTPTTLQFLKVGEPILWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
 Qy 301 STYSTNRTMIRILFAFVSSVARNDGYTTCSSSKPSSQSAALVTIVGKGFINATNSSDEYE 360
 Db 301 STYSTNRTMIRILFAFVSSVARNDGYTTCSSSKPSSQSAALVTIVGKGFINATNSSDEYE 360
 Qy 361 IDOYEEFCFSVRKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHQPGEYIFHA 420
 Db 361 IDOYEEFCFSVRKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHQPGEYIFHA 420
 Qy 421 ENDDAQFTKMTFLNTRRKPOVLAEASASQSCFSDGYPLPSWTWKKCDKSPNCTEITE 480
 Db 421 ENDDAQFTKMTFLNTRRKPOVLAEASASQSCFSDGYPLPSWTWKKCDKSPNCTEITE 480
 Qy 481 GVMNRKANRKVFGQWVSSSTLNNSEAIKGLVKCCAYNSLGTSCETILLNSPGPRFIOQ 540
 Db 481 GVMNRKANRKVFGQWVSSSTLNNSEAIKGLVKCCAYNSLGTSCETILLNSPGPRFIOQ 540
 Qy 541 NISFYATIGVCLLFTIVLTLIICHKYKKQFYESQLOMVQVT-----GSSDN 587
 Db 541 NISFYATIGVCLLFTIVLTLIICHKYKKQFYESQLOMVQVTGSSDNEFYVDVFRSSDN 600
 Qy 588 EYFYVDPREYEDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVQAVKMLK 647
 Db 601 EYFYVDPREYEDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVQAVKMLK 660
 Qy 648 EKADSSREALMSLKMMTOLGSHENIVNLGACTLSGPIYLIFEYCCYGDLLNLYLSKR 707
 Db 661 EKADSSREALMSLKMMTOLGSHENIVNLGACTLSGPIYLIFEYCCYGDLLNLYLSKR 720
 Qy 708 EKFHRTWTETIFKEHNFSFYPTFQSHPNSSMPGSRREVQIHPDSDQISGLHNSFHSDEIE 767
 Db 721 EKFHRTWTETIFKEHNFSFYPTFQSHPNSSMPGSRREVQIHPDSDQISGLHNSFHSDEIE 780
 Qy 768 YENQKRLBEEEDLNLVTEDLLCFAYQYAKGMEFLFKSCVHRDLAARNVLVTHGKWKI 827
 Db 781 YENQKRLBEEEDLNLVTEDLLCFAYQYAKGMEFLFKSCVHRDLAARNVLVTHGKWKI 840
 Qy 828 CDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGIYTIKSDVNSYGILLWEIFSLGVN 887
 Db 841 CDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGIYTIKSDVNSYGILLWEIFSLGVN 900
 Qy 888 PYPGIPVDANFYKLIQNGFKMDQPPFYATEEIVIMQSCWAFDSRKRKPSFNLTSFLGCOL 947
 Db 901 PYPGIPVDANFYKLIQNGFKMDQPPFYATEEIVIMQSCWAFDSRKRKPSFNLTSFLGCOL 960
 Qy 948 ADAEAMTYQNVDGRVSECPHTYQNR 973
 Db 961 ADAEAMTYQNVDGRVSECPHTYQNR 986

RESULT 14

AAW63586

ID AAW63586 standard; Protein; 994 AA.

XX AC AAW63586;

XX DT 12-OCT-1998 (first entry)

XX DE Human receptor type protein kinase FLT3 protein SEQ ID NO:17.

XX KW Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
 KW membrane-vicinal region; tyrosine kinase; juxtamembrane region.

XX XX

OS Homo sapiens.
 PN WO9817808-A1.
 XX 30-APR-1998.
 XX 13-OCT-1997; 97WO-JP03667.
 XX 18-OCT-1996; 96JP-0297329.
 PR (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX
 PI Yokota S;
 XX WPI; 1998-362333/31.
 DR N-PSDB; AAV39039.
 XX
 XX Nucleic acid sequences encoding receptor type protein kinase -
 PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes
 PT M2
 XX
 XX Claim 6; Page 34-39; 80pp; Japanese.
 XX
 CC New nucleic acid sequences have been isolated which encode receptor type
 CC protein kinases (especially a tyrosine kinases) having tandem repeats in
 CC the juxtamembrane region. Also described in the present invention are:
 CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
 CC representing FLT3 juxtamembrane receptor type protein kinases found in
 CC leukaemia patients of FAB subclass M2, M4 or M5 (nucleic acid sequences
 CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
 CC recognising the kinases or their portions including the tandem repeat
 CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
 CC (4) a method for detecting the nucleic acid sequences in human tissue
 CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
 CC gene, and (iii) determining the size of the gene for comparing the size
 CC of the normal gene not containing tandem repeats, and (5) kits for
 CC carrying out the detection. The products and methods may be used for
 CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.
 XX
 XX Sequence 994 AA;
 SQ
 Query Match 97.7%; Score 5153.5; DB 19; Length 994;
 Best Local Similarity 97.9%; Pred. No. 0;
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 DB 61 EDLGCALRPQSSGTVYEAAYVEVDVSASITLQVLVDAPGNISCLWVFKHSLNCPHFDL 120
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 QY 181 ALVCTISESVPEPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
 DB 181 ALVCTISESVPEPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
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 DB 241 CTRLTFTIDLNTQPTTLTLPQLFKVGEPLWIRCKAVVNHVHFGLTWELNKALEEGNYFEM 300
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 DB 541 NISFYATIGVCLLFIIVVLTLLIICHYKKQFRIESOLOQWQVTGSSDNEYFYVDREY 600
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 DB 661 QVAVKMLKEKADSSEREAALMSELKMTQLGSHENIVNLLGACTLSGPIYLIFFEYCCYGD 720
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 DB 901 EIFSLGVNYPGIPVDANFYKLIQNGFMQDPFYATEBIYIMQSCWAFDSRKRPSFPNL 960
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 DB 961 TSFLGCOLADAEAMYQNVDRVSECPHTYQNR 994
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 ID AAR81868 standard; Protein; 1000 AA.
 XX AC
 XX AC AAR81868;
 DT 29-FEB-1996 (first entry)
 XX
 DE Flk2/Flt3 tyrosine kinase receptor.
 XX
 KW Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;
 KW haematopoiesis; hypoplasia; anaemia; thrombocytopenia; stem cell.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..542
 FT /label= Extracellular_domain
 FN W09527062-A1.
 XX
 PD 12-OCT-1995.
 XX
 PP 23-MAR-1995; 95WO-US03718.
 XX
 PR 04-APR-1994; 94US-0222299.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bennett BD, Broz SD, Matthews W, Zeigler FC;
 XX
 DR WPI; 1995-358636/46.

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:59:30 ; Search time 41.0207 Seconds
(without alignments)
2400.704 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDACTVPLLVFSAM.....PFSREMDLGLSPQAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.pap.*
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12: /cgn2_6/ptodata/2/pubpaa/US10 PUBCOMB.pap.*
13: /cgn2_6/ptodata/2/pubpaa/US60 NEW PUB.pap.*
14: /cgn2_6/ptodata/2/pubpaa/US60 PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5274	100.0	993	10	US-09-872-136-4
3	4429.5	84.0	992	10	US-09-919-408-2
4	4429.5	84.0	992	10	US-09-872-136-2
5	1266	24.0	975	9	US-10-192-867-2
6	1251	23.7	976	9	US-10-099-895-32
7	1251	23.7	976	9	US-10-192-867-4
8	1216.5	23.1	972	10	US-09-944-807-10
9	1166.5	22.1	1088	9	US-09-961-403-4
10	1166	22.1	1089	9	US-09-955-363-36
11	1166	22.1	1089	10	US-09-769-987-2
12	1166	22.1	1089	10	US-09-919-497-90
13	1166	22.1	1089	10	US-09-866-510-2
14	1163	22.1	1089	10	US-09-866-510-10
15	1162	22.0	1089	10	US-09-866-510-4
16	1161	22.0	1089	10	US-09-866-510-8
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18	1086.5	20.6	1090	10	US-09-866-510-14
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Sequence 33, Appl
Sequence 2, Appl
Sequence 34, Appl
Sequence 33, Appl
Sequence 32, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl

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1081.5 20.5 1106 10 US-09-866-510-20
1080.5 20.5 1106 10 US-09-866-510-18
990 18.8 1338 9 US-10-059-585-44
957 18.1 386 9 US-09-939-833-6
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957 18.1 386 10 US-09-939-832-6
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951.5 18.0 1356 9 US-10-100-405A-2
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923 17.5 1367 10 US-09-919-408-6
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880.5 16.7 1363 9 US-10-105-901-32
859.5 16.3 367 9 US-09-939-833-9
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846 16.0 367 9 US-09-939-833-12
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ALIGNMENTS

RESULT 1

US-09-919-408-4

; Sequence 4, Application US/09919408

; Patent No. US20020072077A1

; GENERAL INFORMATION:

; APPLICANT: Lemischka, Ihor R.

; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL RECEPTORS AND THEIR LIGANDS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ImClone Systems Incorporated

; STREET: 180 Varick Street

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10014

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/919,408

; FILING DATE: 31-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/977,451

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 07/906,397

; FILING DATE: 26-JUN-1992

; APPLICATION NUMBER: US PCT/US92/05401

; FILING DATE: 26-JUN-1992

; APPLICATION NUMBER: TW 81102961

; FILING DATE: 15-APR-1992

; APPLICATION NUMBER: US PCT/US92/02750

; FILING DATE: 02-APR-1992

; APPLICATION NUMBER: US 07/813,593

; FILING DATE: 24-DEC-1991

; APPLICATION NUMBER: US 07/793,065

; FILING DATE: 15-NOV-1991

; APPLICATION NUMBER: US 07/728,913

; FILING DATE: 28-JUN-1991

APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-919-408-4

Query Match 100.0%; Score 5274; DB 10; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-872-136-4
Sequence 4, Application US/09872136
Patent No. US20020119545A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/208,786
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/021,324
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-872-136-4

Query Match 100.0%; Score 5274; DB 10; Length 993;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-919-408-2
Sequence 2, Application US/09919408
Patent No.: US20020072077A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Ibor R.
TITLE OF INVENTION: TOTIPOENT HEMATOPOIETIC STEM CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/919,408
FILING DATE: 31-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,451
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-919-408-2

Query Match 84.0%; Score 4429.5; DB 10; Length 992;
Best Local Similarity 84.1%; Pred. No. 1.7e-288;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MPALA-RDAGTVPLLVVFSAMIFGTITNODLPVICKVLINHKNDSSVGKSSYPMVSES 59
Db 1 MRALQSRDRRLLLVLSVMILETVNODLPVICKVLISHENNGSAGKPSYRMRGS 60
QY 60 PEDLGCALRPOSSGTVYEAADVEDVSASITLQVLVDAPGNISCLWVFKHSSLNCPHF 119
Db 61 PEDLOCTPRQSGTVYEAATVEAESGSIITLQVLATPGDLSCLVWFKHSSLCQPHFD 120
QY 120 LQNRGVSVMLKMTETQAGEYLLFTQSEATNTTILFTVIRNTLLTLRPFYRKMENQ 179
Db 121 LQNRGIVSMAILNVTETQAGEYLLFTQSEATNTTILFTVIRNTLLTLRPFYRKMENQ 180
QY 180 DALVCISESVPEPIVEMVLCDGSGESCKEESPAVVKKEKVLHFGTDIRCCARNELR 239
Db 181 DALLCISEGPEPTVEWVLCSHRESCKEESGPAVVKKEKVLHFGTDIRCCARNELR 240
QY 240 ECTRLFTIDLNTOTPOTLPQLFKVGEPLMIRCKAVHNVHGFGLTWELNKALEEGNYFE 299
Db 241 ECTKLFTIDLNAQPSLTPQLFKVGEPLMIRCKAVHNVHGFGLTWELNKALEEGSYFE 300
QY 300 MSTYSTNTRMIRILFAPVSSVARNDTGYTCCSSKHPQSOSALVTIVGKFINATNSSEY 359
Db 301 MSTYSTNTRMIRILAFVSSVGRNDGYTCCSSKHPQSOSALVTILEKGFINATSSQEEY 360
QY 360 EIDVKEFCFSVREKAYPOIRCTWTESRKSFCPCOEKGLDNGYSISKFCNKHCHOPGEYIP 419
Db 361 EIDVKEFCFSVREKAYPRIRCTWTESRKSFCPCOEKGLDNGYSISKFCNKHCHOPGEYIF 420
QY 420 AENDDAQFTKMTLNIRKPOVLAEASASQSCFSGYPLPSWTWKCKSDKSPNCTEET 479
Db 421 AENDDAQFTKMTLNIRKPOVLANASASQSCSDGYPLPSWTWKCKSDKSPNCTEET 480
QY 480 EGVNRKANRKYFGQWVSSTLMSBAIKGFLVKCCAYNSLGTSCETILLNSGPPFFIQ 539
Db 481 EGVNRKANRKYFGQWVSSTLMSBAIKGFLVKCCAYNSLGTSCETILLNSGPPFFIQ 540
QY 540 DNISFYATIGVCLLFTVILTLCHIKYKQFRYESQLQVQVGTSSDNEFYVDREY 599
Db 541 DNISFYATIGVCLLFTVILTLCHIKYKQFRYESQLQVQVGTSSDNEFYVDREY 600
QY 600 DLKWFPPRENLEFGKVLGSAFGKVNATAYGISTGVSIOQAVKMLKEKADSSEALM 659
Db 601 DLKWFPPRENLEFGKVLGSAFGKVNATAYGISTGVSIOQAVKMLKEKADSSEALM 660
QY 660 SELKMTQLGSHENIYNLLGACTLSPYLIPIFYCCYGLDLLNLYRSKREKPHRTWTEIP 719
Db 661 SELKMTQLGSHENIYNLLGACTLSPYLIPIFYCCYGLDLLNLYRSKREKPHRTWTEIP 720
QY 720 EHNFSFYPTFOQSHNSMFGSRVQIHPDSQISGLHGSFHSDEIEYENQKRL--EE 777
Db 721 EHNFSFYPTFOQSHNSMFGSRVQIHPDSQISGLHGSFHSDEIEYENQKRLAEE 780
QY 778 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGVKVKICDFGLARDIM 837
Db 781 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGVKVKICDFGLARDIL 840
QY 838 SDSNYVVRGNARLPVKWMAPESEFEGYITIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 897
Db 841 SDSNYVVRGNARLPVKWMAPESEFEGYITIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
QY 898 FYKLQNGKMQOPFYATETIYIIMQSCWAFDSRKPSFNLTSLFGCQLADAEEMAYQN 957
Db 901 FYKLQNGKMQOPFYATETIYIIMQSCWAFDSRKPSFNLTSLFGCQLADAEEMAYQN 957
QY 958 VDGVRSECHTQNRPFREMDLGLLSPQAQVE 991
Db 958 ----IRTSIHLFKQAAPQORG-GLRAQSPORQVK 986

RESULT 4

US-09-872-136-2

; Sequence 2, Application US/09872136

; Patent No. US20020119545A1

GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/208,786
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/021,324
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992

APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-872-136-2

Query Match 84.0%; Score 4429.5; DB 10; Length 992;
Best Local Similarity 84.1%; Pred. No. 1.7e-288;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MPALA-RDAGTVPLLVVFSAMIFGTITNODLPVICKVLINHKNDSSVGKSSYPMVSES 59
Db 1 MRALQSRDRRLLLVLSVMILETVNODLPVICKVLISHENNGSAGKPSYRMRGS 60
QY 60 PEDLGCALRPOSSGTVYEAADVEDVSASITLQVLVDAPGNISCLWVFKHSSLNCPHF 119
Db 61 PEDLOCTPRQSGTVYEAATVEAESGSIITLQVLATPGDLSCLVWFKHSSLCQPHFD 120
QY 120 LQNRGVSVMLKMTETQAGEYLLFTQSEATNTTILFTVIRNTLLTLRPFYRKMENQ 179

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Db 121 LQNRGVSMALNVTQAGEYLLHQSERANYVLTFTVNRDQLVLRPFYFRKMNQ 180
Qy 180 DALVCISESPEPIVWLVCDSCGCKERSPAVVKKEKVLHELFGTDIRCCARNELGR 239
Db 181 DALLCISEGPEPTVWLVCSHRESCKEGBPAVRKEKVLHELFGTDIRCCARNALGR 240
Qy 240 ECTRLPTIDLNQPTTLPOLFLKVEPLWIRKCAVHVNHGFLTWELNKALEEGNYFE 299
Db 241 ECTKLFTIDLNQAPQSTLPOLFLKVEPLWIRKCAVHVNHGFLTWELNKALEEGNYFE 300
Qy 300 MTSYSNRNMIRILFAVSSVANDGTGYTSCSKHPSQALVTIIVCKGINATNSSEY 359
Db 301 MTSYSTNRNMIRILFAVSSVANDGTGYTSCSKHPSQALVTIIVCKGINATNSSEY 360
Qy 360 EIDQVEEFCFVRKAYPQIRCTWTFSRKFPCCEQGLDNGYISKFCNKHOPGEYIFH 419
Db 361 EIDPVEKFCFVRKAYPQIRCTWTFSRKFPCCEQGLDNGYISKFCNKHOPGEYIFH 420
Qy 420 AENDDAQFTMFTLNIRKPKQVLAEASASQASCFSDGYPLPSWTWKCDKSPNCTEEIT 479
Db 421 AENDDAQFTMFTLNIRKPKQVLAEASASQASCFSDGYPLPSWTWKCDKSPNCTEEIT 480
Qy 480 EGVNRKANRKPQGVQVSSSTLNMSAIGFLVKCCAYNSLGHSCETILLNSPGPPFIQ 539
Db 481 EGVNRKANRKPQGVQVSSSTLNMSAIGFLVKCCAYNSLGHSCETILLNSPGPPFIQ 540
Qy 540 DNISFYATIGVCLLFTVLTLCHVKQFRYESOLQVQVQVQVQVQVQVQVQVQVQV 599
Db 541 DNISFYATIGVCLLFTVLTLCHVKQFRYESOLQVQVQVQVQVQVQVQVQVQVQV 600
Qy 600 DLKWEPPRENLEFGLVSGAFGVNATAYGISTKGVSIQVAVKMLKEKADSSEREAALM 659
Db 601 DLKWEPPRENLEFGLVSGAFGVNATAYGISTKGVSIQVAVKMLKEKADSSEREAALM 660
Qy 660 SELKMTQLGSHENIVNLGACTLSPYILIFCYCCVGLLNLVLRKREKPHRTWTEIFK 719
Db 661 SELKMTQLGSHENIVNLGACTLSPYILIFCYCCVGLLNLVLRKREKPHRTWTEIFK 720
Qy 720 EBNFSYPTFQSHNSMPSGSRVQTHPSDQISGLHNSFHSEDEIYENOKEL--EE 777
Db 721 EBNFSYPTFQSHNSMPSGSRVQTHPSDQISGLHNSFHSEDEIYENOKEL--EE 780
Qy 778 EDNLNLTFLDLCLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIM 837
Db 781 EDNLNLTFLDLCLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
Qy 838 SDSYVVRGNARLPVKWMAPESLFEGYITKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
Db 841 SDSYVVRGNARLPVKWMAPESLFEGYITKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Qy 898 FYKLLONGFKMDOPFYATEIIVIMOSWAFDSRKRPSPNLTSFLGCQLADABEAMQN 957
Db 901 FYKLLONGFKMDOPFYATEIIVIMOSWAFDSRKRPSPNLTSFLGCQLADABEAMQN 957
Qy 958 VDRYSECHPTTYQNRPPREMDLGLLSPOAQVE 991
Db 958 ----IRTSIHLFKQAAPQORG-CLRAQSPQRQVK 986

RESULT 5
US-10-192-867-2
; Sequence 2, Application US/10192867
; Publication No. US20030084466A1
; GENERAL INFORMATION:
; APPLICANT: BLUME-JENSEN, Peter
; APPLICANT: HUNTER, Tony
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
; FILE REFERENCE: SALKINS.002C1
; CURRENT APPLICATION NUMBER: US/10/192,867
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/175,625
; 2000-01-11
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; PRIOR APPLICATION NUMBER: PCT/US01/00573
; 2001-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 2
; LENGTH: 975
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-10-192-867-2

Query Match      24.0%; Score 1266; DB 9; Length 975;
Best Local Similarity 33.2%; Pred. No. 1.2e-76;
Matches 336; Conservative 173; Mismatches 330; Indels 172; Gaps 41;

Qy 35 CVLINHKNDSSVGKSSSYPMVSESPEDLGCALRPOSSGTYVEAAAVDVDSASITQLV 94
Db 12 CVLLVLRGGTATQSASGPEFPP-----SIHPAQ-----ELIVEAGDTL--- 54
Qy 95 VDAIGNISCL-----WVFKHSLNCQHPFDLQNRGVVSMVILKMTQTQAGEYILFTQSE 148
Db 55 -----SLTCTIDPDPFVRWTFK-----TYFN-----EMVENKKNEMIQ-EKAE 89
Qy 149 ATNYTILFTVISIRNTL-----LYTLRRPYFRKMNQDQDALVCISESPEPIVE 195
Db 90 ATR-TGTYTCSNSNGLTSSIIYFVRDPAKLFLVGLPLFGK-EDSDALVRCPLTDPO-VSN 146
Qy 196 WVLCDQSOGSCKEESPAV-----VKKEEVLHELFGTDIRCCARNELGRECTRL--- 244
Db 147 YSLIEDCGSLPDLTFVNPKNKAGITIKVRAVHRLC-----VRCAAQ-----RDGTWLHSD 199
Qy 245 -FTIDLNQ-----POTTLPOL--FLKVGEPILWIRCKAVHVNHGFLTW-----E 286
Db 200 KFTLKVREAIKALPVVSVPTSHLLKKGDTFTVCTIKDYSTVNSMWLKNMPOPOHIAQ 259
Qy 287 LENKALEEGNYFEMSYSTNRNMRILFAVSSVANDGTGYTSCSKHPSQSALVT--- 343
Db 260 VKHNSWHRGDF-----NYERQETLT-----ISSARVDDSGVFMCAVNTTSGSANVTTLK 309
Qy 344 IVKGKGINATN-SSEYEDIDQVEEFCFVRKAYPQ-IRCTWTFSRKSFPCEQKGLD--- 398
Db 310 VVEKGIIINISPVKNNTTFTVTDGENVDLWVEYEAIPKPEHQOQWIMNRT--SANKGRDYVK 367
Qy 399 -NGYSIKSKFNHKKH-----QPGEYIFHAENDDAQFTKMTLNIRKPKVOLA--EASAS 448
Db 368 SDNKSNIYVQNQLRLTRLKTEGTTFLVNSDASASVTFNVNTKPELITYDRLING 427
Qy 449 QASCFSDGYPLPSWTWKCDKSPNCTEEITE-GVNRKANRKPQGVQVSSSTLNMSSEAI 507
Db 428 MLQCVAEGFPEPTIDWYFCTGABQRCTTPVSPVDVQVQVSVSPFGKLVQSSIDSSVFR 487
Qy 508 KGFVLKCCAYNSLGTSCETILLNSPGPPFP-----IQDN-----ISFYATIGVCLLPIV 557
Db 488 HNGTVECKASNDVGKS--SAFFN-----FAPKEIQOAHLTFTPLLLIGFVVAAGAIIVMV 541
Qy 558 LTLILCHYKVKQPRYESOLQMV-QVTGSSDNEYFYVDFREYEDLWKEPRENLEFQKVL 616
Db 542 LT-----YKYLQKPMYEVQMKVVEEING-----NNYVYIDPTQLPYDHWKEPFRNLSFGKTL 594
Qy 617 GSGAFGVNATAYGISTKGVSIQVAVKMLKEKADSSEREAALMSLKMOTOLGSHENIVN 676
Db 595 GAGAFGVNATAYGLIKSDAAMTAVKMLKPSAHLTEREALNSELKVLISYLGHNHNVN 654
Qy 677 LLGACTLSGPIYILIFCYCCVGLLNLVLRKREKPF-----HRTWTIRIFKEHNFSFYPTFQ 730
Db 655 LLGACTVGGPTLVITEYCCYCGDLLNFRKRDSFIFSKQBEQAEAAALYKNLLHSTBESCD 714
Qy 731 SHPNSSM---PGSREVOIHPDSDQISGLHNSFHSEDEIYENOKLEEBEEDNLVTFED 787
Db 715 S-SNEYMDMKPGVSIV-VPTKTKRKSARIDSY-----IERDVTPIAIMEDEL-ALDLD 766
Qy 788 LLCFAVQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDSNYVVRGN 847
Db 767 LLSFSYQVAKANAFASKKNICHRDLAARNILLTHGRITKICDFGLARDIRKDSNYVVRGN 826
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Qy 848 ARLPVKMAPESLPGIYTIKSDVMSYGILLWEISLGVNYPGIPVDANFYKLIQNGFK 907
Db 827 ARLPVKMAPESIFSCVYTFESDVMSYGIFLWELFSLGSSPYGMPVDSKFYKMIKGF 886
Qy 908 MDOPFYATEEIIYIMOSWAPDSRRKPSPNLTSFLGCCLADAEAMQNV 958
Db 887 MVSPEHAPAEYDVNKTCDADPLKRPFKQVQVQLIEKQISDSKHIYSNL 937

RESULT 6
US-10-099-895-32
; Sequence 32, Application US/10099895
; Patent No. US2002017186A1
; GENERAL INFORMATION:
; APPLICANT: BERNDT, Michael C
; APPLICANT: STOMSKI, Frank C
; APPLICANT: LOPEZ, Angel F
; APPLICANT: GUTHRIDGE, Mark A
; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
; FILE REFERENCE: 3991/0K379
; CURRENT APPLICATION NUMBER: US/10/099,895
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/AU00/01118
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 32
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-099-895-32

Query Match 23.7%; Score 1251; DB 9; Length 976;
Best Local Similarity 32.7%; Pred. No. 1.2e-75;
Matches 324; Conservative 166; Mismatches 352; Indels 148; Gaps 34;

Qy 47 VQKSSYPMVSESPDLGCALRPQSGTGYEAAAVEVDVSASITLQVLVDAPGNISCLW 106
Db 20 VQTGSSQPSVSPG-EPSPPSIHPGKSDLI-----VRVGEIRLLCTDPPGVK--WT 67
Qy 107 FXHSSILNCQPHDLQNRGVSVVILKWTQAGEYLLFIQSEATN---YTILFTVSIRNT 163
Db 68 FE-----ILDETENKQNEWIT-EKAEATNTGKYCTNKHGLSNS 106
Qy 164 L-----LYTLRPFYFRKMNODALVCISVPEPIVWVLCDSQGESCKEE----- 209
Db 107 IYVVRDPAKFLVDRSLYK-EDNTLVRCLPTDPE-VTNYSLKGCQKPLPKDLRFIP 164
Qy 210 ----SPAVVKEEVLHELFGTDIRCCARNELGRECTRLFTIDL---NOTPTTLPO--L 260
Db 165 DPKAGIMIKSVKRAVHRLC---LHCSVDQEGKSVLSEKFIKVRPAFAKVPVVSVKASY 221
Qy 261 FLKVGEPILIRCKAVNHGFGILTWELEN---KALBEGNYFEMSTYSTNRTMIRILPAFV 317
Db 222 LUREGEEFTVCTIKDVSSTVTKRENSQTKLQEKYNSWHHGDNFYERQAT-----LTI 277
Qy 318 SSVARNDTGYTTCSSSKHPSSQSALVT---IVGKGFINA-----TNSSEYEDIQYE 365
Db 278 SSARVNDSGVFCYANNITGSAVNTTILEVDKGINIPPMINTTVFVNDGENVDL---- 333
Qy 366 EPCFVSFRKAYPO-IRCTWTFSRKSP--PCEQKGLONGYISIKFNKH-----OPGE 415
Db 334 ----IVEYEAFFKPEHQOMIYMNRTFTDKWEDYPKSENEINIRYVSELHLTRLKGTGGT 389
Qy 416 YIFHAENDAOQTKMTLAIIRKPOVLA--EASASQACSFSDGVPPLPSWTWKCSKSPN 473
Db 390 YTFVLSNSDVNAIAFNVYNTTKEPILTYDRLVNGLMQCVAAGFPPEITDIWYFCPGTEQR 449
Qy 474 CTBEEITE-GVNNRKNRKFVGQWSSSTLNWSEAIKGFVLKCCAYNSLGTSCETILLNSP 532
Db 450 CSASVLVDVQTLNNSGPPGKLIVQSSIDSASFKNGTVECKAYDNVGT--SAYFN-- 505
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Qy 533 GPFPFIODN-----ISFYATIGVCLLFIIVLTLLICHKYKQKQFRESQLQM 578
Db 506 --FAFGKNNKQIHPHTLFTPLLIGFVIVAGMCIIVMLT---YKLOKPMYEVQWKV 559
Qy 579 V-QVTGSSDNSEYFYVDREYEDLKWEPFRENLEFGKVLGSCAPKQWNNATAYGISKTV 637
Db 560 VEEING---NNYVYIDPTQLPYDHKEWEPFNRNLSFGKTLGAGAFGVVEATAYGLIKSDA 616
Qy 638 SIQVAVKMLKEKADSSEREALMSLKMMTQGLGSHENIVNLLGACTLSGPIYLIFEYCCYV 697
Db 617 AMTAVKMLKPSAHLTEREALMSLKVLISLGNHWNIVNLLGACTIGGPTLVITETCCYV 676
Qy 698 DLLNLYLRKREKFRHTWTE-----IFKEHNFSTYPTFQSHPNSSM---PGSREVOIHPD 748
Db 677 DLLNFRKRRKDSFICKQEDHAAALYKNLLHSKESSCSDSTNEYMDMKPGVSYV-VPTK 735
Qy 749 SDQISGLHNSPHSEDEIYENQKLEBEDLNVTFFEDLLCFAYQVAKGMFLEFKSCV 808
Db 736 ADKRRSVRIGSY-----IERDVTPAIMDEDEL-ALDLELLSFSYQVAKGMFLASKNCI 789
Qy 809 HRDLAARNVLVTHGKVKIKCDFGLARDIMSDSNVVRGNARLPVKWMAPESELEGIYTIK 868
Db 790 HRDLAARNILLTHGRITTKICDFGLARDIKDSDNYVVGKGNARLPVKWMAPESEIFNCVYTFE 849
Qy 869 SDVWSYGILLWEISLGVNYPGIPVDANFYKLIQNGFKMDOPFYATEEIIYIMOSWAF 928
Db 850 SDVWSYGIFLWELFSLGSSPYGMPVDSKFYKMIKGFNRNLSPEHAPAEYMDIMKTCWDA 909
Qy 929 DSRKPSFPNLTSFLGCCLADAEAMQNV 958
Db 910 DPLKRPFKQIVQLIEKQISESTNHIYSNL 939

RESULT 7
US-10-192-867-4
; Sequence 4, Application US/10192867
; Publication No. US20030084466A1
; GENERAL INFORMATION:
; APPLICANT: BLUME-JENSEN, Peter
; APPLICANT: HUNTER, Tony
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
; FILE REFERENCE: SALKINS.002C1
; CURRENT APPLICATION NUMBER: US/10/192,867
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/175,625
; PRIOR APPLICATION NUMBER: PCT/US01/00573
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 976
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-192-867-4

Query Match 23.7%; Score 1251; DB 9; Length 976;
Best Local Similarity 32.7%; Pred. No. 1.2e-75;
Matches 324; Conservative 166; Mismatches 352; Indels 148; Gaps 34;

Qy 47 VQKSSYPMVSESPDLGCALRPQSGTGYEAAAVEVDVSASITLQVLVDAPGNISCLW 106
Db 20 VQTGSSQPSVSPG-EPSPPSIHPGKSDLI-----VRVGEIRLLCTDPPGVK--WT 67
Qy 107 FXHSSILNCQPHDLQNRGVSVVILKWTQAGEYLLFIQSEATN---YTILFTVSIRNT 163
Db 68 FE-----ILDETENKQNEWIT-EKAEATNTGKYCTNKHGLSNS 106
Qy 164 L-----LYTLRPFYFRKMNODALVCISVPEPIVWVLCDSQGESCKEE----- 209
Db 107 IYVVRDPAKFLVDRSLYK-EDNTLVRCLPTDPE-VTNYSLKGCQKPLPKDLRFIP 164
Qy 210 ----SPAVVKEEVLHELFGTDIRCCARNELGRECTRLFTIDL---NOTPTTLPO--L 260
Db 165 DPKAGIMIKSVKRAVHRLC---LHCSVDQEGKSVLSEKFIKVRPAFAKVPVVSVKASY 221
Qy 261 FLKVGEPILIRCKAVNHGFGILTWELEN---KALBEGNYFEMSTYSTNRTMIRILPAFV 317
Db 222 LUREGEEFTVCTIKDVSSTVTKRENSQTKLQEKYNSWHHGDNFYERQAT-----LTI 277
Qy 318 SSVARNDTGYTTCSSSKHPSSQSALVT---IVGKGFINA-----TNSSEYEDIQYE 365
Db 278 SSARVNDSGVFCYANNITGSAVNTTILEVDKGINIPPMINTTVFVNDGENVDL---- 333
Qy 366 EPCFVSFRKAYPO-IRCTWTFSRKSP--PCEQKGLONGYISIKFNKH-----OPGE 415
Db 334 ----IVEYEAFFKPEHQOMIYMNRTFTDKWEDYPKSENEINIRYVSELHLTRLKGTGGT 389
Qy 416 YIFHAENDAOQTKMTLAIIRKPOVLA--EASASQACSFSDGVPPLPSWTWKCSKSPN 473
Db 390 YTFVLSNSDVNAIAFNVYNTTKEPILTYDRLVNGLMQCVAAGFPPEITDIWYFCPGTEQR 449
Qy 474 CTBEEITE-GVNNRKNRKFVGQWSSSTLNWSEAIKGFVLKCCAYNSLGTSCETILLNSP 532
Db 450 CSASVLVDVQTLNNSGPPGKLIVQSSIDSASFKNGTVECKAYDNVGT--SAYFN-- 505
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Db 165 DPKAGIMIKSVKRAVHRLC---LHCSVDQSGKSVLSEKFIKVRPAKPAVVPVSVSKASY 221
Qy 261 FLKVGEPILWIRCKAVVNHGFLTWLEN---KALBEGNYFEMSTYSTNRTMIRILPAFV 317
Db 222 LLREGEFTVTCTIKDVSSSVSTWKRNSQTLQKBYNSWHHGDYFNERQAT---LTI 277
Qy 318 SSVARNDTCVYTCSKSHPSQSALVT---IVGKGFINA-----TNSSEYVEIDQYE 365
Db 278 SARVNDSGVFWCYANNTTGVANVTTLTLEVDKGFNIFPMINTVFNVDGENVDL--- 333
Qy 366 EFCFSVRKAYPO-IRCTWTFRSKF--PCEQKGLDNGYSISKPCNHKH-----QPGE 415
Db 334 ----IVEYEAFKPEHQOQIYNNRTFTDKWEDYPKSENEINRYVSELHLTRLKGTEGT 389
Qy 416 YLPHANDDAQFTQMTILIRKQPQVLA--EASASQASCFSDGYPLPSWTWKCSKSPN 473
Db 390 YTLVNSDVNAIAFNVVNTKPEILTYDRLVNGMLQCVAAAGPEPTIDWYFCPGTEQR 449
Qy 474 CTEETE-CVMNRKANRKYFGOWSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLNSP 532
Db 450 CSASLPVDQTLNNSGPPFGKLVQOSSDSAFKNGTVECKAYINDVGKT--SAYFN-- 505
Qy 533 GPFPTQDN-----ISFYATIGVCLLFTVVLTLILCHIKYKQFYESQLOM 578
Db 506 --PAFGNNKEQIHPTLFTPLLIGFVIVAGMCIIVMLT----XYLOKPMYEQWKV 559
Qy 579 V-QVTGSSDNEYVDREYEDLKWEPRENLEFGKVLGSGAGFKVMNATAYGISKTGV 637
Db 560 VEEING---NNVYIDPTQLPYDHKWEFPENRLSPGKTLGAGAFKQVVEATAYGLIKSDA 616
Qy 638 SIQVAVKMKELKADSSEREAALSELKQMTQLGSHENIVNLLGACTLSGPIYLIFFEYCCYG 697
Db 617 AMTAVAKMLKPSAHLTEREALMSLVLSYLGNNHMINVLLGACTTGGEPLVITEYCCYG 676
Qy 698 DLLNVLRSKREKFRHTWTE-----IPKEHNFSTYPTFQSHPNSSM---PGSREVOIHPD 748
Db 677 DLLNVLRSKREKFRHTWTE-----IPKEHNFSTYPTFQSHPNSSM---PGSREVOIHPD 748
Qy 749 SDOIISGLHNSHSEDEIBEYENQKLEEBEDNLVTFEDLLCFAYQVAKMEFLFKSCV 808
Db 736 ADKRSVRIGSV-----IERDVTAPIMEDDEL-ALDLEDLLSPSYQVAKMAFLASKNCI 789
Qy 809 HRDLAARNVLVTHGKVKIKCDGLARDIMSDNSYVVRGNARLPVKWMAPESEFEGIYTIK 868
Db 790 HRDLAARNVLVTHGKVKIKCDGLARDIMSDNSYVVRGNARLPVKWMAPESEFEGIYTIK 868
Qy 869 SDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGEKMDQPFYATEEYIIMQSCWAF 928
Db 850 SDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGEKMDQPFYATEEYIIMQSCWAF 928
Qy 929 DSRKRPSFNLTSLFLGCLQADAEAMQYV 958
Db 910 DPKRPTFKQIQLIEKQISESTNHIYSNL 939

RESULT 8
US-09-944-807-10
; Sequence 10, Application US/09944807
; Patent No. US2002011949A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10

; LENGTH: 972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-10
Query Match 23.1%; Score 1216.5; DB 10; Length 972;
Best Local Similarity 32.8%; Pred. No. 2.5e-73;
Matches 325; Conservative 156; Mismatches 316; Indels 195; Gaps 33;
Qy 75 VYEAAVEVDV--SASITQLVADAPGNISCLWFKHSSLNCPHFLQNRGVVSMWLK 132
Db 22 VIEPSVPELVKFGATVTLRCV---GNGSVEWDGPPS-----PHMTLYSDGSSILSTN 72
Qy 133 MTE-----TOAGEYL-----LFTQSEATNTILFTVSIIRNTLLVTLRPPYRKM 176
Db 73 NATFQNTGYRCTEPDGLGSAIIHLYVKDPAHPNVL-----AQEVVVF----- 118
Qy 177 ENQDALV-CISESVPEPIVEWLVCLDSQGESCKEESPAVVKKEK-----VLHE--- 223
Db 119 EDQDALLPCL---LTPVLE-----AGVSLVRVRGRPLMRHTNYSFSPMHGFTIHRKF 169
Qy 224 LFGTDIRCCARNELGRECTRLFTIDNQTPTLP-----QLFLKVGEPILWIRCK 273
Db 170 IQSDYQCSALMG-GR---KWSISIRLKVKQVIPGPPALTLPVPAELVIRGEAAQIVCS 225
Qy 274 AVHNVHGFGLTWELENKALEEGNYFEMSTYSTNRTMIRILPAFVSSVARNDTGYTTCSS 333
Db 226 ASSVDYVDFVLOHNNTKLA---IPOQSDPHNNRYQ-KVLTLLNDQVDFQHAGNYSVAS 281
Qy 334 ---KHPSQSALVTIYVKGFINATNSSED---YEIDQYEEFCFSVRKAYPOIR-CTWTF 385
Db 282 NVQCKH-STSMFRVVEBSAYLNL---SSEQNLIOEVTVEGELNLKMWVEAYPGICGFNTY 338
Qy 386 SRKSPPEQKGLDNGYSISKFCNKHQP-----GYEIF 418
Db 339 -----LGFSDHQPEKPLANATTKDYRHTFTLSLPLKPSAGRYSP 381
Qy 419 HAENDDAQTKMFTLIRKQVLAASASQAS-----CFSDGYPLPSWTWKSKSDKSPNC 474
Db 382 LARNPGWRALTFELTRYPPPEVSVIWTFTNGSGTLTCAASGYPOPNTVTLQCSGHTDRC 441
Qy 475 TTEITGVWN---RKANRKYFGOWSSSTLNMSEAIKGFVKKCCAYNSLGTSCETILLN 530
Db 442 DEAOVLQWDDPYPEVLSQEPHFKVTVQSLLTVEHNTQTECRHNSVSGSSWAFPI 501
Qy 531 SFGPPFPIODNISFYATIGVC---LLFIVVLTLLIHKYKQKQFYESQLOMVQVGTSSDN 587
Db 502 SAGATHPPDEFLLTPVVVACHSIMALLLLLLLLLLYKQKPKYQVRWKIIE--SYEGN 559
Qy 588 EYFYVDREYEDLKWEPRENLEFGKVLGSGAGFKVMNATAYGISKTGVSIQVAVKMLK 647
Db 560 SYTFIDPTQLPYNEKWEFPENRLQFCKTLGAGAFKQVVEATAFGLGKEDAVLKVAVKMLK 619
Qy 648 EKADSSEREAALMSLKMMTQLGSHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNYSKR 707
Db 620 STAHADEKALMSSELKIMSHLOHENIVNLLGACTHGGPVLVITEYCCYGDLLNYSKR 679
Qy 708 E-----KFHRTWTETIFKEHNFSTYPTFQSHPNSSMPGSRVQIHP 747
Db 680 EAMLGPSLSPGQDPGCVVDYKNIHLEKKYVRDSDGFS-----SQGVDTYV 724
Qy 748 DSDQISGLHNSHSEDEIBEYENQKLEEBEDNLVTFEDLLCFAYQVAKMEFLFKSC 807
Db 725 EMRPVSTNSDSF-SBQDLKEDGRPLE-----LRDLLHFSQVAGQMAFLASKNC 774
Qy 808 VHRDLAARNVLVTHGKVKIKCDPLARDIMSDNSYVVRGNARLPVKWMAPESEFEGIYTI 867
Db 775 IHRDVAARNVLLTNGHVAKIGDFGLARDIMSDNSYVVRGNARLPVKWMAPESEFDCVY 834
Qy 868 KSDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGEKMDQPFYATEEYIIMQSCWA 927
Db 835 QSDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGEKMDQPFYATEEYIIMQSCWA 894

Qy 928 FDSRKRPSFNLTSFLGCOL-ADAEAMYNV 958
Db 895 LEPTHRPTFQQICSLFLOEQADRRERYTNL 926

RESULT 9

US-09-961-403-4
; Sequence 4, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-4

Query Match 22.1%; Score 1166.5; DB 9; Length 1088;
Best Local Similarity 30.4%; Pred No. 6.3e-70;
Matches 336; Conservative 165; Mismatches 365; Indels 241; Gaps 36;

Qy 12 PLLVVFSAIFG---TITNQDLFVI-----KCVLINHNKNDSSVGKSS---SYPMVSES 59
Db 6 PAFLVGLCLLTGLSLILCOLSLPSILPNEKNVQLNSSFSLRCFGESEVSWQYPMSEEE 65
Qy 60 PEDLCALRPOSG---TYEAAAEVVDVSAITLQVLVDAPGNISCLVWFHSSLNCP 116
Db 66 SSDVEIRNEENNSGLFVTVLEVSS-----ASAHT-----GLYTCYNNHTQTEEN--- 110
Qy 117 HFDLQNRGV-----VSMVILKMTQTQAGEYLLFIQSEATNYTILFTVSIRNTLLYTL 168
Db 111 --ELGRRHIYIVPPDPDAFVLGMT-----DYLIVE----- 141
Qy 169 RPYFRKMNQDALVCISBSVPEPIVWVLCDSQG-----ESCKE 208
Db 142 -----DDSAIIPCRITTDPTPV--TLHNSGVVPASYSRQGFNGFTVGPYIC-- 189
Qy 209 ESPAVVKEEVLHELFGTDIRCCARNELGRECTRLFTIDLQTPQTTLPOLKVGEBPL 268
Db 190 EATVKGKKFTIPPNVYALK-----ATSELDLEMEALKTV-----YKSGETI 231
Qy 269 WIRCKAVVNHGFGITW-----ELEKNA---LEBGNVFMSTYSTNRTMIRILFAP-VSSV 320
Db 232 VVTC-AVFNNVVDLQWTVGKVGIGITWLEB-----IKVPSIKLVITLTVPEA 280
Qy 321 ARNDTGYTCCSSK-----HPSQALVTIVGKGFINATNSSDEYE-IDQVEEFCFSVRFK 374
Db 281 TVKDSGDYECARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHVKHFVVEVR 340
Qy 375 AVPQIRCTWTFRKRKSPCKQKGLDNGYSIS-----KFCNHKQ-POEYIF 418
Db 341 AYPPPRISMLKNLTL-----IENLTETITDVEKIQEIRYSKILIRAKEDSGHYTI 394
Qy 419 HAENDDAQTKMFTNIRKQVQL-----AEASQASQCPDGYPLPSWTWKCSDKS 471
Db 395 VAQNEADVSKSYTFELTQVPSLIDLVDHGGTGGQTVRCRTAEGTLPDIEMWICKD-I 453
Qy 472 PNCITEITGVWNRKANRVFGOWSS-----STLNMSEATKGLFVKCCAY 517
Db 454 KCKNETS---WTILANN-----VSNIIITEHSRDRSTVEGRVTFKVEETIAVRCLAK 504

Qy 518 NSLGTSCETILINSGPPFPFIQDNISFYATICVCLLFIWVLTLLCHKYKQFRYESQLO 577
Db 505 NLLGAENRELKVA---PTLRSELTVAALVLLVIVLVIISLVLVWVWKQPRYBIRWR 560
Qy 578 MVQVTGSSDNEYFYVDFREYEDLKWEPRENLEFGKVLGSGAFGKVMNATAYGSKTGV 637
Db 561 VIESISPDGHEIYYVDPMLQPLPYDSRWEFPRDGLVLRVLGSGAFGKVEGTAYGLSRQP 620
Qy 638 SIQVAVKMLKEKADSSEREALMSLKMTQLGSHENIVNLLGACTLSGPIYILIFEYCCVG 697
Db 621 VMKAVKMLKPTARSEKQALMSLKIMTHLGPLHLNIVNLLGACTKSGPIYIITEYCFYG 680
Qy 698 DLLNLYLRKREKF-----HRTWTEIFKEHNFSTFYPTFQSHPN 734
Db 681 DLVNYLHNKRDLSFLSHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDKQADTT 740
Qy 735 SSMPSGREVQIHPDSQISGLHGN--SPHSEDEIEYENOKRLEEBEDLNVLFEDLLCEA 792
Db 741 QYVPMLEKREVSYSIORSLYDRPASVYKSKMLDSE-VKNLLSDNSEGLTLLDLLSFT 799
Qy 793 YQVAKGMEFLEPKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIMSDSNVYVGNARLPV 852
Db 800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYSVSGSTFLPV 859
Qy 853 KWMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNVPYGPIDANFYKLIQNGFKMDQPF 912
Db 860 KWMAPESFDNLYTTLSDVWSYGILLWEIFSLGCTPYPGMWVDSTFYNKIKSYRAKPD 919
Qy 913 YATEIYIMQSCWAFDRKPSFPNLTSLFLGCOLADAEAMYNV--DGRVSECPH--- 967
Db 920 HATSEYVEIMVCMNSEPEKPSFYHLSBIVENLLPGQYKYSYEKIHLDLFLKSDHPAVAR 979
Qy 968 -----TYQNRPPSREMDLGL 983
Db 980 MVDSDNAYIGVTVKNEEDKLDWEGGL 1006

RESULT 10

US-09-955-363-36
; Sequence 36, Application US/09955363
; Patent No. US20020173621A1
; GENERAL INFORMATION:

APPLICANT: Sledziewski Ph.D., Andrzej Z

Bell, Lillian A.

Kindsvogel Ph.D., Wayne R.

TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

FUSIONS

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA: US/09/955,363

FILING DATE: 18-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,510

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/347,291

FILING DATE: 02-MAY-1989

ATTORNEY/AGENT INFORMATION:

NAME: Maki J.D., David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-955-363-36

Query Match 22.1%; Score 1166; DB 9; Length 1089;
Best Local Similarity 30.3%; Pred. No. 6.8e-70;
Matches 336; Conservative 165; Mismatches 365; Indels 242; Gaps 36;
QY 12 PLVAFSAMIFG---TITNQDLFVI-----KCVLNHNKNDSSVGKSS---SYPMVSES 59
DB 6 PAFVLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYPMSEEE 65
QY 60 PEDLGCALRPQSSG---TVYEAADVDSASITLQVLVDAPGNISCLWVFKHSLNCQP 116
DB 66 SSDVEIRNEENSGLFVTVLVSS---ASAHT-----GLYTCYNHTQTEEN--- 110
QY 117 HFDLQNRGV-----VSMVILKMTQTQAGEYLLFIQSEATNTILFTVSIRNTLLYTL 168
DB 111 --ELEGRIIYVDPDPVAFPLGMT-----DYLVIVE----- 141
QY 169 RRPYFRMENQDALVCISSEVPEPVEWVLCDSQG-----ESCKE 208
DB 142 -----DDDSAIIPCRITDPTPV--TLHNSGVVPASYSRQGFNGFTVGPYIC-- 189
QY 209 ESPAVKKEKVLHELPGTDIRCCARNEELGRECTRLFTIDLNQTPQTLQFLKVGSEPL 268
DB 190 EATVKGKKTQIPFNVAALK-----ATSELDLEMAELKTV-----YKSGETI 231
QY 269 WIRCKAVHVNHGFLTW-----ELENKA---LEEGNYEMSTYSTNRTMIRILPAF-VSSV 320
DB 232 VVTC-AVFENNEVDLQWYGEVKGKGITILE-----IKVPSIKLVYTLTVPEA 280
QY 321 ARNDTGYTCSSK-----HPSQALVTIVKGFINATNSSEDEY-IDOYEFCFSVRPK 374
DB 281 TVKDSGDYCAARQATREVEMKKTIVSHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVR 340
QY 375 AYPQIRCTWTFSRKSPCEQKGLDNGYSIS-----KFCNKHQ-PGEYIF 418
DB 341 AYPPIPRISLKNLTL-----IENLTETITDVEKIQEIRYRSKLIRAKESDSGHYTI 394
QY 419 HAENDDAQFTKMTLIRKPOVL-----AEASASQASCFSDGYPLPSMTWKCKSDKS 471
DB 395 VAQNEADVKSFTFELLTQVPSLIDLVDHGHSTGGTVRCETAGTLPDIEWMICKD-I 453
QY 472 PNCTEITEGVNMRKANRVFGOWSS-----STLNMSEAIKGLVKCCAY 517
DB 454 KCKNNETS---WTILANN-----VSNIIITEIHSRDRSTVEGRTVAKVETIAVRCLAK 504
QY 518 NSLGTSCETILNSPPFPFIQNIISFYATIGVCLLFIIVLTLILCHYKQKPFYSQLQ 577
DB 505 NULGAENRELKIVA-----PTLSELATAAAVLLVLIIVLSILVAVVWVKQKRYEIRWR 560
QY 578 MYQVTGSSNNEYFYVDREYEDLWKEFFRENLEFGKVLGSGAGFKMKNATAYGISKTGV 637
DB 561 VIESISPDGHEIYVDPMLQPLDSRWEFFRDGLVGLGSGAGFKVVEGTAYGLRSRQP 620
QY 638 SIQVAVKMLKEKADSSERELMSKMTQLGSHENIVNLLGACTLSGPIYLIFEYCCYV 697
DB 621 VMKVAVKMLKPTARSEKQALMSKALMTLGLPHINIVNLLGACTLSGPIYIITEYCFYV 680
QY 698 DLLNLYRSKREXF-----HRTWEIFKEHNFSEFYPTFQSHPN 734
DB 681 DLVNVLHKNRDGSFLSHHPEKPKELDI FGLNPADESTRSVILSFENNNGYDMQKADIT 740

QY 735 SSMPGSEVQIHPDSQDOTISGLHGN--SPHSEDEIEYENQKLEEBEDLNVLTFFDLCLCA 792
DB 741 QYVPMLEKKEVSKYSDIQRSYLDPRPASVYKKSMLDSE-VKNLLSDDNSEGUTLLDLLSFT 799
QY 793 YQVAKGMEFLEFKSCVHRDLAARNVLTGHVKVVKICDFGLARDIMSDSNVYVGNARLPV 852
DB 800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYSVSKGSTFLPV 859
QY 853 KWMAPESLPEGIYTIKSDVMSYGILLMEIFSLGVNPPYGIIVDANFYKLIQNGFKMDQPF 912
DB 860 KWMAPESIFONLYTTLSDVMSYGILLMEIFSLGTPPYGMVVDSTFYNKIKSGYRMAKPD 919
QY 913 YATIEIYIIMQSCWAFDSRKRPSFNLTSFLGCOLADAEAEAMQNV--DGRVSECPH--- 967
DB 920 HATSEVEIWMKWNSEPEKPSFYHLSEIVENLLPGQYKKSIEYKIHLDLFLKSDHPAVAR 979
QY 968 -----TYONRRPFSREMDLGL 983
DB 980 MRVDSNDNAYIGVTYKNEEDKLKDWEGGL 1007

RESULT 11

US-09-769-987-2
Sequence 2, Application US/09769987
Patent No. US20020055129A1
GENERAL INFORMATION:
APPLICANT: Matsui, Toshimitsu
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Recept.
FILE REFERENCE: 14014.0266U2
CURRENT APPLICATION NUMBER: US/09/769,987
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 08/460,656
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: US 08/439,095
PRIOR FILING DATE: 1995-05-11
PRIOR APPLICATION NUMBER: US 07/915,884
PRIOR FILING DATE: 1992-07-20
PRIOR APPLICATION NUMBER: US 07/308,282
PRIOR FILING DATE: 1989-02-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1089
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1e =
US-09-769-987-2

Query Match 22.1%; Score 1166; DB 10; Length 1089;
Best Local Similarity 30.3%; Pred. No. 6.8e-70;
Matches 336; Conservative 165; Mismatches 365; Indels 242; Gaps 36;

QY 12 PLVAFSAMIFG---TITNQDLFVI-----KCVLNHNKNDSSVGKSS---SYPMVSES 59
DB 6 PAFVLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSSFSLRCFGESEVSWQYPMSEEE 65
QY 60 PEDLGCALRPQSSG---TVYEAADVDSASITLQVLVDAPGNISCLWVFKHSLNCQP 116
DB 66 SSDVEIRNEENSGLFVTVLVSS---ASAHT-----GLYTCYNHTQTEEN--- 110
QY 117 HFDLQNRGV-----VSMVILKMTQTQAGEYLLFIQSEATNTILFTVSIRNTLLYTL 168
DB 111 --ELEGRIIYVDPDPVAFPLGMT-----DYLVIVE----- 141
QY 169 RRPYFRMENQDALVCISSEVPEPVEWVLCDSQG-----ESCKE 208
DB 142 -----DDDSAIIPCRITDPTPV--TLHNSGVVPASYSRQGFNGFTVGPYIC-- 189

Db 800 YQVARGMEFLASKNCVHRDLAARNVLLAQAQKIVKICDFGLARDIMHDSNYKSGSTFLPV 859
QY 853 KMAPESLFGIYTIKSDVMSYGILLWEIFSLGVNPPGIPVDANFYKLIQNGFKMDQPF 912
Db 860 KMAPESIFDNLTYLSDVMSYGILLWEIFSLGTPFGMVDSTFFYNKIKSGYRMAKPD 919
QY 913 YATEEYIIQMSWAFDSRKPSFNLTSLFLGCOLADAEAMYQNV--DGRVSECPH--- 967
Db 920 HATSEVVEIMVKWNSPEKRPSPFYLSEIVENLLPGQYKSKYEKIHLDFLKSHPAVAR 979
QY 968 -----TYQNRPPSPREMDLGL 983
Db 980 MRVDSNAYIGVTYKNEEDKLKDWEGGL 1007

RESULT 13

US-09-866-510-2
; Sequence 2, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-2

Query Match 22.1%; Score 1166; DB 10; Length 1089;
Best Local Similarity 30.3%; Pred. No. 6.8e-70;
Matches 336; Conservative 165; Mismatches 365; Indels 242; Gaps 36;

QY 12 PLLVFSAMIFG---TITNQLDLPVI-----KCVLINHKNDSSVGKSS---SYPMVSES 59
Db 6 PAFVLGCLLTGLSLILCOLSLPSILPNEKVKVQLNSFSLRCFGESEVSWQPMSEEE 65
QY 60 PEDLGCALRQSSG---TYVEAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQP 116
Db 66 SSDVEIRNEENNSGLFTVLEVS-----ASAHT-----GLYTCYNNHTQTEEN--- 110
QY 117 HFDLQNRGV-----VSMVILKMTETOAGEVLLFTQSEATNYTLFTVSIINTLLYTL 168
Db 111 --ELEGRIHYIVDPDPAFVPLGMT-----DYLIVIVE----- 141
QY 169 RRPYFRKMNQDALVCISBSVPPIVVEWLCDSQG-----ESCKE 208
Db 142 -----DDSDAIICRTDTPPV--TLHNSGVVPPASYSRQGFNGFTVGPVIC-- 189
QY 209 ESPAVVKEEVLHELFGTDIRCCARNEIGRECTRLFTIDNQTPTTLPOLFLKVGPEPL 268
Db 190 EATVKGKFTQTFPNVYALK---ATSELDLEMEALKTV-----YKSGETI 231
QY 269 WTRCAVHVNHGFLTW-----ELEKVA---LEGNFEMSTYSTNTMTIRILFAP-VSSV 320
Db 232 VVTC-AVFNEVVDLQWTPGVEVKGIGITMLEE-----IKVPSIKLVTLVPEA 280
QY 321 ARNDTGYTCSKK-----HPSQALVTIVGKGFINATNSSEIYE-IDQVEEFCFSVRFX 374
Db 281 TVKSGDVEACARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHVEKHFVVEVR 340
QY 375 AYPQIRCTWTFSRKSPFCQKGLDNGYSIS-----KFCNKHQ-PGEYIF 418

Db 341 AYPPIRISWLKNNLTL-----IENLTEITTDVEKIQBIYRYSKLKLIRAKEEDSGHYTI 394
QY 419 HAENDAOQFTQMTFLNIRRKPOVL-----AEASASQASCFSDGYPLPSTWTKCSDKS 471
Db 395 VAQNEADAVKSTVFELLTQVPSIILDLVDDHGGTGGQVTRCTAEGTPLPDIEMWICKD-I 453
QY 472 PNCTEEITEGVNMRKANRKFVQWVSS-----STLNMSEAIKGFVKKCCAY 517
Db 454 KCKNNETS---WTLANN-----VSNLITEHSRDRSTVEGRVTFKAVEETIAVRCLAK 504
QY 518 NSLGTSCETILLSPGPPFIQDNI SFYATIGVCLLFLFVLTLLICHKYKQKFRYESQLQ 577
Db 505 NLLGAENRELKVA---PTLRSELTVAALVLLVLIISLIVLVVWIKQKPRYEIRWR 560
QY 578 MVQVGTSSDNEYFYVDPREYEDLKWEFFRENLEFGLVSGSAGFKGMNATAYGISKTV 637
Db 561 VIESISPDGHEIYVDPMQLPYDSRWEFFPRDGLVGLVSGGAFGVKVEGTAYGLSRQP 620
QY 638 SIQVAVKMLKADSSERREALMSLKMTOIGSHENIVNLGACTLSGPIYLIPEYCCYG 697
Db 621 VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPLHNLVNLGACTKSGPIYLIPEYCFYG 680
QY 698 DLLNLYLRSKREKF-----HRTWTEIFKEHNFSPYPTFQSHPN 734
Db 681 DLVNYLHKNRDPSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNNDYMDMKQADTT 740
QY 735 SSMGSGREVOIHPDSDOISGLHGN--SFHSEDEIYEYENOKLEEEEDLNVITFEDLLCFA 792
Db 741 QYVPMLEKEVSKYSYDIQSRSLYDRPASYSKKSMLDSE--VKNLLSDNSEGLTLLDLLSFT 799
QY 793 YQVAKGMEFLFKSCVHRDLAARNVLTGKVKVVICDFGLARDIMSDSNVYVGNARLPV 852
Db 800 YQVARGMEFLASKNCVHRDLAARNVLLAQAQKIVKICDFGLARDIMHDSNYKSGSTFLPV 859
QY 853 KMAPESLFGIYTIKSDVMSYGILLWEIFSLGVNPPGIPVDANFYKLIQNGFKMDQPF 912
Db 860 KMAPESIFDNLTYLSDVMSYGILLWEIFSLGTPFGMVDSTFFYNKIKSGYRMAKPD 919
QY 913 YATEEYIIQMSWAFDSRKPSFNLTSLFLGCOLADAEAMYQNV--DGRVSECPH--- 967
Db 920 HATSEVVEIMVKWNSPEKRPSPFYLSEIVENLLPGQYKSKYEKIHLDFLKSHPAVAR 979
QY 968 -----TYQNRPPSPREMDLGL 983
Db 980 MRVDSNAYIGVTYKNEEDKLKDWEGGL 1007

RESULT 14

US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-10

Query Match 22.1%; Score 1163; DB 10; Length 1089;
Best Local Similarity 30.2%; Pred. No. 1.1e-69;
Matches 335; Conservative 166; Mismatches 365; Indels 242; Gaps 36;

Db 505 NLGAENRELKVA---PTIRSELTVAAAVLVLVIVIIISLIVLVIVWKQRYEIRWR 560
QY 578 MVQVTGSSDNEYFYVDPREYEDLKWEFFRENLEFGVLGSGAFGKVMNATAYCISKTV 637
Db 561 VIESISPDGHEYIYVPMQLPYDSRWKFPKRDGLVLRVLGSGAFGVVEGTAYGLSRQP 620
QY 638 SIQVAVKMLKEKADSSEREALMSELKMTQLGSHENIVNLLGACTLSGPIYLIFEYCCYG 697
Db 621 VMKVAVKMLKPTARSSKQALMSELKIMTHLPHLNIIVNLLGACTKSGPIYIITEYCFYG 680
QY 698 DLLNYLRSKREKF-----HRTWTEIFKEHNFsfYPTFOSHFN 734
Db 681 DLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTT 740
QY 735 SSMPGSRVQIHPDSQISGLHGN--SFHSEDSIEYENOKRELEEDLNVLTFEDLLCPA 792
Db 741 QYVPMLEKEVSKYSDIORSLYDRPASYYKKSMDDSE-VKNLLSDDNSEGLTLLDLLSFT 799
QY 793 YQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMGDSNYYVVRGNARLPV 852
Db 800 YQVARGMEFLASKNCVHRDLAARNVLLAQOKIVIKICDFGLARDIMHDSNYYVSKGSTFLPV 859
QY 853 KMWAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGFKMDQPF 912
Db 860 KMWAPESIADNLYTTLSDVMSYGILLWEIFSLGCTPYPGMWVDSTFYNNKIKSGYRWAKPD 919
QY 913 YATEEYIIMQSCWAFDSKRPSPNLTSLGCOLADAEEMYNQV--DGRVSECPH--- 967
Db 920 HATSEYIEMVKNWSEPEKRPSPFVHLSIVENLFLPGQYKYSYEKIHLDFLAKSDHPAVAR 979
QY 968 -----TYQNRPPFSREMDLGL 983
Db 980 MRVDSNAYIGVYTKNEEDKLDWEGGL 1007

Search completed: May 24, 2003, 17:10:20
Job time : 45.0207 secs

GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2003, 16:54:10 ; Search time 14.0071 seconds
(without alignments)
2085.875 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVELLVFSAM.....PFSREMDLGLSPQAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5274	100.0	993	1	US-07-977-451-4
2	5274	100.0	993	1	US-08-252-517-4
3	5274	100.0	993	1	US-07-906-397A-4
4	5274	100.0	993	1	US-08-601-891-4
5	5274	100.0	993	2	US-09-021-324-4
6	5274	100.0	993	5	PCT-US92-09893-4
7	5274	100.0	1160	5	PCT-US92-05401-4
8	5240	99.4	993	1	US-08-222-299-4
9	5240	99.4	993	2	US-08-434-878-4
10	5240	99.4	993	5	PCT-US95-03718-4
11	5238	99.3	993	1	US-08-183-211-2
12	5238	99.3	993	5	PCT-US95-00176A-2
13	4533.5	86.0	1000	1	US-08-222-299-2
14	4533.5	86.0	1000	2	US-08-434-878-2
15	4533.5	86.0	1000	5	PCT-US95-03718-2
16	4429.5	84.0	992	1	US-07-813-593-2
17	4429.5	84.0	992	1	US-07-977-451-2
18	4429.5	84.0	992	1	US-07-946-507-2
19	4429.5	84.0	992	1	US-08-252-517-2
20	4429.5	84.0	992	1	US-07-906-397A-2
21	4429.5	84.0	992	1	US-08-601-891-2
22	4429.5	84.0	992	2	US-09-021-324-2
23	4429.5	84.0	992	5	PCT-US92-02750-2
24	4429.5	84.0	992	5	PCT-US92-05401-2
25	4429.5	84.0	992	5	PCT-US92-09893-2
26	1654	31.4	481	4	US-07-912-122-4
27	1654	31.4	481	5	PCT-US93-06404-4

28 1251 23.7 976 3 US-08-750-141A-1 Sequence 1, Appli
29 1216.5 23.1 972 3 US-08-750-141A-2 Sequence 2, Appli
30 1166 22.1 1089 1 US-08-180-195-36 Sequence 36, Appli
31 1166 22.1 1089 1 US-08-168-917-4 Sequence 4, Appli
32 1166 22.1 1089 1 US-08-477-329-36 Sequence 36, Appli
33 1166 22.1 1089 2 US-08-475-458-36 Sequence 36, Appli
34 1166 22.1 1089 2 US-08-460-510-4 Sequence 4, Appli
35 1166 22.1 1089 3 US-08-460-490-4 Sequence 4, Appli
36 1166 22.1 1089 3 US-08-980-400-36 Sequence 36, Appli
37 1166 22.1 1089 3 US-08-462-728-2 Sequence 2, Appli
38 1166 22.1 1089 4 US-09-583-459A-36 Sequence 36, Appli
39 1166 22.1 1089 4 US-09-583-210-36 Sequence 36, Appli
40 1166 22.1 1089 4 US-09-583-449A-36 Sequence 36, Appli
41 1166 22.1 1089 4 US-09-435-059-36 Sequence 36, Appli
42 1166 22.1 1089 4 US-08-461-917-2 Sequence 2, Appli
43 1166 22.1 1089 5 PCT-US92-00730-4 Sequence 4, Appli
44 1166 22.1 1089 5 PCT-US92-00862-4 Sequence 4, Appli
45 1086.5 20.6 1106 1 US-08-180-195-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-07-977-451-4
; Sequence 4, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-977-451-4

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTLLVVFSAIMFGTITNQLPVIKVLIHKNNDSSVGKSSSPYMWSESP 60
Db 1 MPALARDAGTLLVVFSAIMFGTITNQLPVIKVLIHKNNDSSVGKSSSPYMWSESP 60

Qy 61 EDLGCALRPQSSGTVYAAAEVDVDSASITLQVLDPAGNISCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRPQSSGTVYAAAEVDVDSASITLQVLDPAGNISCLWVFKHSSLNCQPHFDL 120

Qy 121 QNRGVVSVILKMTQAGYLLFIOSEATNYTILFTVSRINTLLYLRPPYPRKMNQD 180
Db 121 QNRGVVSVILKMTQAGYLLFIOSEATNYTILFTVSRINTLLYLRPPYPRKMNQD 180

Qy 181 ALVCISSEVPEIVENVLCDOSGESCCKESPAVKKKEKVLHFLGTDIRCCARNELGRE 240
Db 181 ALVCISSEVPEIVENVLCDOSGESCCKESPAVKKKEKVLHFLGTDIRCCARNELGRE 240

Qy 241 CTRLETIDLNQPTTLPOLFLKVGEPMLRCKAVHNVHFGLTWLENKALEEGNYFEM 300
Db 241 CTRLETIDLNQPTTLPOLFLKVGEPMLRCKAVHNVHFGLTWLENKALEEGNYFEM 300

Qy 301 STYSNTRMTIRILFAFVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSDYE 360
Db 301 STYSNTRMTIRILFAFVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSDYE 360

Qy 361 IDQYEEFCFSVRKAYPQIRCTWTFSRKSPFCEQKGLDNGYSISKFCNKHQGEYIFHA 420
Db 361 IDQYEEFCFSVRKAYPQIRCTWTFSRKSPFCEQKGLDNGYSISKFCNKHQGEYIFHA 420

Qy 421 ENDDAQFTKMTINIRKQVLAESASQASCFSDGYPLPSWTWKKCSKSPNCTEEITE 480
Db 421 ENDDAQFTKMTINIRKQVLAESASQASCFSDGYPLPSWTWKKCSKSPNCTEEITE 480

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Db 481 GWNKANKRVFGQWSSSTLNNSEAIKFLVKCCAYNSLGTSCETILLNSPGPPFFIOD 540

Qy 541 NISFYATIGVCLLFIIVLTLCHIKYKQFRYESQLQWQVGTSSDNEYFYVDREYED 600
Db 541 NISFYATIGVCLLFIIVLTLCHIKYKQFRYESQLQWQVGTSSDNEYFYVDREYED 600

Qy 601 LKWEFPRENLEKGLGSAFGKVMNATYIGISKTGVSTQAVKMLKEKADSSEREAALS 660
Db 601 LKWEFPRENLEKGLGSAFGKVMNATYIGISKTGVSTQAVKMLKEKADSSEREAALS 660

Qy 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYGDLLNLYRSKREKPHRTWTIFKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYGDLLNLYRSKREKPHRTWTIFKE 720

Qy 721 HNFSPYTFQSHNSMPGSRVQIHDPDSQISGLHNSFHSDETEYENQKRLBEEEDL 780
Db 721 HN'FYPTFQSHNSMPGSRVQIHDPDSQISGLHNSFHSDETEYENQKRLBEEEDL 780

Qy 781 NVLTPEDLICFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTPEDLICFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840

Qy 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900

Qy 901 LIQNGFKMDQPPVATYEEIYIMQSCWAFDSRKRPSPNLTSFLGCCOLADAEAEAMYQNVDG 960
Db 901 LIQNGFKMDQPPVATYEEIYIMQSCWAFDSRKRPSPNLTSFLGCCOLADAEAEAMYQNVDG 960

Qy 961 RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS 993

RESULT 2
US-08-252-517-4
Sequence 4, Application US/08252517
Patent No. 5548055
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/252,517
FILING DATE: 31-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-517-4

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKVCLINHNKNDSSVGKSSSPMVSESP 60

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DB 181 ALVCISESPEPIVEVILCDQESCKEESPAVVKKEKVLHFLFGTDIRCCARNELGRE 240

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DB 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360

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DB 481 GVMNRKANRKFQGWSSSTLNNSEAIKGLVKCCAYNSLGTSCETILLNSPGPFPIQD 540

QY 541 NISFYATIGVCLLFIIVLLILLCHVKYKQPRYSQLOMVQVGTSSDNEYPYVDFREYED 600
DB 541 NISFYATIGVCLLFIIVLLILLCHVKYKQPRYSQLOMVQVGTSSDNEYPYVDFREYED 600

QY 601 LKWEFPRENLEFGKVLGSGAFGVMNATAGISKTGVSIOVAVKMLKEKADSSERBALMS 660
DB 601 LKWEFPRENLEFGKVLGSGAFGVMNATAGISKTGVSIOVAVKMLKEKADSSERBALMS 660

QY 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNLYRSKREKPHRTWTIFKE 720
DB 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNLYRSKREKPHRTWTIFKE 720

QY 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNPSHSEDEIYENQKLEEEEDL 780
DB 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNPSHSEDEIYENQKLEEEEDL 780

QY 781 NVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDPLGLARDMSDS 840
DB 781 NVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDPLGLARDMSDS 840

QY 841 NYVVRGNARLPVKWMAPESLFEGITYIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900

DB 841 NYVVRGNARLPVKWMAPESLFEGITYIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
QY 901 LIQNGFKMDQFFYATBEIYIIMOSWAFDSRKPSFNNLTSLFCQLADAEAMYNQVNDG 960
DB 901 LIQNGFKMDQFFYATBEIYIIMOSWAFDSRKPSFNNLTSLFCQLADAEAMYNQVNDG 960

QY 961 RVSECPHTYQNRPPFRREMDLGLLSPOAQVEDS 993
DB 961 RVSECPHTYQNRPPFRREMDLGLLSPOAQVEDS 993

RESULT 3
US-07-906-397A-4
Sequence 4, Application US/07906397A
Patent No. 5621090
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,397A
FILING DATE: 19920626
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-906-397A-4

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKVCLINHNKNDSSVGKSSSPMVSESP 60
DB 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKVCLINHNKNDSSVGKSSSPMVSESP 60

QY 61 EDLGCALRPQSSGTVYEAADVEVDVSGASITLQVLVDAPGNISCLWVFKHSSSLNCQPHFDL 120

Db 61 EDLGCALRQSSGTVVEAAAEVDVSASITLQVLVDAPGNISCLWFKHSSLNQCQPHFDL 120
Qy 121 QNRGVVSVILKMTQTOAGEYLLFQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMNQD 180
Db 121 QNRGVVSVILKMTQTOAGEYLLFQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMNQD 180
Qy 181 ALVCISESVPEIPEVWVLCDSOGESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEIPEVWVLCDSOGESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLFTIDLNTQPTTLPOLFLKVGPELWIRKAVVNHGFGLTWELENKALEEGNYFEM 300
Db 241 CTRLFTIDLNTQPTTLPOLFLKVGPELWIRKAVVNHGFGLTWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVANDGYTCSSSKHPSQSALVTIYKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVANDGYTCSSSKHPSQSALVTIYKGFINATNSSEDEYE 360
Qy 361 IDOYEEFCFVRFKAYPQIRCTWTFSRKFPCQKGLDNGYISIKPCNHKHQPGYIFHA 420
Db 361 IDOYEEFCFVRFKAYPQIRCTWTFSRKFPCQKGLDNGYISIKPCNHKHQPGYIFHA 420
Qy 421 ENDDAQFTKMTFLNIRRKQVLAESAASQSCFSDGYPLPSMTWKCKSDKSPNCTEEITE 480
Db 421 ENDDAQFTKMTFLNIRRKQVLAESAASQSCFSDGYPLPSMTWKCKSDKSPNCTEEITE 480
Qy 481 GWNKRNKRVQGWSSSTLNSEAIKGLVKKCCAYNSLGTSCETILLNSPGPPFIOD 540
Db 481 GWNKRNKRVQGWSSSTLNSEAIKGLVKKCCAYNSLGTSCETILLNSPGPPFIOD 540
Qy 541 NISFYATTGVCLLFIVLTLCHYKVKQFRYESQLOMVOVQVGTSSDNEYFYVDFREYED 600
Db 541 NISFYATTGVCLLFIVLTLCHYKVKQFRYESQLOMVOVQVGTSSDNEYFYVDFREYED 600
Qy 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGSKTGVSIQVAVKMLKEXADSSEREALMS 660
Db 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGSKTGVSIQVAVKMLKEXADSSEREALMS 660
Qy 661 ELKMTQLGSHENIYNLLGACTLSGPIYLIPEYCCYGDLLNLYRSKREKPHRTWTIEFKE 720
Db 661 ELKMTQLGSHENIYNLLGACTLSGPIYLIPEYCCYGDLLNLYRSKREKPHRTWTIEFKE 720
Qy 721 HNFSPYPTFQSHPSNMPGSRVQIHPDSDQISGLHNSFHSDEIEYENOKRLEEBEEL 780
Db 721 HNFSPYPTFQSHPSNMPGSRVQIHPDSDQISGLHNSFHSDEIEYENOKRLEEBEEL 780
Qy 781 NVLTPEDDLFCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVKVVICDFGLARDIMSDS 840
Db 781 NVLTPEDDLFCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVKVVICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWMAPESLFPGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLFPGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
Qy 901 LIQNGFKMDQPYATEEIIYIMQSWAFDSRKRPSPNLTSLGCOLADAEEMYNQVGD 960
Db 901 LIQNGFKMDQPYATEEIIYIMQSWAFDSRKRPSPNLTSLGCOLADAEEMYNQVGD 960
Qy 961 RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS 993

RESULT 4

US-08-601-891-4
; Sequence 4, Application US/08601891
; Patent No. 5747651
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:

ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601.891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977.451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906.397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813.593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793.065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728.913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679.666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-891-4

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVVFSAIEGTITNODLPVTKCVLIHKNKNDSSVGKSSSPMVSESP 60
Db 1 MPALARDAGTVLLVVFSAIEGTITNODLPVTKCVLIHKNKNDSSVGKSSSPMVSESP 60
Qy 61 EDLGCALRQSSGTVVEAAAEVDVSASITLQVLVDAPGNISCLWFKHSSLNQCQPHFDL 120
Db 61 EDLGCALRQSSGTVVEAAAEVDVSASITLQVLVDAPGNISCLWFKHSSLNQCQPHFDL 120
Qy 121 QNRGVVSVILKMTQTOAGEYLLFQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMNQD 180
Db 121 QNRGVVSVILKMTQTOAGEYLLFQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMNQD 180

QY 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEVLHFGTDIRCCARNELGRE 240
DB 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEVLHFGTDIRCCARNELGRE 240
QY 241 CTRLFTIDLNOTPOTTLPOLFLKVGGBPLWIRCKAVHVNHGFGLTWELNKALBEGNYFEM 300
DB 241 CTRLFTIDLNOTPOTTLPOLFLKVGGBPLWIRCKAVHVNHGFGLTWELNKALBEGNYFEM 300
QY 301 STYSTNRTMIRILFAFVSSVARNDTGYYTSSSKHPSQSALVTIVGKGFNATNSSEDYE 360
DB 301 STYSTNRTMIRILFAFVSSVARNDTGYYTSSSKHPSQSALVTIVGKGFNATNSSEDYE 360
QY 361 IQYBEFCFSVRKAYPQIRCTWTFGRKPPCEQKGLDNGYSISKFNHKKHQGEVIFHA 420
DB 361 IQYBEFCFSVRKAYPQIRCTWTFGRKPPCEQKGLDNGYSISKFNHKKHQGEVIFHA 420
QY 421 ENDDAQFTKMTLNIRRKQVLAESAASQSCFSDGYPPLPSWTWKCKSDKSPNCTBEITE 480
DB 421 ENDDAQFTKMTLNIRRKQVLAESAASQSCFSDGYPPLPSWTWKCKSDKSPNCTBEITE 480
QY 481 GYWNKANKRVGOWYSSSTLAMEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
DB 481 GYWNKANKRVGOWYSSSTLAMEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
QY 541 NISFVATICVCLLFIVVLTLILCHYKKQPRYESQLOMVQVGTSSDNEYFYVDFREVEYD 600
DB 541 NISFVATICVCLLFIVVLTLILCHYKKQPRYESQLOMVQVGTSSDNEYFYVDFREVEYD 600
QY 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOQAVKMLKEKADSSEREALMS 660
DB 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOQAVKMLKEKADSSEREALMS 660
QY 661 ELKMTQLGSHENIVNLLGACTLSGDIYILIFECYCCYGDLLNLYRSKREKPHRTWTIFKE 720
DB 661 ELKMTQLGSHENIVNLLGACTLSGDIYILIFECYCCYGDLLNLYRSKREKPHRTWTIFKE 720
QY 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSDQISGLHNSFHSDEIYENOKLEBEEDL 780
DB 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSDQISGLHNSFHSDEIYENOKLEBEEDL 780
QY 781 NVLTPEDDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIMSDS 840
DB 781 NVLTPEDDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIMSDS 840
QY 841 NVTVRGNARLPVKWAPESLFEIGIYTIKSDVWSYGILLWEIFSLGVPNPGIPIVDANFYK 900
DB 841 NVTVRGNARLPVKWAPESLFEIGIYTIKSDVWSYGILLWEIFSLGVPNPGIPIVDANFYK 900
QY 901 LIQNGFKMDOPFYATEEIIYIMOSWAFDSRKRPSPNLTSFLGCQLADAEABMYQNVDG 960
DB 901 LIQNGFKMDOPFYATEEIIYIMOSWAFDSRKRPSPNLTSFLGCQLADAEABMYQNVDG 960
QY 961 RVSECPHTYQNRPPFSREMDGLLSLSPQAQVEDS 993
DB 961 RVSECPHTYQNRPPFSREMDGLLSLSPQAQVEDS 993

RESULT 5

US-09-021-324-4

; Sequence 4, Application US/09021324

; Patent No. 5912133

; GENERAL INFORMATION:

; APPLICANT: Lemischka, Ihor R.

; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ImClone Systems Incorporated

; STREET: 180 Varick Street

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,324
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-021-324-4

Query Match

100.0%; Score 5274; DB 2; Length 993;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKCVLINHKNDSSVGKSSSPMWSESP 60
DB 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKCVLINHKNDSSVGKSSSPMWSESP 60

QY 61 EDLGCALRPQSSGTVEAAAAYVDVSASITLQVLVDAPGNISCLWVFKHSSLCQPHFDL 120
DB 61 EDLGCALRPQSSGTVEAAAAYVDVSASITLQVLVDAPGNISCLWVFKHSSLCQPHFDL 120

QY 121 QNRGVVSWILKMTETQAGEYLLFIQSEATNYTILFTVSRINTLLTYLRPFYFRKMENQD 180
DB 121 QNRGVVSWILKMTETQAGEYLLFIQSEATNYTILFTVSRINTLLTYLRPFYFRKMENQD 180

QY 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEVLHFGTDIRCCARNELGRE 240
DB 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEVLHFGTDIRCCARNELGRE 240

QY 241 CTRLFTIDLNOTPOTTLPOLFLKVGGBPLWIRCKAVHVNHGFGLTWELNKALBEGNYFEM 300
DB 241 CTRLFTIDLNOTPOTTLPOLFLKVGGBPLWIRCKAVHVNHGFGLTWELNKALBEGNYFEM 300

Db 241 CTRLFTIDLNOTPOTTLPOLFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Qy 361 IDQYEEFCFVSFRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 420
Db 361 IDQYEEFCFVSFRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 420
Qy 421 ENDDAQFTKMTNIRRKQVLAASASQASCFSDGYPLPSWTWKCKSDKSPNCTEITE 480
Db 421 ENDDAQFTKMTNIRRKQVLAASASQASCFSDGYPLPSWTWKCKSDKSPNCTEITE 480
Qy 481 GWNKRNKRVFGQWSSSTLANSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIOD 540
Db 481 GWNKRNKRVFGQWSSSTLANSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIOD 540
Qy 541 NISFYATIGVCLLFIIVLLTLLCHYKKQFRYESQIQVAVKMLKEKADSSEREAALMS 600
Db 541 NISFYATIGVCLLFIIVLLTLLCHYKKQFRYESQIQVAVKMLKEKADSSEREAALMS 600
Qy 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREAALMS 660
Db 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREAALMS 660
Qy 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYCGDLLNLYRSKREKPHRTWTBIFKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYCGDLLNLYRSKREKPHRTWTBIFKE 720
Qy 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSDQISGLHNSFHSEDEIYENQKLEBEEDL 780
Db 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSDQISGLHNSFHSEDEIYENQKLEBEEDL 780
Qy 781 NVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Qy 841 NVVVRGNARLPVKWAPESLFEIGIYTKSDVMSYGILLWEIFSLGYNPYPGIPVDANFYK 900
Db 841 NVVVRGNARLPVKWAPESLFEIGIYTKSDVMSYGILLWEIFSLGYNPYPGIPVDANFYK 900
Qy 901 LIONGFKMDOPFVATEEIIYIMOSWAFPSRKPSPNLTSLFGCOLADAEAEAMYNQVDG 960
Db 901 LIONGFKMDOPFVATEEIIYIMOSWAFPSRKPSPNLTSLFGCOLADAEAEAMYNQVDG 960
Qy 961 RVSECPHTYQNRPPFREMDDLGLLSPOAQVEDS 993
Db 961 RVSECPHTYQNRPPFREMDDLGLLSPOAQVEDS 993

RESULT 6

PCT-US92-09893-4

; Sequence 4, Application PC/TUS9209893

; GENERAL INFORMATION:

; APPLICANT: Lemischka, Ihor R.

; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Imclone Systems Incorporated

; STREET: 180 Varick Street

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10014

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/09893

; FILING DATE: 19921116
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7PT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09893-4

Query Match 100.0%; Score 5274; DB 5; Length 993;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPDLLVVFSAIMFGTTITNQDLPIVKVLINHKNDSSVGKSSSPMVSSESP 60
Db 1 MPALARDAGTVPDLLVVFSAIMFGTTITNQDLPIVKVLINHKNDSSVGKSSSPMVSSESP 60
Qy 61 EDLGCALRPQSSGTYYEAAAEVDVSATITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRPQSSGTYYEAAAEVDVSATITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDL 120
Qy 121 QNRGVVSMVLKMTETQAGEYLLFTIQSEATNTILFTVSI RNTLLYLRPRPKMENQD 180
Db 121 QNRGVVSMVLKMTETQAGEYLLFTIQSEATNTILFTVSI RNTLLYLRPRPKMENQD 180
Qy 181 ALVCISSEVPEPIVBMVLCDSSQESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISSEVPEPIVBMVLCDSSQESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLETTIDLNOTPOTTLPOLFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
Db 241 CTRLETTIDLNOTPOTTLPOLFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Qy 361 IDQYEEFCFVSFRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 420
Db 361 IDQYEEFCFVSFRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 420
Qy 421 ENDDAQFTKMTNIRRKQVLAASASQASCFSDGYPLPSWTWKCKSDKSPNCTEITE 480
Db 421 ENDDAQFTKMTNIRRKQVLAASASQASCFSDGYPLPSWTWKCKSDKSPNCTEITE 480
Qy 481 GWNKRNKRVFGQWSSSTLANSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIOD 540
Db 481 GWNKRNKRVFGQWSSSTLANSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIOD 540
Qy 541 NISFYATIGVCLLFIIVLLTLLCHYKKQFRYESQIQVAVKMLKEKADSSEREAALMS 600
Db 541 NISFYATIGVCLLFIIVLLTLLCHYKKQFRYESQIQVAVKMLKEKADSSEREAALMS 600
Qy 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREAALMS 660
Db 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREAALMS 660
Qy 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYCGDLLNLYRSKREKPHRTWTBIFKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYCGDLLNLYRSKREKPHRTWTBIFKE 720
Qy 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSDQISGLHNSFHSEDEIYENQKLEBEEDL 780
Db 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSDQISGLHNSFHSEDEIYENQKLEBEEDL 780

QY 781 NVLTPEDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGKVVKICDFGLARDIMSDS 840
Db 781 NVLTPEDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGKVVKICDFGLARDIMSDS 840
QY 841 NVVVRGNARLPVKWMAPESLFEGIIYIKSDVWSYGILLWEIFSLGVNPPYGPVDFANFYK 900
Db 841 NVVVRGNARLPVKWMAPESLFEGIIYIKSDVWSYGILLWEIFSLGVNPPYGPVDFANFYK 900
QY 901 LIQNGFKMDQPPFYATEBEIYIMOSCWAFDSRKRKPSFPNLTSLFCGLADAEAEAMYQNDG 960
Db 901 LIQNGFKMDQPPFYATEBEIYIMOSCWAFDSRKRKPSFPNLTSLFCGLADAEAEAMYQNDG 960
QY 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993
Db 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993
RESULT 7
PCT-US92-05401-4
; Sequence 4, Application PC/TUS9205401
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOPIOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05401
; FILING DATE: 19920626
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1160 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-05401-4
Query Match 100.0%; Score 5274; DB 5; Length 1160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPALARDAGTPLLVLVFSAMIFGTITNQDLPVILKCVLINHKNDSSVGKSSSYPMWSESP 60
Db 20 MPALARDAGTPLLVLVFSAMIFGTITNQDLPVILKCVLINHKNDSSVGKSSSYPMWSESP 79
QY 61 EDLGCALRPQSSGTVYAAAEVDVVSASITLQVLDPAGNISCLWVFKSSLNCQPHFDL 120
Db 80 EDLGCALRPQSSGTVYAAAEVDVVSASITLQVLDPAGNISCLWVFKSSLNCQPHFDL 139
QY 121 QNRGVVSVILKMTQAGEYLLFIQSEATNYTLFTVSRINLTLLYLRPPYFRKMNQD 180
Db 140 QNRGVVSVILKMTQAGEYLLFIQSEATNYTLFTVSRINLTLLYLRPPYFRKMNQD 199
QY 181 ALVCISSEVPETIVEVWLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

Db 200 ALVCISSEVPETIVEVWLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 259
QY 241 CTRLFITIDLNQPTTLPOLFLKVGEPILMIRCKAVAVNHGFGLTWELNKALEBGNFEM 300
Db 260 CTRLFITIDLNQPTTLPOLFLKVGEPILMIRCKAVAVNHGFGLTWELNKALEBGNFEM 319
QY 301 STYSTNRTMIRILFAFVSSVARNDTGYTTCSSSKHPSQSALVTIVGKGFINATNSSSEDEYE 360
Db 320 STYSTNRTMIRILFAFVSSVARNDTGYTTCSSSKHPSQSALVTIVGKGFINATNSSSEDEYE 379
QY 361 IDOYBFCFSVRPKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 420
Db 380 IDOYBFCFSVRPKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 439
QY 421 ENDDAQTQMTFLNIRKQVLAESASQASCFSDGVPPLPSWTWKCSKSPNCTEITE 480
Db 440 ENDDAQTQMTFLNIRKQVLAESASQASCFSDGVPPLPSWTWKCSKSPNCTEITE 499
QY 481 GWNRRKANRKFQGWVSSSTLNNSSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 500 GWNRRKANRKFQGWVSSSTLNNSSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 559
QY 541 NISFYATIGVCLLFIVVLTLILCHIKYKQFYESQLQMVQVGTSSDNEYFYVDFREYEYD 600
Db 560 NISFYATIGVCLLFIVVLTLILCHIKYKQFYESQLQMVQVGTSSDNEYFYVDFREYEYD 619
QY 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOAVKMLKEKADSSREALMS 660
Db 620 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOAVKMLKEKADSSREALMS 679
QY 661 ELKMTQLGSHENIVNLGACTLSGPTIYLFYCCYCGDLLNLYRSRKEKFRHTWTEIFKE 720
Db 680 ELKMTQLGSHENIVNLGACTLSGPTIYLFYCCYCGDLLNLYRSRKEKFRHTWTEIFKE 739
QY 721 HNFSPYFTTQSHENSPMGSRREVQIHPDSDQISGLHNSFHSDEIEYENQKRLSEEDL 780
Db 740 HNFSPYFTTQSHENSPMGSRREVQIHPDSDQISGLHNSFHSDEIEYENQKRLSEEDL 799
QY 781 NVLTPEDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGKVVKICDFGLARDIMSDS 840
Db 800 NVLTPEDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGKVVKICDFGLARDIMSDS 859
QY 841 NVVVRGNARLPVKWMAPESLFEGIIYIKSDVWSYGILLWEIFSLGVNPPYGPVDFANFYK 900
Db 860 NVVVRGNARLPVKWMAPESLFEGIIYIKSDVWSYGILLWEIFSLGVNPPYGPVDFANFYK 919
QY 901 LIQNGFKMDQPPFYATEBEIYIMOSCWAFDSRKRKPSFPNLTSLFCGLADAEAEAMYQNDG 960
Db 920 LIQNGFKMDQPPFYATEBEIYIMOSCWAFDSRKRKPSFPNLTSLFCGLADAEAEAMYQNDG 979
QY 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993
Db 980 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 1012
RESULT 8
US-08-222-299-4
; Sequence 4, Application US/08222299
; Patent No. 5635388
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Susan D.
; APPLICANT: Matthews, William
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-299-4

Query Match 99.4%; Score 5240; DB 1; Length 993;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 987; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVVSAMIGTINQDLPIVKVILNHKNDSVGVKSSYPVMUSEP 60
Db 1 MPALARDAGTVLLVVSAMIGTINQDLPIVKVILNHKNDSVGVKSSYPVMUSEP 60
Qy 61 EDLGCALRQSSGTVYAAAVEVDVVSASITLQVLDPAGNISCLWVFKSSLNCQPHFDL 120
Db 61 EDLGCALRQSSGTVYAAAVEVDVVSASITLQVLDPAGNISCLWVFKSSLNCQPHFDL 120
Qy 121 QNRGVVSMVLKMTQAGEYLLFIQSEATNYTLFTVSRINLLYTLRRPYRKMENQD 180
Db 121 QNRGVVSMVLKMTQAGEYLLFIQSEATNYTLFTVSRINLLYTLRRPYRKMENQD 180
Qy 181 ALVCISSEVPEIVELWVLCDSQGESCKEESPAVVKKEKVLHFLGTDIRCCARNELGRE 240
Db 181 ALVCISSEVPEIVELWVLCDSQGESCKEESPAVVKKEKVLHFLGTDIRCCARNELGRE 240
Qy 241 CTRLFTIDNQTPTTLPOLFLKVGRLPMTIRCAVHVNHGFGTLWELENKALEEGNYFEM 300
Db 241 CTRLFTIDNQTPTTLPOLFLKVGRLPMTIRCAVHVNHGFGTLWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Qy 361 IDQYEEFCFSVRKAYPQIRCTWTFRRKPPCEQKGLDNGYSISKFCNKHQDGEYIFHA 420
Db 361 IDQYEEFCFSVRKAYPQIRCTWTFRRKPPCEQKGLDNGYSISKFCNKHQDGEYIFHA 420
Qy 421 ENDDAQFTKMTFLNIRRKQVLAESAASQSCFSDGVPPLSPWTWKCKSDKSPNCTEITE 480
Db 421 ENDDAQFTKMTFLNIRRKQVLAESAASQSCFSDGVPPLSPWTWKCKSDKSPNCTEITE 480
Qy 481 GVMNRKANRKFQGWVSSSTLANMSEAIKGLFLVKCCAYNSLGTSCTILLNSPGFPFFIQD 540
Db 481 GVMNRKANRKFQGWVSSSTLANMSEAIKGLFLVKCCAYNSLGTSCTILLNSPGFPFFIQD 540
Qy 541 NISFYATIGVCLLFIWVLLILCHIKYKQPRYESQLQMVQVGTSSDNEYPYVDFREYED 600
Db 541 NISFYATIGVCLLFIWVLLILCHIKYKQPRYESQLQMVQVGTSSDNEYPYVDFREYED 600
Qy 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOQVAVKMLKEKADSSEREALMS 660

Db 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOQVAVKMLKEKADSSEREALMS 660
Qy 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIPEYCCVGDLLNLYRSKREKPHRTWTIFKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIPEYCCVGDLLNLYRSKREKPHRTWTIFKE 720
Qy 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNFSHSEDEIEYENQKLEEEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNFSHSEDEIEYENQKLEEEEDL 780
Qy 781 NVLTPEDDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTPEDDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWAPESLFGIYTIKSDVMSYGILLWEIIFSLGVNPPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWAPESLFGIYTIKSDVMSYGILLWEIIFSLGVNPPGIPVDANFYK 900
Qy 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPPSPNLTSLFGCOLADAEAEAMYQNVDG 960
Db 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPPSPNLTSLFGCOLADAEAEAMYQNVDG 960
Qy 961 RVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS 993
Db 961 PVSECPHTYQNRPPFSREMDLGLLSPQAQVEDS 993

RESULT 9

US-08-434-878-4
Sequence 4, Application US/08434878
Patent No. 5997865
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William C.
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES 1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,878
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-434-878-4

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Query Match      99.4%; Score 5240; DB 2; Length 993;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 987; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVVFSAI FGTITNQDLPVTKVLIHKNNDSSVGKSSSYPMVSESP 60
Db 1 MPALARDGQLPLLVVFSAI FGTITNQDLPVTKVLIHKNNDSSVGKSSSYPMVSESP 60

Qy 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120

Qy 121 QNRGVVSMVLKWTQAGEYLLFIQSEATNYTILFTVSRINTLLYLTPRPFKRMENQD 180
Db 121 QNRGVVSMVLKWTQAGEYLLFIQSEATNYTILFTVSRINTLLYLTPRPFKRMENQD 180

Qy 181 ALVCISVPPIVWVLCDSQGESCKESPAVVKKEKVLHFGDTRCCARNELGRE 240
Db 181 ALVCISVPPIVWVLCDSQGESCKESPAVVKKEKVLHFGDTRCCARNELGRE 240

Qy 241 CTRLFTIDLNTQPTTLPLQFLKVGEP LIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
Db 241 CTRLFTIDLNTQPTTLPLQFLKVGEP LIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360

Qy 361 IDQYEEFCFSVRFKAYPOIRCTWTFSRKSFPCEQKGLDNGYSISKFNHKGQGEYIFHA 420
Db 361 IDQYEEFCFSVRFKAYPOIRCTWTFSRKSFPCEQKGLDNGYSISKFNHKGQGEYIFHA 420

Qy 421 ENDDAQFTKMTNIRKPKQVLAESAASQSCFSDGYPLPSMTWKCKSDKSPNCTBEITE 480
Db 421 ENDDAQFTKMTNIRKPKQVLAESAASQSCFSDGYPLPSMTWKCKSDKSPNCTBEITE 480

Qy 481 GWNKRNKRVQGWSSSTLANSEAIKGLVKCCAYNSLGTSCTILLNSPGPPFFIQD 540
Db 481 GWNKRNKRVQGWSSSTLANSEAIKGLVKCCAYNSLGTSCTILLNSPGPPFFIQD 540

Qy 541 NISFYATIGVCLLFIWVLLCHKVKQFRYESQLOMQVQTGSSDNEYFYVDFREYED 600
Db 541 NISFYATIGVCLLFIWVLLCHKVKQFRYESQLOMQVQTGSSDNEYFYVDFREYED 600

Qy 601 LKWEPPRENLEFGKVLGSAFGKVMNATAYGISKTVGSIQAVKMLKEKADSSEREA LMS 660
Db 601 LKWEPPRENLEFGKVLGSAFGKVMNATAYGISKTVGSIQAVKMLKEKADSSEREA LMS 660

Qy 661 ELKMTQLGSHENI VNLGACTLSGPIYLI FEYCCYGDLLNVLRSKREKPHRTWTBIFKE 720
Db 661 ELKMTQLGSHENI VNLGACTLSGPIYLI FEYCCYGDLLNVLRSKREKPHRTWTBIFKE 720

Qy 721 HNFSPYPTFQSHPNSSMPGSRVQHPDSDQISGLHNSFHSDEDEI EYENQKRLBEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPGSRVQHPDSDQISGLHNSFHSDEDEI EYENQKRLBEEDL 780

Qy 781 NVLTFEDLLCFAYQVAKGMFELEKSCVHRDLAARNVLVTHGKVVKICDPGLARDLMSDS 840
Db 781 NVLTFEDLLCFAYQVAKGMFELEKSCVHRDLAARNVLVTHGKVVKICDPGLARDLMSDS 840

Qy 841 NYVVRGNARLPVKWMAPESLFEGITIKSDVMSYIGILLWEIFSLGWNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLFEGITIKSDVMSYIGILLWEIFSLGWNYPGIPVDANFYK 900

Qy 901 LIQNGFKMDQPPYATEEYII IQSCWAFPSRKRPPPNLTSLFGCOLADAEAMYNQVDG 960
Db 901 LIQNGFKMDQPPYATEEYII IQSCWAFPSRKRPPPNLTSLFGCOLADAEAMYNQVDG 960

Qy 961 RVSECPHTYQNRPPFSREMDLGLLPQAQVEDS 993
Db 961 RVSECPHTYQNRPPFSREMDLGLLPQAQVEDS 993
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RESULT 10
PCT-US95-03718-4
; Sequence 4, Application PC/TUS9503718
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 879PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-03718-4

Query Match      99.4%; Score 5240; DB 5; Length 993;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 987; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVVFSAI FGTITNQDLPVTKVLIHKNNDSSVGKSSSYPMVSESP 60
Db 1 MPALARDGQLPLLVVFSAI FGTITNQDLPVTKVLIHKNNDSSVGKSSSYPMVSESP 60

Qy 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120

Qy 121 QNRGVVSMVLKWTQAGEYLLFIQSEATNYTILFTVSRINTLLYLTPRPFKRMENQD 180
Db 121 QNRGVVSMVLKWTQAGEYLLFIQSEATNYTILFTVSRINTLLYLTPRPFKRMENQD 180

Qy 181 ALVCISVPPIVWVLCDSQGESCKESPAVVKKEKVLHFGDTRCCARNELGRE 240
Db 181 ALVCISVPPIVWVLCDSQGESCKESPAVVKKEKVLHFGDTRCCARNELGRE 240

Qy 241 CTRLFTIDLNTQPTTLPLQFLKVGEP LIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
Db 241 CTRLFTIDLNTQPTTLPLQFLKVGEP LIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360

Qy 361 IDQYEEFCFSVRFKAYPOIRCTWTFSRKSFPCEQKGLDNGYSISKFNHKGQGEYIFHA 420
Db 361 IDQYEEFCFSVRFKAYPOIRCTWTFSRKSFPCEQKGLDNGYSISKFNHKGQGEYIFHA 420
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Qy 421 ENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPPLSWTWKCKSDKSPNCTEEITE 480
Db 421 ENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPPLSWTWKCKSDKSPNCTEEITE 480
Qy 481 GWNKRNKRVFGQWSSSTLNSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNKRNKRVFGQWSSSTLNSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Qy 541 NISFYATIGVCLLFIVLTLCHYKKQFRYESQLOQWQVGTSSDNEFYVDREYED 600
Db 541 NISFYATIGVCLLFIVLTLCHYKKQFRYESQLOQWQVGTSSDNEFYVDREYED 600
Qy 601 LKWEPPRENLEFGKVLGSGAFKVMNATAYGISTKGTGSIQVAVKMLKEKADSSEREALMS 660
Db 601 LKWEPPRENLEFGKVLGSGAFKVMNATAYGISTKGTGSIQVAVKMLKEKADSSEREALMS 660
Qy 661 ELKMMTQLGSHENIVNLGACTLSGPIYLIIFYCCYGDLLNLYLRKREKFRHTWTEIFKE 720
Db 661 ELKMMTQLGSHENIVNLGACTLSGPIYLIIFYCCYGDLLNLYLRKREKFRHTWTEIFKE 720
Qy 721 HNFSPYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEEDL 780
Qy 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSDS 840
Db 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWMAPESLFEGITIKSDVMSYGILLWEIFSLGVNPPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLFEGITIKSDVMSYGILLWEIFSLGVNPPGIPVDANFYK 900
Qy 901 LIQNGFKMDQFPYATEEYIIMQSCWAFDSRKRPFPPNLTSLGLCOLADAEAMTQNVDG 960
Db 901 LIQNGFKMDQFPYATEEYIIMQSCWAFDSRKRPFPPNLTSLGLCOLADAEAMTQNVDG 960
Qy 961 RVSECPHYQNRPPFSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHYQNRPPFSREMDLGLLSPQAQVEDS 993

RESULT 11
US-08-183-211-2
; Sequence 2, Application US/08183211
; Patent No. 5618709
; GENERAL INFORMATION:
; APPLICANT: Alan M. Gewirtz, Donald Small, Curt I. Civin.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEO- TIDES
; TITLE OF INVENTION: SPECIFIC FOR STK-1 AND METHOD FOR
; TITLE OF INVENTION: INHIBITING EXPRESSION OF THE STK-1 PROTEIN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL GONDA LAVORGNA & MONACO
; STREET: Suite 1800, Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/183.211
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
```

```
; REFERENCE/DOCKET NUMBER: 3957-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8393
; TELEFAX: (215) 568-5549
; TELEX: No. 5618709e
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-183-211-2
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Query Match 99.3%; Score 5238; DB 1; Length 993;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 991; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Qy 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVVKVLINHKNDSSVGKSSYPMVSESP 60
Db 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVVKVLINHKNDSSVGKSSYPMVSESP 60
Qy 61 EDLGCALRPOSSGTYEAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRPOSSGTYEAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120
Qy 121 QNRGVVSVILKMTETQAGEYLLFIQSEATNTYITLFTVSIKRTLLYLRPYPFRKMNOD 180
Db 121 QNRGVVSVILKMTETQAGEYLLFIQSEATNTYITLFTVSIKRTLLYLRPYPFRKMNOD 180
Qy 181 ALVCISSEVPPIVSWVLCDQSQESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISSEVPPIVSWVLCDQSQESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLTIDNLTQPTTLPLQFLKVGEPDWIRCKAVVHNHGPGLTWELENKALEEGNYFEM 300
Db 241 CTRLTIDNLTQPTTLPLQFLKVGEPDWIRCKAVVHNHGPGLTWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAPVSSVARNDGYTCSSSKHPSQSALVTIVKGFINATNSSDEYE 360
Db 301 STYSTNRTMIRILFAPVSSVARNDGYTCSSSKHPSQSALVTIVKGFINATNSSDEYE 360
Qy 361 IDQEEFCFSVRKAYPOIRCTWTFSRKSFPCQCKQLONGYSISKPCNKHQPGEYIFH- 419
Db 361 IDQEEFCFSVRKAYPOIRCTWTFSRKSFPCQCKQLONGYSISKPCNKHQPGEYIFH- 419
Qy 420 AENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPPLSWTWKCKSDKSPNCTEEIT 479
Db 420 AENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPPLSWTWKCKSDKSPNCTEEIT 479
Qy 480 EGVWNRKANRVFGQWSSSTLNSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQ 539
Db 480 EGVWNRKANRVFGQWSSSTLNSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQ 539
Qy 540 DNISFYATIGVCLLFIVLTLCHYKKQFRYESQLOQWQVGTSSDNEFYVDREYED 599
Db 540 DNISFYATIGVCLLFIVLTLCHYKKQFRYESQLOQWQVGTSSDNEFYVDREYED 599
Qy 600 DLKWEPPRENLEFGKVLGSGAFKVMNATAYGISTKGTGSIQVAVKMLKEKADSSEREALM 659
Db 600 DLKWEPPRENLEFGKVLGSGAFKVMNATAYGISTKGTGSIQVAVKMLKEKADSSEREALM 659
Qy 660 SELKMMTQLGSHENIVNLGACTLSGPIYLIIFYCCYGDLLNLYLRKREKFRHTWTEIFK 719
Db 660 SELKMMTQLGSHENIVNLGACTLSGPIYLIIFYCCYGDLLNLYLRKREKFRHTWTEIFK 719
Qy 720 EHNFSFYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEED 779
Db 720 EHNFSFYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEED 779
Qy 780 LNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSD 839
Db 780 LNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSD 839
Qy 840 SNYVVRGNARLPVKWMAPESLFEGITIKSDVMSYGILLWEIFSLGVNPPGIPVDANFY 899
```

Db 840 SNVVRGNARLPVKWMAPESLFEGITIKSDVMSYGLLWEIFSLGWNYPGIPVDANFY 899
Qy 900 KLIONGFKMDQPPYATEEYIIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Db 900 KLIONGFKMDQPPYATEEYIIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Qy 960 GRVSECPHTYQNRPPFSREMDLGLSPQAQVEDS 993
Db 960 GRVSECPHTYQNRPPFSREMDLGLSPQAQVEDS 993

RESULT 12
PCT-US95-00176A-2
; Sequence 2, Application PC/TUS9500176A
; GENERAL INFORMATION:
; APPLICANT: Alan M. Gewirtz, Donald Small, Curt I. Civin.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
; SPECIFIC FOR STK-1 AND METHOD FOR INHIBITING EXPRESSION OF THE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL GONDA LAVORGNA & MONACO
; STREET: Suite 1800, Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00176A
; FILING DATE: 6 January 1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/183,211
; FILING DATE: 14 January 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 3957-14 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 993 amino acids
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
PCT-US95-00176A-2

Query Match 99.3%; Score 5238; DB 5; Length 993;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 991; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy 1 MPALARDAGTVLLVVFSAIFGTTINQDLPVVKVLIHKNKNDSSVGKSSSYPMVSESP 60
Db 1 MPALARDAGTVLLVVFSAIFGTTINQDLPVVKVLIHKNKNDSSVGKSSSYPMVSESP 60
Qy 61 EDLGCALRQSSGTVYEAADVVSASITLQVLDAPGNISCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRQSSGTVYEAADVVSASITLQVLDAPGNISCLWVFKHSSLNCQPHFDL 120
Qy 121 QNRGVSVMLKMTQAGEYLLFTQSEATNTYLTFTVSRNTLLYLRPFYRKMENQD 180
Db 121 QNRGVSVMLKMTQAGEYLLFTQSEATNTYLTFTVSRNTLLYLRPFYRKMENQD 180
Qy 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240

Db 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
Qy 241 CTELFITIDLNOTQTTLPOLFLKVGELWIRCKAVHVNHGFLTWELNKALEBGNFYEM 300
Db 241 CTELFITIDLNOTQTTLPOLFLKVGELWIRCKAVHVNHGFLTWELNKALEBGNFYEM 300
Qy 301 STYSTNRTMIRILFAPVSSVARNDTGYTCTSSSKHPSQSALVTIVGKGFINATNSSDEYE 360
Db 301 STYSTNRTMIRILFAPVSSVARNDTGYTCTSSSKHPSQSALVTIVGKGFINATNSSDEYE 360
Qy 361 IDQYEFPCFSVRFPKAYPQIRCTWTFSRKSPPCEQKGLDNGYSISKFCNHKHQPGYEYIFH- 419
Db 361 IDQYEFPCFSVRFPKAYPQIRCTWTFSRKSPPCEQKGLDNGYSISKFCNHKHQPGYEYIFH 420
Qy 420 AENDDAQFTKMTLNTRRRKPOVLAEASASQSCFSDGYPL-SWTWKCKSDKSPNCTEIT 479
Db 421 AENDDAQFTKMTLNTRRRKPOVLAEASASQSCFSDGYPL-SWTWKCKSDKSPNCTEIT 479
Qy 480 EGVNKRKANRKFQGVQWSSSTLNMSAIGFLVKCCAYNSLGTSCETILLNSPGFPFFIQ 539
Db 480 EGVNKRKANRKFQGVQWSSSTLNMSAIGFLVKCCAYNSLGTSCETILLNSPGFPFFIQ 539
Qy 540 DNISFYATIGVCLLFIVLTLTLLCHIKYKQFRYESQLMQVQVTGSSDNEYFYVDFREY 599
Db 540 DNISFYATIGVCLLFIVLTLTLLCHIKYKQFRYESQLMQVQVTGSSDNEYFYVDFREY 599
Qy 600 DLKWEFPRENLEPGKVLGSGAFGKVMNATAYGISKTVSIOQAVKMLKEKADSSERELM 659
Db 600 DLKWEFPRENLEPGKVLGSGAFGKVMNATAYGISKTVSIOQAVKMLKEKADSSERELM 659
Qy 660 SELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCVGLLNLRSKREKPHRTWTIEFK 719
Db 660 SELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCVGLLNLRSKREKPHRTWTIEFK 719
Qy 720 EHNFSFYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSSEDEIEYENQKLESEED 779
Db 720 EHNFSFYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSSEDEIEYENQKLESEED 779
Qy 780 LNVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNLVTHGKVKICDFGLARDIMSD 839
Db 780 LNVLPEDLLCFAYQVAKGMEFLFKSCVHRDLAARNLVTHGKVKICDFGLARDIMSD 839
Qy 840 SNVVRGNARLPVKWMAPESLFEGITIKSDVMSYGLLWEIFSLGWNYPGIPVDANFY 899
Db 840 SNVVRGNARLPVKWMAPESLFEGITIKSDVMSYGLLWEIFSLGWNYPGIPVDANFY 899
Qy 900 KLIONGFKMDQPPYATEEYIIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Db 900 KLIONGFKMDQPPYATEEYIIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Qy 960 GRVSECPHTYQNRPPFSREMDLGLSPQAQVEDS 993
Db 960 GRVSECPHTYQNRPPFSREMDLGLSPQAQVEDS 993

RESULT 13
US-08-222-2999-2
; Sequence 2, Application US/08222299
; Patent No. 5635388
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Susan D.
; APPLICANT: Matthews, William C.
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES 1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-299-2

Query Match 86.0%; Score 4533.5; DB 1; Length 1000;

Best Local Similarity 85.6%; Pred. No. 0;
Matches 851; Conservative 56; Mismatches 84; Indels 3; Gaps 2;

QY 1 MPALA-RDAGTVPLAVFSAFAMIFGITNODLPVVKVLIHKNNDSSVGKSSYPMVSES 59
DB 1 MRALQSRDRRLVLLVLSWILETVTNDLPVVKVLIHSHENNGSSAGKPSRYNRVRS 60
QY 60 PEDLCALRPOSSGTVYEAADVEDVDSAITLQVLVDAPGNTSCLWFKHSSLNCPHED 119
DB 61 PEDLQCTPRQSEGTVYEAATVEAEGSITLQVLATPGDLSCLWFKHSSLGCPHED 120
QY 120 LQNRGWSNVILKMTQAGEYLLFTQSBATNYTLFTVTSIRNTLYTLRRPYFRKQENQ 179
DB 121 LQNRGIVSMALNVETQAGEYLLHQSEAAANYTLFTVNRDTQYVLRPYFRKQENQ 180
QY 180 DALVCISSEVPPIVENVLDCSQGCKESPAVVKKEKVLHELFGTDIRCCARNELGR 239
DB 181 DALLCISEGVPEVWVLCSSHRESCKEGEPAVVRKEKVLHELFGTDIRCCARNALGR 240
QY 240 ECTRLFTIDLNOTPOTLPQLFKVGEPLWIRCKAVHNVHFGLTWELNKALEEGNYFE 299
DB 241 ESTKLFTIDLNOAPSTLPQLFKVGEPLWIRCKAVHNVHFGLTWELNKALEEGSYFE 300
QY 300 MSTYSTNRTMIRILFAPVSSVARNDTGYTCSKSHPSQSALVTIVGKGFINATNSSEDY 359
DB 301 MSTYSTNRTMIRILAFVSSVGRNDTGYTCSKSHPSQSALVTILEKGFINATSSQEEY 360
QY 360 BIDQVEECFCFVRKAYPOIRCTWTFPSRKFCEQKGLONGYSISKFCNKHQKQPGYVIFH 419
DB 361 EIDPYEKEFCFVRKAYPIRCTWTFPSRKFCEQKGLONGYSISKFCNKHQKQPGYVIFY 420
QY 420 AENDDAQFTKMTLNIRRRPQVLAESAQSCFSDGYPLPSWTWKCKSDKSPNCTEIT 479
DB 421 AENDDAQFTKMTLNIRKQVLANASAQSCSDGYPLPSWTWKCKSDKSPNCTEITP 480
QY 480 EGWNRKANRVKFGQWVSSTLNMSBAIKGFLVKCCAYNSLGTSCETILLNSGPPFFIQ 539
DB 481 EGWNRKANRVKFGQWVSSTLNMSBAGKGLLVKCCAYNSMGTSCTIFLNSGPPFFIQ 540
QY 540 DNISYATIGVCLLFTVTLILCHYKQFVRESOLQMVQVTGSSDNEYFYVDREY 599
DB 541 DNISYATIGVCLLFTVTLILCHYKQFVRESOLQMVQVTGSSDNEYFYVDREY 600
QY 600 DLKWEFPRENLEFGKVLGSGAFGRVNMATAYGISKTVGSIQVAVKMLKEKADSSREALM 659

DB 601 DLKWEFPRENLEFGKVLGSGAFGRVNMATAYGISKTVGSIQVAVKMLKEKADSSREALM 660
QY 660 SELXMTOLGSHENIVNLLGACTLSGPIYLIIEYCCYGDLLNLYRSKRKFHRTWTIEPK 719
DB 661 SELXMTOLGSHENIVNLLGACTLSGPIYLIIEYCCYGDLLNLYRSKRKFHRTWTIEPK 720
QY 720 EHNFSFYFTFQSHPNSSMPGSRVQIHDPDSQISGLHGNPSHSEDEIEYENQKRL--EEE 777
DB 721 EHNFSFYFTFQSHPNSSMPGSRVQIHDPDSQISGLHGNPSHSEDEIEYENQKRL--EEE 780
QY 778 EDNLVLTTFEDLLCFAYQVAKGMEFLEPKSCVHRDLAARNVLTGHKVVKICDFGLARDIM 837
DB 781 EDNLVLTTFEDLLCFAYQVAKGMEFLEPKSCVHRDLAARNVLTGHKVVKICDFGLARDIL 840
QY 838 SDSNVYVRGNARLPVKWMAPELSLFGIYTIKSDVMSYIGILLWEIFSLGVPNPGIPVDAN 897
DB 841 SDSNVYVRGNARLPVKWMAPELSLFGIYTIKSDVMSYIGILLWEIFSLGVPNPGIPVDAN 900
QY 898 FYKLIQNGFQMDQPFYATEEIIYIMQSWAFDSRKRPSFNLTSFLGCOLADAEAMYQN 957
DB 901 FYKLIQNGFQMDQPFYATEEIIYIMQSWAFDSRKRPSFNLTSFLGCOLADAEAMYQN 960
QY 958 VDGRVSECPHTYQNRPRPSREMDLGLLSPOAQUE 991
DB 961 MCGNVPEHPSIYQNRPLSRREAGSEPPSPQAQVK 994

RESULT 14

US-08-434-878-2
Sequence 2, Application US/08434878
Patent No. 5997865
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES 1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,878
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-434-878-2

Query Match 86.0%; Score 4533.5; DB 2; Length 1000;

[illegible]

RESULT 15

PCT-US95-03718-2
; Sequence 2, Application PC/TUS9503718
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 879PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-03718-2

Query Match 86.0%; Score 4533.5; DB 5; Length 1000;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 851; Conservative 56; Mismatches 84; Indels 3; Gaps 2;

QY	1	MPALA-RDAGTVPLLVVFSAMIFGITNQDLPVVKVLINHKNDSSVGKSSSYPMVSES	59
DB	1	MRLAQRSDRLLLVLSVILFTVTNQDLPVVKVLISHENNGSSAGKPSYRWGRS	60
QY	60	PEDIGCALRPOSSGTVYEAATAVEVDVSASITLQVLVADPAGNISCLWFKHSSLNCPHED	119
DB	61	PEDLQTPRRQSEGTVEAATVEAESSITLQVLATPGDLSCLVWFKHSSLGCPHED	120
QY	120	LQNRGVSMVLKMTQTQAGYLYLFIOSEATNYTLFTVSTIRNTLLYTLRRPYFRMENQ	179
DB	121	LQNRGVSMAILNVTQTAGEYLLHIQSEAAANYTVLFTVNRDTQLYVLRPYFRMENQ	180
QY	180	DALVCISESPPEPVEVWVCLDQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGR	239
DB	181	DALLCISEGPEPVEVWVCLSHRESCKEGBAVRKEEKVLHFGTDIRCCARNALGR	240
QY	240	ECTRLFTIDLNQTPQTTLPOLFLKVGEPFLWIRCKAVHVNHGFGLTWELNKALESGNYFE	299
DB	241	ESTKLFTIDLNAQPSLTPQLFLKVGEPFLWIRCKAIHVNHGFGLTWELNKALESGNYFE	300
QY	300	MSYTSYTRNTRIRILPAFVSSVARNDTGYTTCSSKHPSQSALVTIVGKGFINATSSBDEY	359
DB	301	MSYTSYTRNTRIRILLAAVSSVGRNDTGYTTCSSKHPSQSALVTILEKGFINATSSQBEY	360
QY	360	EIDQYEEFCFSVRFKAYPOLRCTWTFGRKSPCCQKGLDNGYSISKFCNHHKQPCGYIFH	419
DB	361	EIDPYEFCFSVRFKAYPRIRCTWTFGRKSPCCQKGLDNGYSISKFDHKNKQPCGYIFH	420
QY	420	AENDDAQFTKMTFLNIRRKPOLVAESAQSCFSDGYPFLPSWTWKKCSKSPNCTEIT	479

Query Match	86.0%;	Score	4533.5;	DB	5;	Length	1000;
Best Local Similarity	85.6%;	Pred.	No. 0;				
Matches	851;	Conservative	56;	Mismatches	84;	Indels	3;
Gaps	2;						
Qy	1	MPALA-RDAGTVP	LLVVFSSAMIFGTITNODLPV	KVLINHKNDSSVGKSSSYPMVSES	59		
Db	1	MRALQSRDR	LLLVLSVMILETTNODLPV	KVLSHENNNGSSAGKPSRYMVRGS	60		
Qy	60	PEDIGCALRPO	SSGTGYEAAAEVVDVSA	SITLQVLVDAPGNISCLVWFKHSSLNCOHPFD	119		
Db	61	PEDLOCTPR	RSQSGTYEATVEASSGSIT	LQVLQATPEDLSCLVWFKHSSLCQCPHD	120		
Qy	120	LQNRGVVSM	VLKMTETOAGEXLLFTQSEATN	YTLFTVTSIRNTLLYTLRRPYFRKQENQ	179		
Db	121	LQNRGIVSM	ALNVTTOAGEXLLHQSEAA	NTVLFTVNVKDTQYVLRPFYFRKQENQ	180		
Qy	180	DALVCSIES	VPPIVEVWLCDOSGEC	KEESPAAVVKKEKVLHELFGTDIRCCARNELGR	239		
Db	181	DALLCISG	VEPTVBMWLCSSHRE	CKEKGPAVVRKEEKVLHELFGTDIRCCARNALGR	240		
Qy	240	ECTRLFTID	LNONPOTLPOLFLK	VGPELWIRCKAVVNHGFGLTWELENKALEEGNYFE	299		
Db	241	ESTRLFTID	UNQAPQSTLPQLFK	VGPELWIRCKALHVNHGFGLTWELEDKALEEGSYFE	300		
Qy	300	MSTYSTNR	TMRIRLIPAFSVS	VARNDTGYTTCSSSKHPSQSALVTIVGKGFINATNSSEY	359		
Db	301	MSTYSTNR	TMRIRLLAFVS	VGSRNDTGYTTCSSSKHPSQSALVTILEKGFINATSSQEEY	360		
Qy	360	EIDDYEEPC	FVSFRKAYPOIRCT	WTSFRKSPCEQKGLDNGYSISKFCNNHKQPGEYIFH	419		
Db	361	EIDPYBKFC	FVSFRKAYPIR	CTWIPFSQASFPCEQRGLDEGYSISKFCDDHKKPGEYIFY	420		
Qy	420	AENDDAQFT	KMFNTINRRK	PQVLAEASASQACSF	DGYPLPSWTWKCKSDKSPNCTEEIT	479	

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Db 421 AENDDAQFTKFTLNIRKQVLANASASQASCSGDPPLPSWTWKCSKSPNCTEIP 480
Qy 480 EGVNKRKANRVFGQWSSSTLNMSIAKGLVKCCAYNSLGTSCETILLNSPGPPFIQ 539
Db 481 EGVNKRKANRVFGQWSSSTLNMSIAKGLVKCCAYNSLGTSCETILLNSPGPPFIQ 540
Qy 540 DNISFYATIGVCLLFIIVLTLLI CHYKKQFYESOLOQWQVVTGSSDNEYFYVVDREY 599
Db 541 DNISFYATIGVCLLFIIVLTLLI CHYKKQFYESOLOQWQVVTGSSDNEYFYVVDREY 600
Qy 600 DLKWEFFRENLEFGKVLGSGAFKGMATAYGISKTGYSIQVAVKMLKEKADSSREALM 659
Db 601 DLKWEFFRENLEFGKVLGSGAFKGMATAYGISKTGYSIQVAVKMLKEKADSSREALM 660
Qy 660 SELKMTOLGSHENIVNLLGACTLSGPVLIPEYCCYGDLLNLSKREKPHRTWTEIFK 719
Db 661 SELKMTOLGSHENIVNLLGACTLSGPVLIPEYCCYGDLLNLSKREKPHRTWTEIFK 720
Qy 720 EHNFSFYPTFQSHPNSSMPGSRVQIHSDSDQISGLHGNSFHSDEIEYENOKRL--EEE 777
Db 721 EHNFSFYPTFQSHPNSSMPGSRVQIHSDSDQISGLHGNSFHSDEIEYENOKRLAE 780
Qy 778 EDLNVLTEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLTGHGVKVICDFGLARDIM 837
Db 781 EDLNVLTEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLTGHGVKVICDFGLARDIL 840
Qy 838 SDSNVVVRGNARLPVKWMAPESLFEGIVTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
Db 841 SDSNVVVRGNARLPVKWMAPESLFEGIVTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Qy 898 FYKLIQNGFKMDOPYATEEYIIWQSWAFDSRKRPSFPNLTSLGCOLADAEAMYQN 957
Db 901 FYKLIQSGFKMEQPFYATEGIYFVNQSWAFDSRKRPSFPNLTSLGCOLADAEAMYQN 960
.Qy 958 VDGRVSECPHTYQNRPRPFSREMDLGLLSPQAOVE 991
Db 961 MGGNVPEHPSYQNRRLPSREAGSEPPSPQAVK 994
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Search completed: May 24, 2003, 17:01:10
Job time : 18.0071 secs